

**Discrimination of Pathogenic Species Using
Oligonucleotide Frequencies of Barcoding**

*A Major Project dissertation submitted
in partial fulfilment of the requirement for the degree of*
Master of Technology

In

Bioinformatics

Submitted by

Pratibha

(DTU/12/M.Tech/403)

Delhi Technological University, Delhi, India

Under the supervision of
Dr. Asmita Das



Department of Biotechnology
Delhi Technological University
(Formerly Delhi College of Engineering)
Shahbad Daultpur, Main Bawana Road,
Delhi-110042, INDIA



CERTIFICATE

This is to certify that the dissertation entitled **Discrimination of pathogenic species using oligonucleotide frequencies of barcoding** submitted by **Pratibha (DTU/12/M.Tech/403)** in the partial fulfilment of the requirements for the award of the degree of Master of Technology, Delhi Technological University (Formerly Delhi College of Engineering, University of Delhi), is an authentic record of the candidate's own work carried out by him/her under my guidance.

The information and data enclosed in this thesis is original and has not been submitted elsewhere for honoring of any other degree.

Date:

Dr. Asmita Das

(Project Mentor)

Department of Bio-Technology

Delhi Technological University

(Formerly Delhi College of Engineering, University of Delhi)

Certificate (on letter head) from the second mentor in case project has been done outside DTU

DECLARATION

I hereby declare that this thesis is my own work and effort and that it has not been submitted anywhere for any award. Where other sources of information have been used, They have been acknowledged

Signature:

Date:

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2K12/BIO/21

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LIST OF ABBREVIATIONS

COI	Cytochrome c oxidase subunit 1
DNA	Deoxy Nucleic Acid
EMBL	European Molecular Biology Lab
FISH-BOL	The Fish Barcode of Life Initiative
NCBI	National Centre for Bioinformatics Information
PCR	Polymerase Chain Reaction
RNA	Ribo Nucleic Acid

Discrimination of pathogenic species using oligonucleotide frequencies of barcoding

Pratibha

Delhi Technological University, Delhi, India

ABSTRACT

Now days, molecular taxonomy has become a more targeted tool to classify enormous diversity of the organisms present on earth. As a part of molecular taxonomy DNA based methods especially DNA bar coding serves as a more precise tool for identification and subsequent targeted techniques. The genres of worms which are chosen are the popular organisms of various human and animal diseases. Currently, only physiological mode of diagnoses is available to detect the type of infection.

Our proposed technique works on knowledge based methods of diagnosis where the basis of diagnosis is taken as the whole genome of the organism. The characteristic of this sequence based method is based on the nucleotide indices and DNA bar coding techniques. This technique will help in a more precise and rapid diagnosis. This approach has been extended to other pathogenic organisms for accurate diagnosis and personalized treatment measures. The analytical tool has been developed in JAVA for better user interface and ease of use by researchers. Currently the tool is in offline standalone format but it can also be made an online tool hosted by a server with very minor changes.

1. INTRODUCTION

DNA barcoding is a method for characterizing types of species of organism utilizing a short DNA sequence chosen from a standard and concurred upon position in the genome. DNA standardized tag successions are short with respect to the whole genome and they might be acquired sensibly rapidly and efficiently. The cytochrome c oxidase subunit 1 mitochondrial area (COI) is developing as the standard standardized tag locale for higher creatures. DNA barcoding was especially helpful for marine living beings (Shander and Willassen, 2005), including fishes (Mason, 2003; Ward et al., 2005); soil microbes (Blaxter et al., 2004) and freshwater meiobenthos (Markmann and Tautz, 2005); and extinct birds (Lambert et al., 2005). In the rainforests, quick DNA-based entomological inventories were so compelling (Monaghan et al., 2005; Smith et al., 2005) that tropical biologists were the most dynamic advocates of DNA barcoding (Janzen, 2004). All the more practically, DNA standardized tags have ended up being valuable in bio security, e.g. for observation of infection vectors (Besansky et al., 2003) and obtrusive bugs (Armstrong and Ball, 2005), and in addition for law authorization and primatology (Lorenz et al., 2005).

A new approach, Oligonucleotide Frequency Range (OFR) of barcode loci for discrimination of species has been proposed. OFR of the loci which discriminates between species is characteristic of a species, i.e., the maxima and minima within a species did not overlap with that of other species. The species resolution ability of the barcode loci using p-distance, Euclidean distance of oligonucleotide frequencies, nucleotide-character based approach and OFR method has been compared in many species. The species resolution by OFR was either higher or comparable to the other methods (Tyagi *et al.*, 2010). We have used the same approach in discriminating the various species of pathogenic worms. The dinucleotide frequency and trinucleotide frequency of the species was calculated and compared for different species.

The diseases and epidemiological conditions caused by worms are as diverged as the types of worms which are responsible for them. The diseases caused by them varies from malaria to eye infections (Nimir *et al.*, 2012). The technique can enable the non-taxonomists to identify these pathogens, thereby helping to understand and curb disease carrying pests and pathogens. The program can be used as a confirmatory test to various diagnostic tools.

2. REVIEW OF LITERATURE

2.1 Divergence in pathogenicity of worms

According to a report published by NIA, diseases and epidemiological conditions caused by worms are as diverged as the types of worms which are responsible for them. The diseases caused by them varies from malaria to eye infections (Nimir *et al.*, 2012). Worms that behave as parasites come in thousands of different species, including, tapeworms, flatworms, flukes, roundworms and leeches. The worms can be as small as microscopic, or they may be as long as 9 meters.

Some worms cause sore and deforming conditions, while others are simply noticed by the host. Some worm infestations get cleared up after a short time, while others cause long-term problems that affect many distinct body organs and may even result into death.

2.2 Gene based Diagnosis

The diagnosis of any pathological condition is essentially based on the microscopic structure of cells and tissues. This continues as the standard procedure through which all other diagnostic tests are measured. Now days, the pathologists are dependent on the examination of the tissue section stained by histochemical methods. This method is supported by the advanced biochemical, immunological and molecular techniques. It is one of the ways that can be used to unravel the molecular mechanism in detecting the disease process. Technologies which are used for studying cellular process are same for both normal and abnormal cell. The cellular process can be analyzed either from protein to gene or from gene to protein. Previously both biochemical analysis and genetic analysis were separate. But in this era with the advances in recombinant DNA technology it has become possible to have a connection between the biochemical and genetic analysis (Premalatha *et al.*, 2014). Recently PCR amplification has been used to detect and compare various species like *P. vivax* and *P. falciparum* (Pattakorn *et al.*, 2010).

2.3 DNA barcoding

DNA barcoding was created as of late as a strategy for animal types distinguishing proof over a wide scope of eukaryotes taxa by sequencing an institutionalized short DNA part. Because of present day innovations, it is conceivable to do this with a small bit of any tissue taken from a life form at any formative stage, frequently without harming it. A variable 5' a large portion of mitochondrial gene Co1 is recommended as a standard locale for the greater part of creatures; it is not distinguished yet for organisms and plants. "The Barcode of Life Initiative" infers making and creating the scanner tag library for all the species on Earth to encourage both relegating of recently got examples to the known species and for finding new and obscure species or at any rate their temporary distinguishment. This methodology has an extraordinary potential for the utilization in worldwide biodiversity studies, particularly on account of inadequately explored taxa and situations. The activity being referred to includes finish of another electronic succession database with thorough standards for taxonomic data on the examples and records of their stockpiling and in addition for norms of grouping quality and their passage. Discriminating complaints of rivals to DNA barcoding are audited

and additionally impediments of the methodology, the issues to be mulled over, and the fields where it might be utilized. Various late studies on distinctive creature aggregates convincingly show the viability of DNA barcoding and its possibilities. The last relies on upon accessibility of extensive and fair-minded reference database inferring right distinguishing proof of the source examples and sufficient information of intraspecies variety, so the Barcode Initiative would be more effective as a piece of the integrative examination of the taxa being bar-coded (Shneer, VS. 2009).

Species identification is an elementary part in recognizing and classifying biodiversity. Traditionally, identification is based on morphological features provided by taxonomic studies. Only taxonomy experts and trained technicians can identify taxa accurately, because it requires extensive experience and special skills. Moreover the classical method of species classification suffers from various drawbacks. Firstly, the two prime characters employed for species recognition viz phenotypic plasticity and genetic variability can lead to inaccurate identifications. Secondly, the approach neglects morphologically cryptic taxa that are common in several groups (Knowlton 1993; Jarman & Elliott 2000). Thirdly, as morphological keys are often valid only for a specific life stage or gender, many individuals cannot be identified. Finally, although new interactive versions serve as a major advance, the use of keys often calls for such a high level of expertise that misdiagnoses are frequent. (Herbert et al., 2003).

One of the most promising ways is the use of molecular in place of morphological data for taxa identification, which has been a fundamental idea of many biologists from a long period of time (Busse et al. 1996; Blaxter 2003). DNA barcoding, developed in 2003 to identify species, has helped to rejuvenate taxonomic research. DNA barcoding is a technique for identifying organisms based on a short, standardized fragment of genomic DNA. As a Linnaean binomial is an abbreviated label for the morphology of a species, the short sequence is an abbreviated label for the genome of the species (Vernooy et al., 2010). DNA barcoding allows researchers to develop a system for species identification based on digital characters, ultimately allowing for automated identifications, therefore promising to raise the capacity to identify, monitor, and manage biodiversity, with subtle societal and economic benefits. It also lifts the possibility of identifying the vectors of zoonotic diseases as well as the disease organisms themselves.

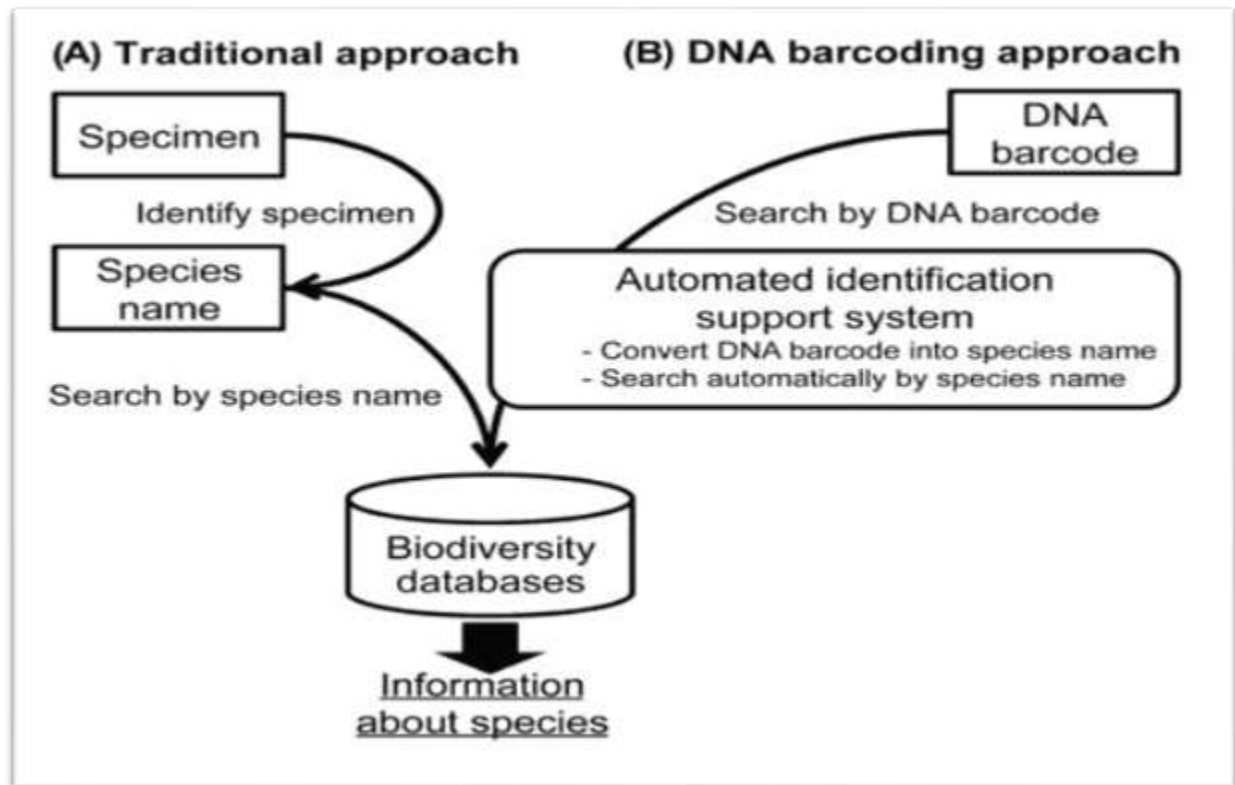


Figure 1: Workflow of traditional and DNA barcode approach of species identification

The 13 protein-coding genes in the animal mitochondrial genome are better targets because indels are rare since most lead to a shift in the reading frame. There is no compelling a priori reason to focus analysis on a specific gene, but the cytochrome c oxidase I gene (COI) does have two important advantages. First, the universal primers for this gene are very robust, enabling recovery of its 59 end from representatives of most, if not all, animal phyla (Folmer et al. 1994; Zhang & Hewitt 1997). Second, COI appears to possess a greater range of phylogenetic signal than any other mitochondrial gene. In common with other protein coding genes, its third-position nucleotides show a high incidence of base substitutions, leading to a rate of molecular evolution that is about three times greater than that of 12S or 16S rDNA (Knowlton & Weigt 1998). In fact, the evolution of this gene is rapid enough to allow the discrimination of not only closely allied species, but also phylogeographic groups within a single species (Cox & Hebert 2001; Wares & Cunningham 2001). Although COI may be matched by other mitochondrial genes in resolving such cases of recent divergence, this gene is more likely to provide deeper phylogenetic insights than alternatives such as cytochrome b (Simmons & Weller 2001).

2.3.1 Criteria to Select Barcode Gene

- **Universability:** The gene used for barcoding should be present in a wide range of taxa.
- **Specificity to variation :** it should have high variability between species but should be conserved within the species so that intraspecific variation becomes insignificant
- **Easiness on Employment:** the gene should be retrievable by single primer pair and should be amenable to bidirectional sequencing. The gene should be short.

2.3.2 DNA Barcodes

- For Plants:

Two regions of chloroplast DNA, ribulose–bisphosphate carboxylase (rbcL) and maturase K (matK) are used as standard barcodes in plants

- For Fungi:

Internal transcribed spacer (ITS) are used as barcode in Fungi

- For Animals:

A ~648 base-pair region of the mitochondrial cytochrome c oxidase subunit I (COI) gene is used as barcode in animals.

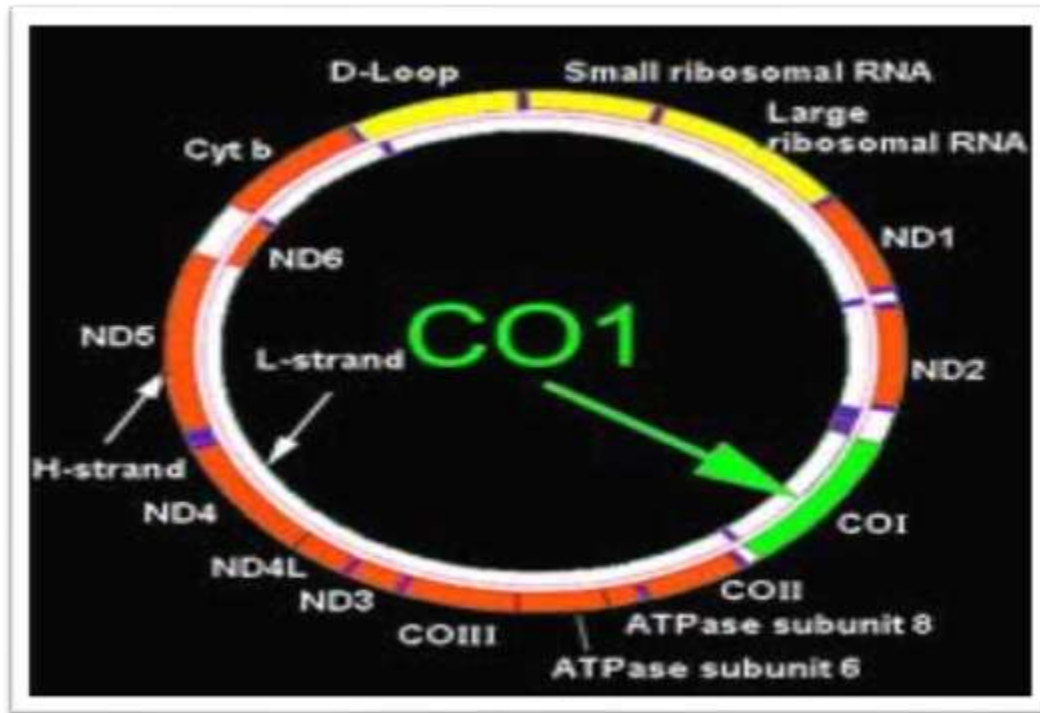


Figure 2: Depicting COI gene in mitochondria

2.3.3 Advantages of using COI gene as barcode

Mitochondrial genome is especially suitable for identifying species because of its high copy number, greater differences among species, few differences within species and absence of introns. COI is used as a gold standard for barcode because it is flanked by conserved regions and has a limited exposure to recombination. Moreover rate of molecular evolution is high in COI and it lacks indels.

2.3.4 DNA Barcoding in different species

DNA barcoding has also been used to identify marine metazoan species. More than 230,000 known species speaking to 31 metazoan phyla populate the world's seas. Maybe an alternate 1,000,000 or more species stay to be uncovered. There is a worry that species terminations may out-pace disclosure, particularly in assorted and jeopardized marine territories, for example, coral reefs. DNA standardized tags are helpful instruments to quicken species-level examination of marine biodiversity and to encourage preservation deliberations. The method used is based on standardized identification of metazoans using a 648 base-pair sequence of the mitochondrial cytochrome c oxidase subunit I (COI) gene. Scanner tags have additionally been utilized for populace hereditary and phylogeographic dissection, identification of prey in gut substance, location of obtrusive species, and fish wellbeing. All the more questionably, standardized identifications have been utilized to delimit species limits, uncover secretive species, and run across new species. Today there is a concern on the utilization of standardized tags for fast and progressively robotized biodiversity appraisal by high-throughput sequencing, including ecological barcoding and the utilization of standardized tags to locate species for which formal distinguishing features may never be conceivable (Bucklin *et al.*, 2010).

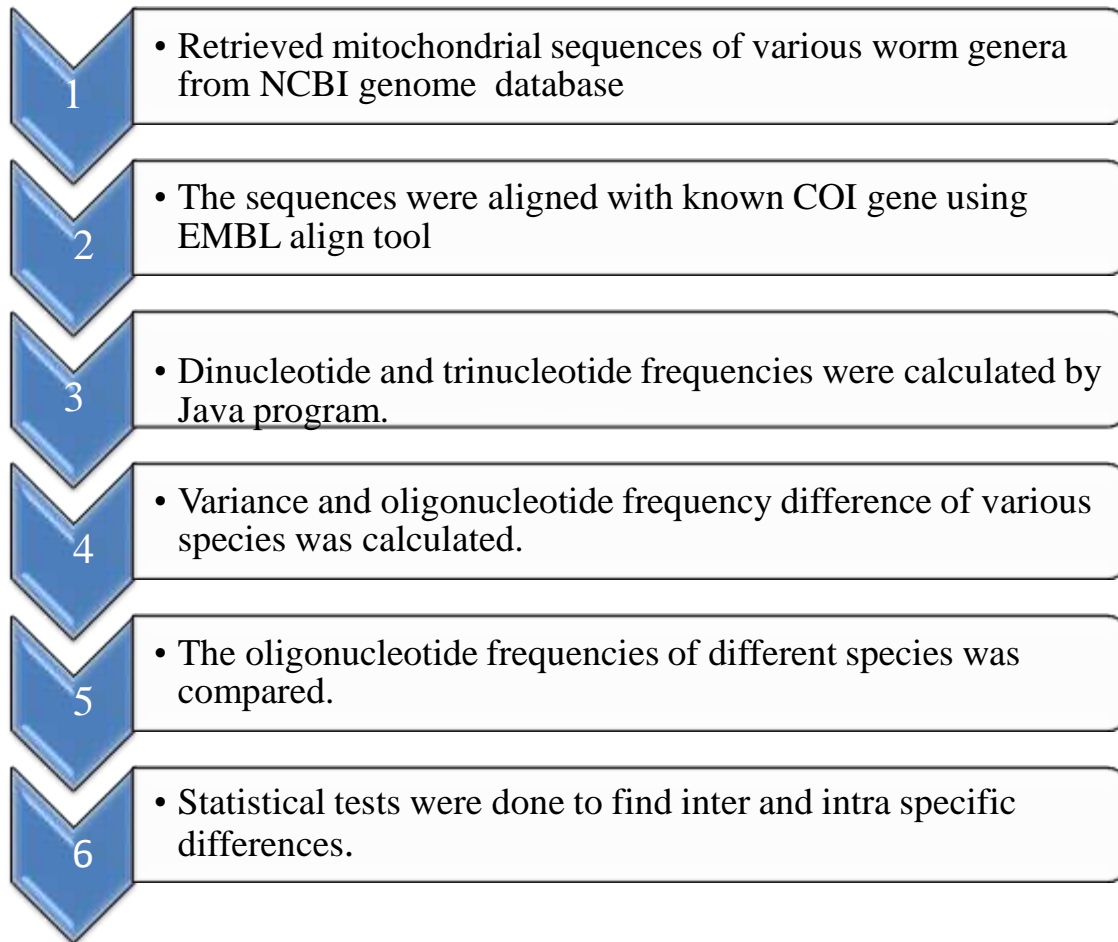
FISH-BOL is a deliberate worldwide examination venture initiated in 2005, with the objective to gather and analyse the associated DNA standardized tag arrangements and related voucher provenance information in a curated reference succession library to support the sub-atomic distinguishing proof of all fish species. Of the more or less 31,000 presently known fish species, 25% have been transformed effectively, with no less than one animal varieties from 89% of all families bar-coded so far(Becker *et al.*, 2011).

Fungal research is encountering another wave of methodological upgrades that most likely will help mycology as significantly as atomic phylogeny has done amid the most recent 15 years. Particularly the next generation sequencing advances might be relied upon to have a huge impact on fungal biodiversity and biology research. So as to understand the true ability of these promising strategies by quickening biodiversity appraisals, identification methods of parasites need to be adjusted to the developing requests of advanced huge scale biological studies. While the response may appear unimportant to most microbiologists, taxonomists working with organisms may have different perspectives. Barcoding has been used successfully in fungal research and has identified a number of species (Begerow *et al.*, 2011).

DNA barcoding was proposed as a strategy for identification of eukaryotic species through correlation of successions of a standard short DNA part -DNA standardized identification - from an obscure example to a library of reference arrangements from known species. These permits recognizing an organic entity at any phase of improvement from a little tissue test, fresh or saved numerous years ago. Molecular identification proof of plant specimens might be utilized as a part of different investigative and connected fields. It would likewise help to discover new species, which is especially helpful for cryptogamic plants. An ideal DNA scanner tag locale is a little section exhibit in all types of a real taxonomic gathering, having perpetual nucleotide arrangement in all parts of the same species, yet with sufficient variety to segregate among the species. This part ought to be flanked by low-variable sequences for

utilization of general first stages in PCR for intensification and sequencing. The DNA standardized identification that is entrenched in creatures is a grouping of a part of the mitochondrial cytochrome c oxidase gene Co1. Be that as it may, hunting down DNA standardized identification in plants turned out to be an additionally difficult assignment. No DNA locale generally suitable for all plants and gathering the majority of the vital criteria has been found. Evidently, a multilocus or two-stage methodology ought to be requisitioned this reason. A few sections of the chloroplast genome (trnh-psba, matk, rpoc, rpob, rbc1) in consolidations of a few areas were proposed as applicant districts with most noteworthy potential, yet more illustrative specimens ought to be analyzed to pick the best competitor. The likelihood is examined to use as DNA standardized tag inner translated spacers (ITS) of atomic rRNA genes, which are profoundly variable, generally utilized in sub-atomic phylogenetic studies at the species level, additionally have a few impediments (Shneer, VS. 2009).

3.1 METHODOLOGY



3.1 Sequence retrieval

The whole mitochondrial genome of different species of worms was retrieved from organelle resource database of NCBI.

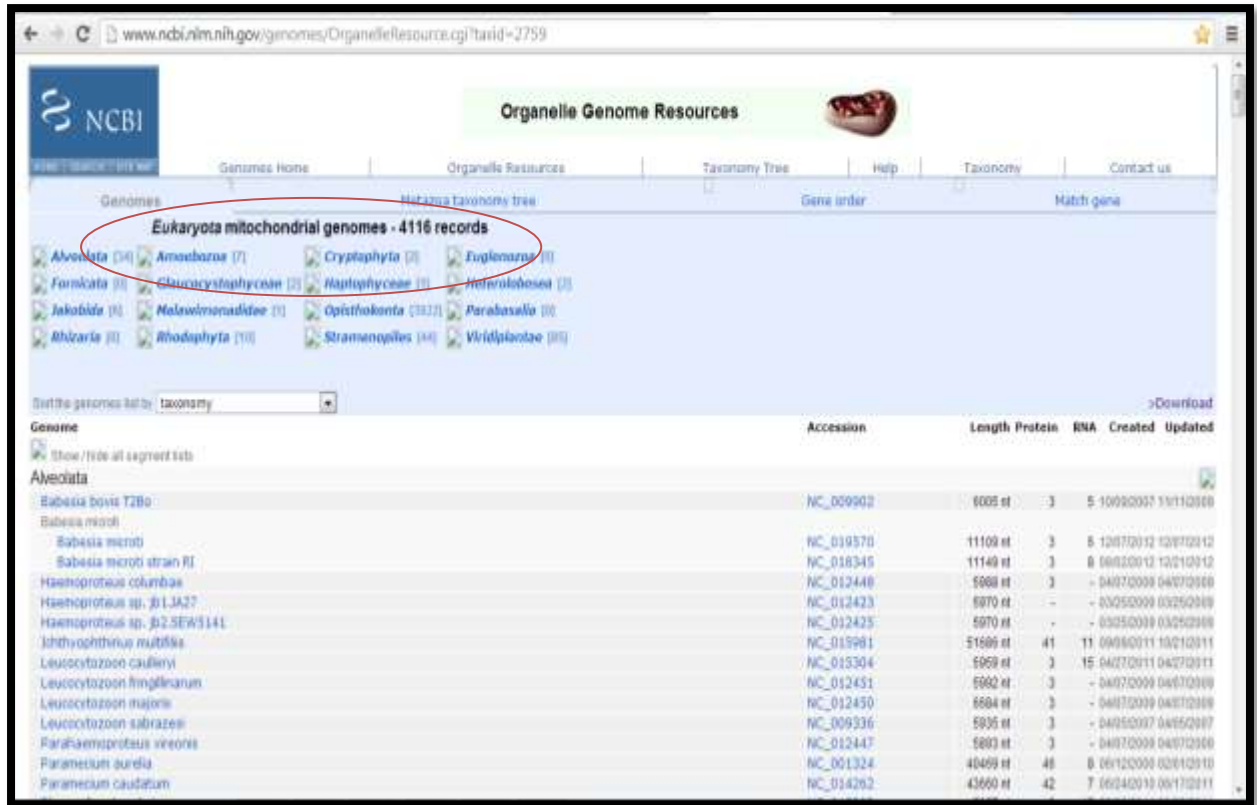


Fig 3: Depicting Organelle resource database of NCBI

Different worm genes were identified and retrieved using their accession numbers. The number of characters or base pairs present in the mitochondrial genome was mentioned in the database.

S no.	Genus	Species
1	<i>Angiostrongylus</i>	<i>Angiostrongylus cantonensis</i> <i>Angiostrongylus costaricensis</i> <i>Angiostrongylus vasorum</i>
2	<i>Diplogonoporus</i>	<i>Diplogonoporus balaenopterae</i> <i>Diplogonoporus balaenopterae</i>
3	<i>Dictyocaulus</i>	<i>Dictyocaulus eckerti</i> <i>Dictyocaulus viviparous</i>
4	<i>Ascaris</i>	<i>Ascaris lumbricoides</i> <i>Ascaris suum</i>
5	<i>Baylisascaris</i>	<i>Baylisascaris ailuri</i> <i>Baylisascaris procyonis</i> <i>Baylisascaris schroederi</i> <i>Baylisascaris schroederi</i>
6	<i>Toxocara</i>	<i>Toxocara canis</i> <i>Toxocara cati</i> <i>Toxocara malaysiensis</i>
7	<i>Taenia</i>	<i>Taenia asiatica</i> <i>Taenia crassiceps</i> <i>Taenia hydatigena</i> <i>Taenia krepkogorski</i> <i>Taenia laticollis</i> <i>Taenia madoquae</i> <i>Taenia martis</i> <i>Taenia multiceps</i> <i>Taenia mustelae</i> <i>Taenia ovis</i>

	<p><i>Taenia parva</i></p> <p><i>Taenia pisiformis</i></p> <p><i>Taenia saginata</i></p> <p><i>Taenia serialis</i></p> <p><i>Taenia solium</i></p> <p><i>Taenia twitchelli</i></p> <p><i>Taeniopygia guttata</i></p>
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Table 1 List of different worm genera

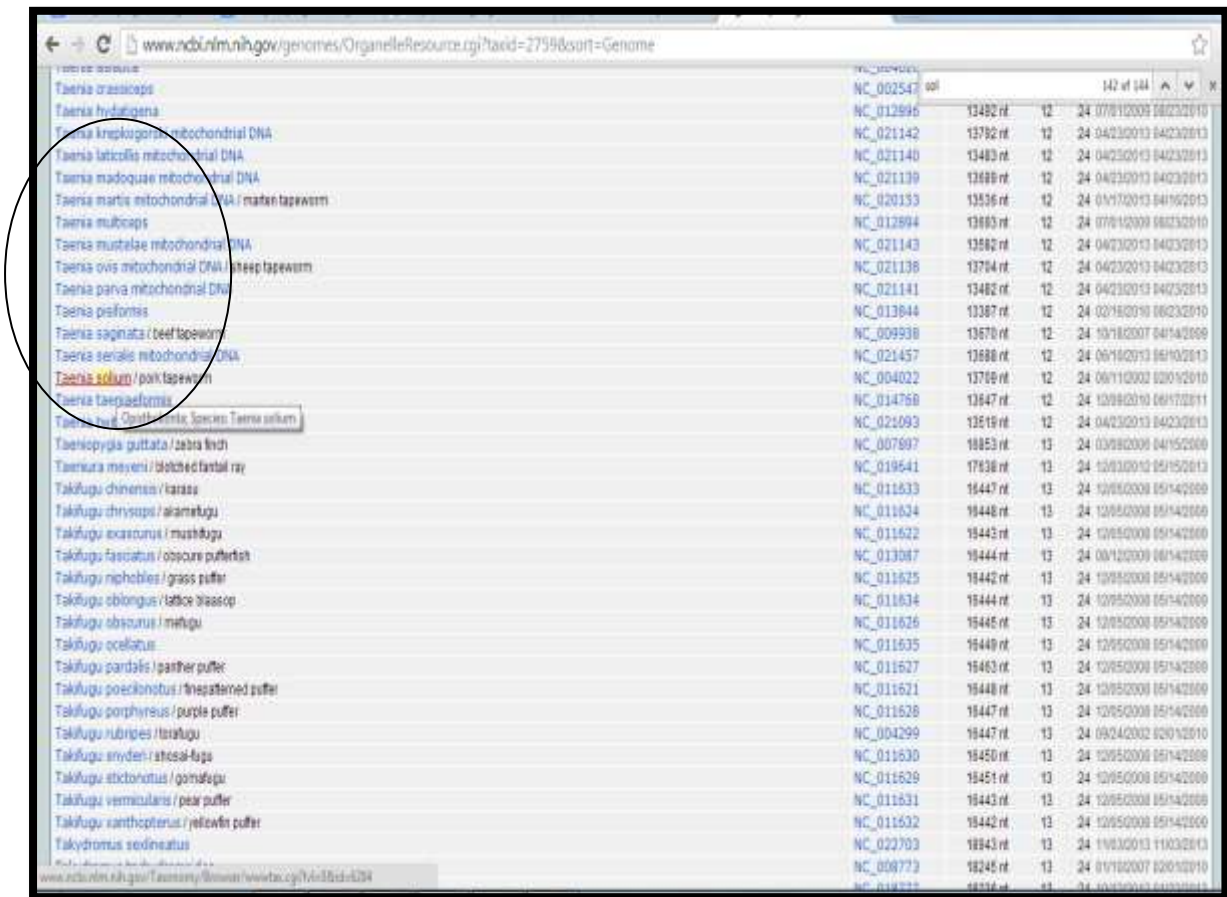


Fig 4: Depicts mitochondrial genome retrieval of *taenia* genus

The fasta sequence of all the species listed above was downloaded from NCBI database. Different folders were made for different genus.

3.2 Extraction of COI gene

The whole sequence of COI gene (1527 bp) and partial sequence of COI gene (327 bp) was retrieved from NCBI database. The above sequences were aligned with both COI gene sequences using EMBL alignment tools.

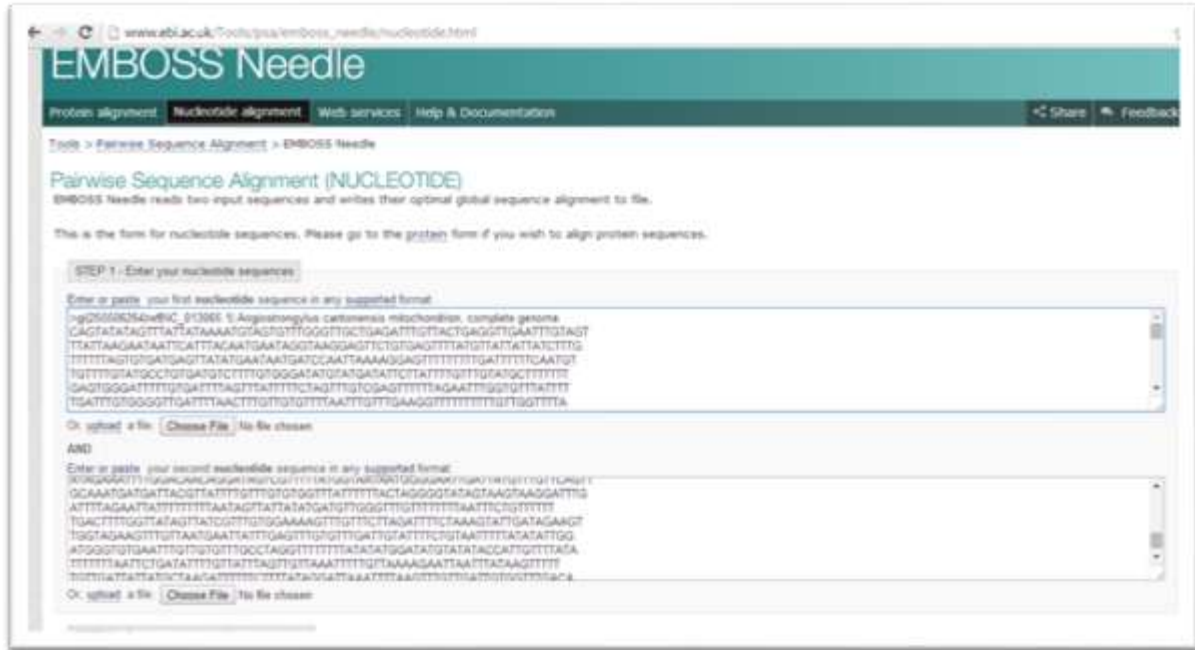


Figure 5 : Depicting EMBOS Needle alignment.

3.3 Discrimination of species using java program

The selected values in the combo boxes are stored in two string variables named as s and t respectively. After getting the name of the species from the combo boxes, the corresponding DNA sequence is taken using the if else statement and the sequence is stored in a temporary string variable q. The string q is then processed for the functions like calculating frequencies.

3.3.1 Oligonucleotide frequency calculation

➤ For dinucleotide frequencies :

- Sixteen integer variables namely AA,AC,AG,AT,.....,TT are declared and initialized to zero.
- The sequence is then parsed, and as any of the variables is encountered the value of that particular variable is incremented by 1 using the unary operator “++”.
- The variables are then divided by total length of the sequence.
- Then the results are rounded of and stored in an array and displayed on the screen.

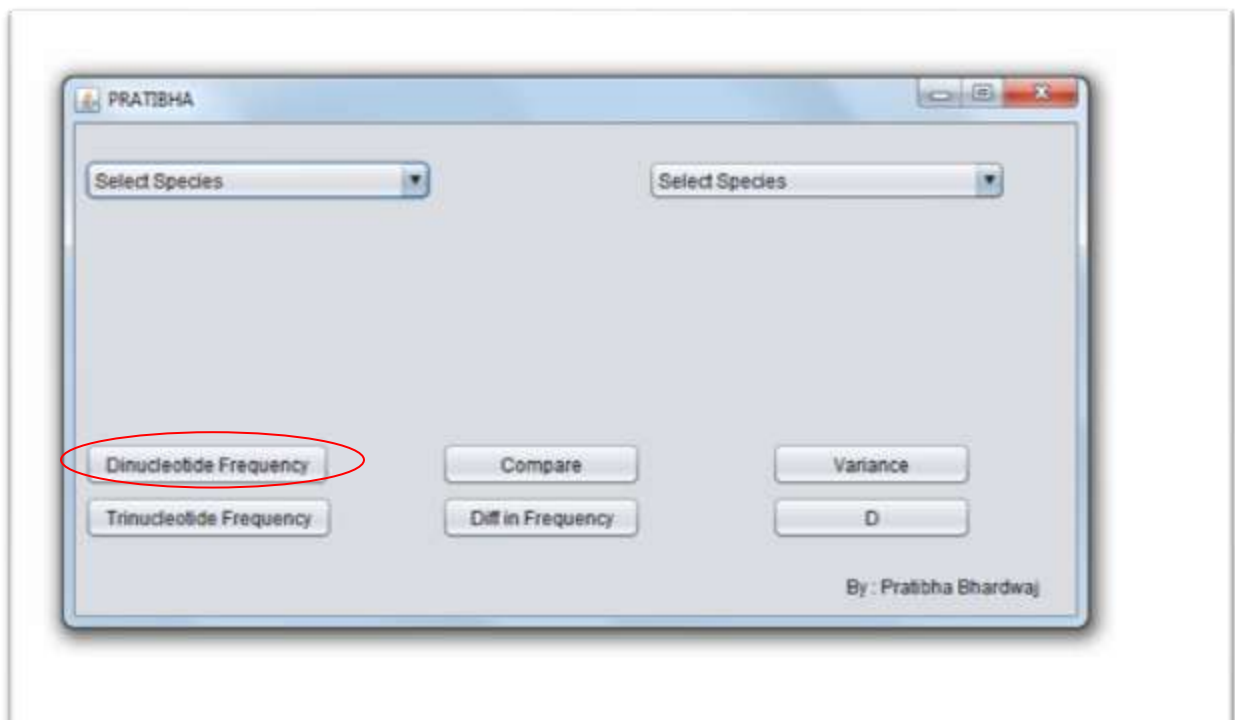


Figure 6: Depicting home screen with option for Dinucleotide Frequency.

➤ For trinucleotide frequency :

- For trinucleotide frequencies sixty four integer variables namely AAA,AAC,.....,TTT are declared and initialised to zero.
- The sequence is then parsed and as any of the variables is encountered the value of that particular variable is incremented by 1 using the unary operator “++”.
- The variables are then divided by total length of the sequence.
- Then the results are rounded of and stored in an array and displayed on the screen.

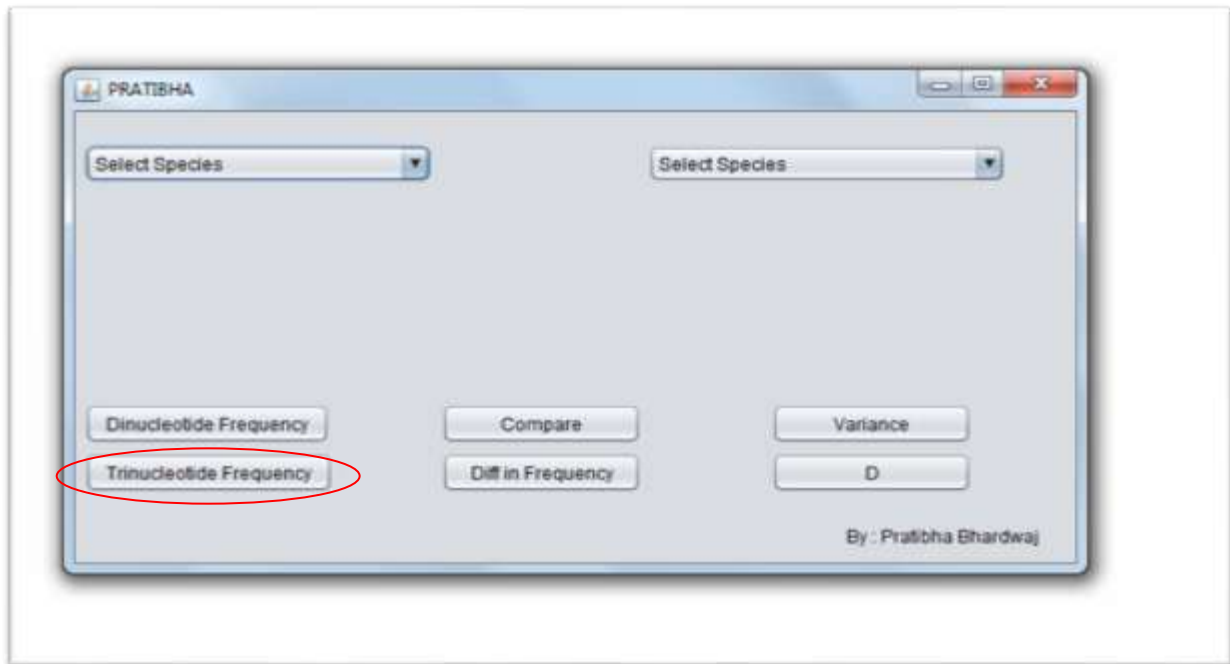


Figure7: Depicting home screen with option for Trinucleotide Frequency.

3.3.2 Variance calculation

- First the di and trinucleotide frequencies are obtained.
- The frequencies are then stored in two different arrays.
- Then the mean for di and tri nucleotide frequencies is obtained separately.
- The mean for dinucleotide frequencies is then subtracted from them and the mean for trinucleotide frequencies is subtracted from them.
- The sum of all the elements of array is then obtained for both the arrays.
- The sum is then divided by the no. of elements in the array.
- This result is the variance.
- This is then displayed on the screen.

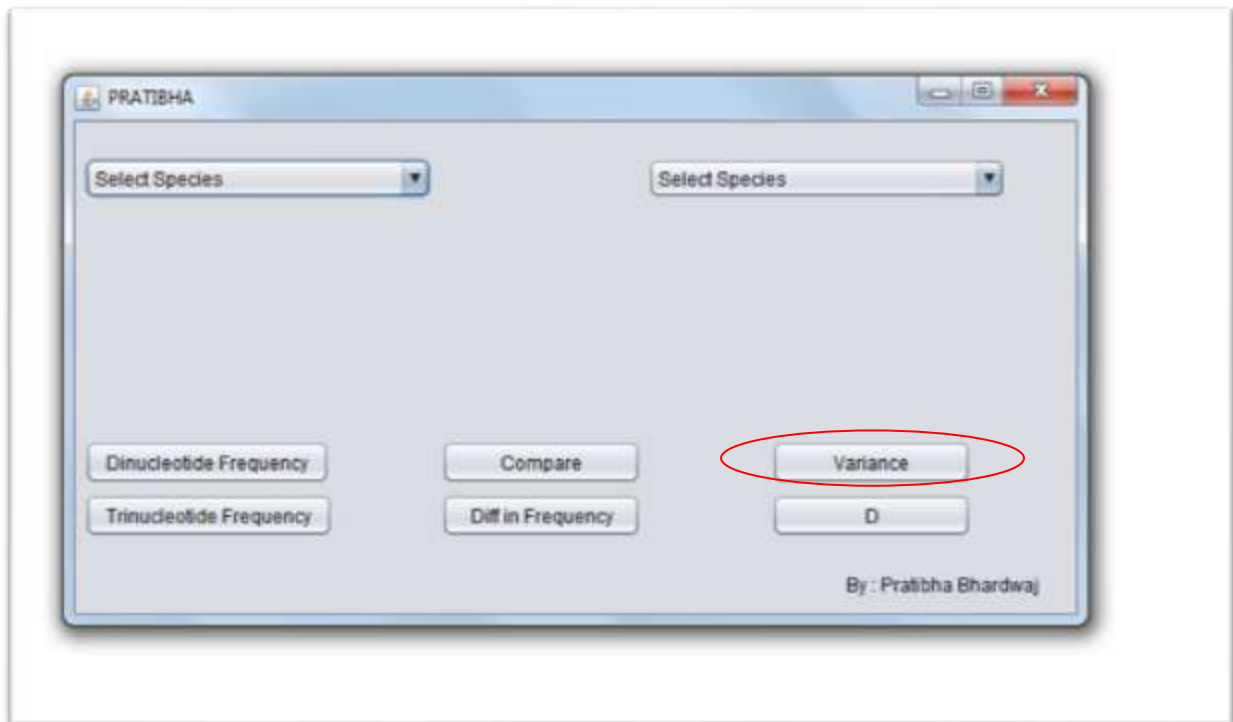


Figure 8: Depicting home screen with option for Variance.

3.3.3 Calculation of Oligonucleotide frequency difference

- This button allows user to know the difference in the maximum and minimum di and trinucleotide frequencies of the species.
- First the di and trinucleotide frequencies are obtained.
- Then four variables are declared namely max1, max2, min1, min2.
- Max1 represents the maximum dinucleotide frequency, min1 represents the minimum dinucleotide frequency.
- Max2, Min2 in the same way represent the maximum and minimum trinucleotide frequencies.
- The differences are then obtained by subtracting min1 from max1 and min2 from max 2.
- The differences are then displayed on the screen.

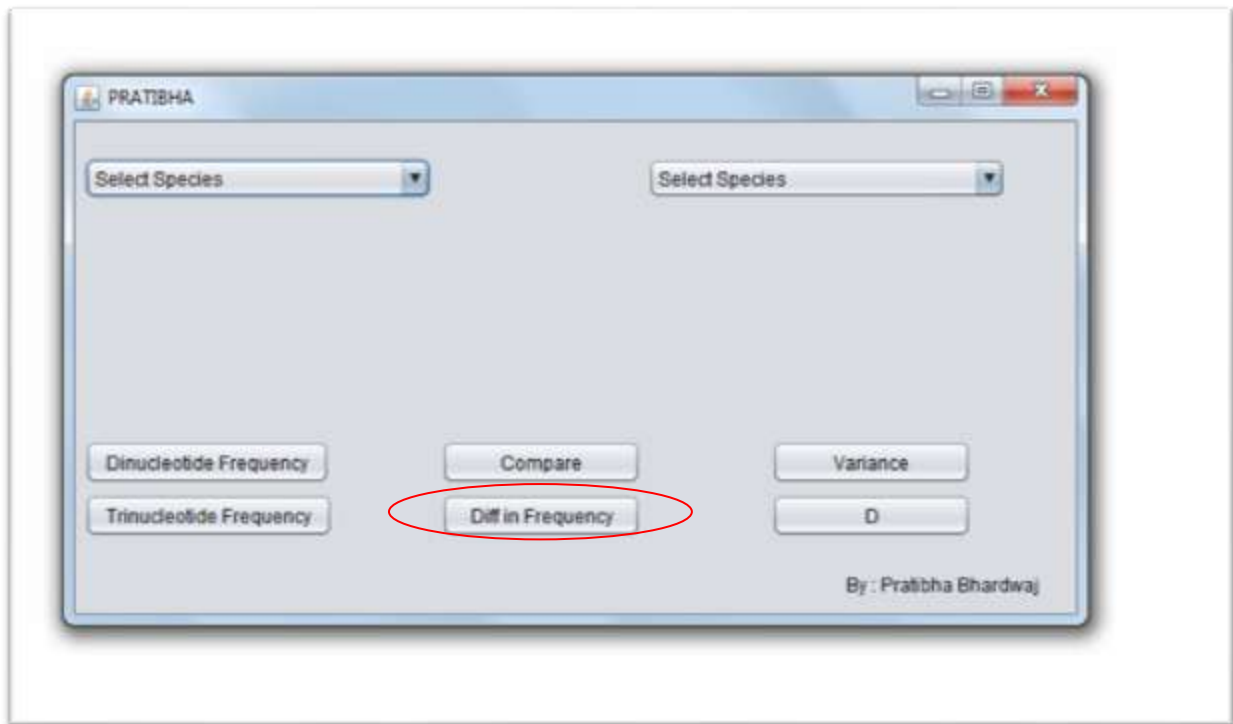


Figure9: Depicting home screen with option for Difference in Frequency.

3.3.4 Comparison of Oligonucleotide frequency

- For comparing two species, it plots two graphs between the di and trinucleotide frequencies of the two species.
- The di and trinucleotide frequencies for the two species are first obtained by the same procedure as discussed above.
- Then datasets are created for both the species.
- Then using the “jfree chart” library provided by the java, the graphs are displayed.

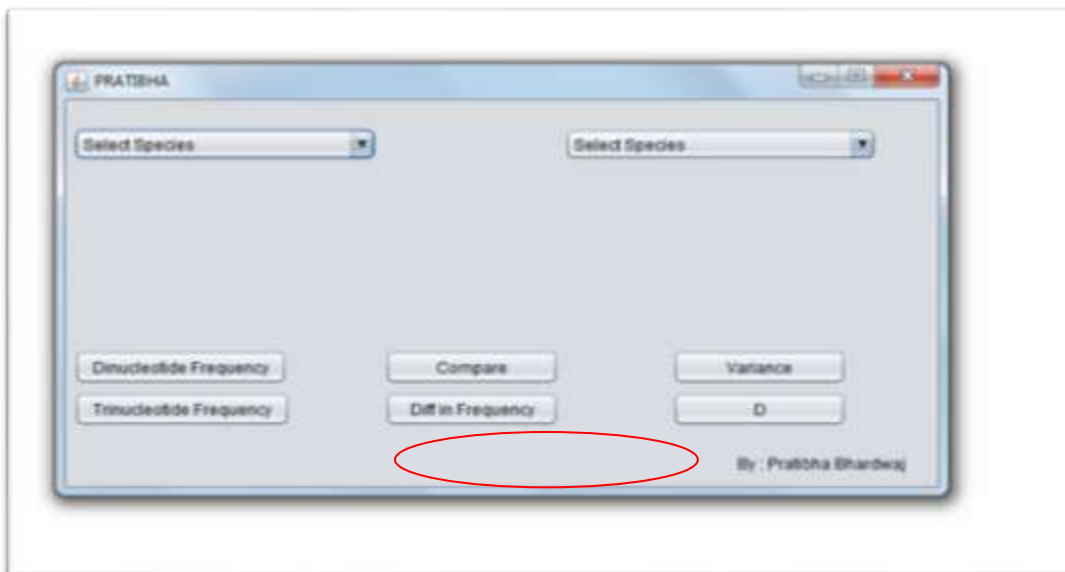


Figure10: Depicting home screen with option for comparison.

3.3.5 Statistical Analysis

The Euclidean distances (D) based on oligonucleotide frequency differences were calculated as follows.

$$D = \sqrt{\sum_{i=1}^N |F1 - F2|^2}$$

Where, N is the number of oligonucleotides, F1 and F2 represent the frequency of each type of oligonucleotide for species 1 and 2 respectively. Each distance was calculated from di- and trinucleotide frequencies.

- First the di and trinucleotide frequencies are obtained, and stored in arrays.
- The dinucleotide frequencies of one sequence are subtracted from the other.
- In the same way trinucleotide for one sequence are subtracted from the other.
- Then the sum is obtained for both the arrays.
- The sum is then rounded off and displayed.

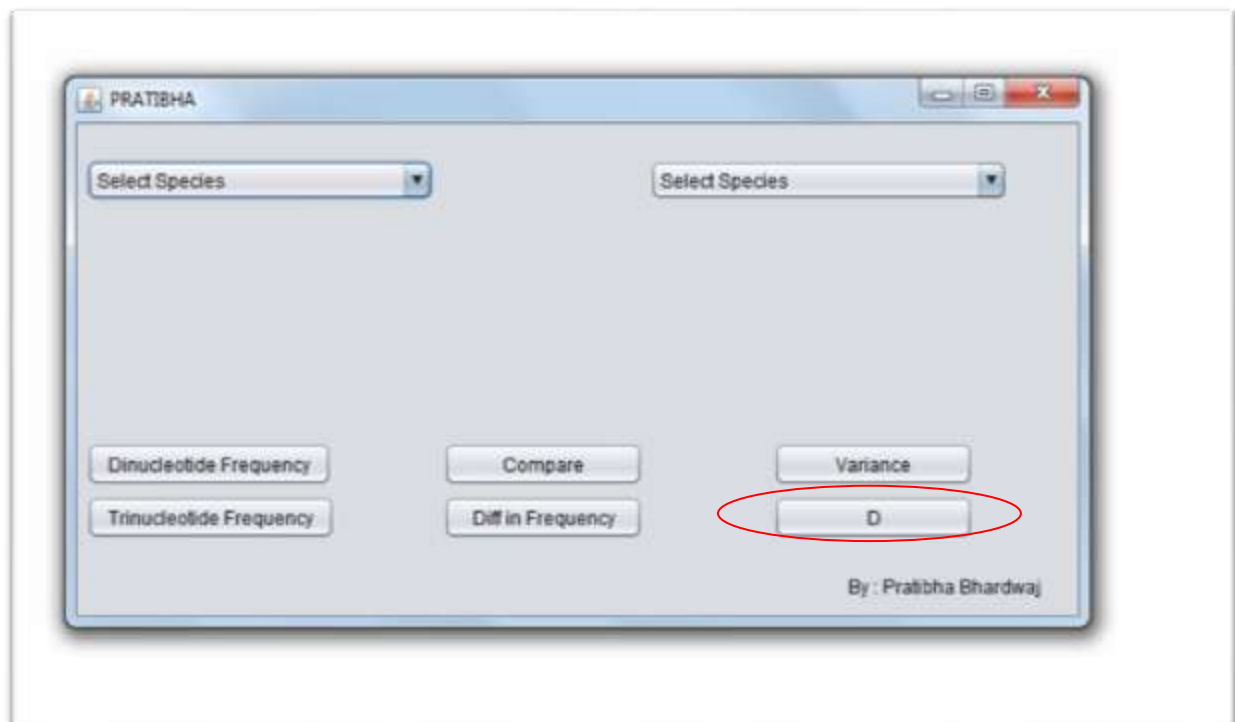
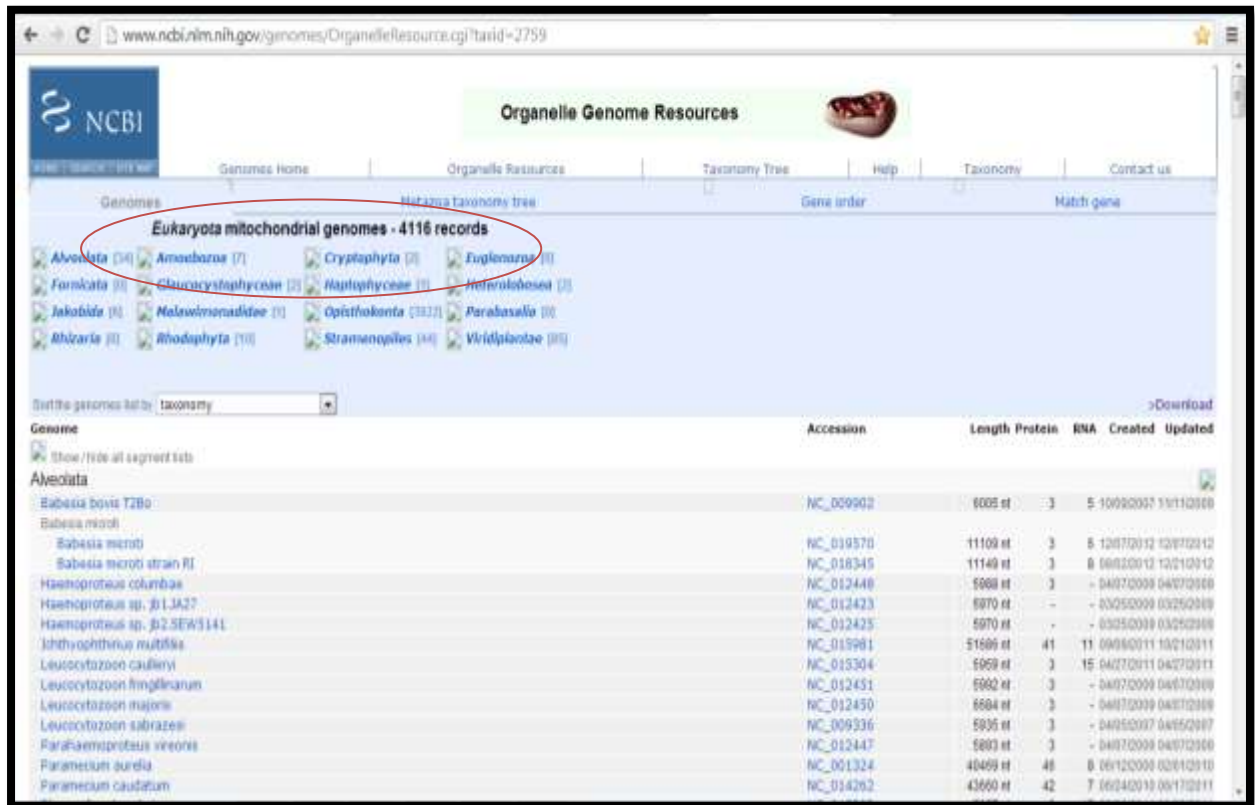


Figure11: Depicting home screen with option for D calculation.

4. RESULTS

4.1 Sequence retrieval

The whole mitochondrial genome of different species of worms was retrieved from organelle resource database of NCBI.



The screenshot displays the NCBI Organelle Genome Resources website. The page title is "Organelle Genome Resources" and the URL is "www.ncbi.nlm.nih.gov/genomes/OrganelleResource.cgi?taxid=2759". The main content area is titled "Eukaryota mitochondrial genomes - 4116 records". A red circle highlights this title. Below the title, there is a grid of taxonomic categories with their respective record counts: Amoebozoa (7), Cryptophyta (2), Euglenozoa (1), Fungi (1), Glaucocystophyceae (2), Harpacticoida (1), Heterolobosea (2), Jakobids (1), Metamonadidae (1), Opisthokonta (332), Parabasalids (1), Rhizaria (1), Rhodophyta (1), Stramenopiles (44), and Viridiplantae (10). Below this grid, there is a table of mitochondrial genomes. The table has columns for "Genome", "Accession", "Length", "Protein", "RNA", "Created", and "Updated". The "Genome" column is expanded to show a list of species names. The "Accession" column shows the NCBI accession numbers for each species. The "Length" column shows the length of the mitochondrial genome in base pairs (nt). The "Protein" and "RNA" columns show the number of protein-coding genes and rRNA genes, respectively. The "Created" and "Updated" columns show the dates when the records were created and last updated.

Genome	Accession	Length	Protein	RNA	Created	Updated
<i>Babesia bovis</i> T2Bo	NC_009902	6005 nt	3	5	10/09/2007	11/11/2010
<i>Babesia microti</i>						
<i>Babesia microti</i>	NC_019570	11109 nt	3	5	12/07/2012	02/07/2012
<i>Babesia microti</i> strain RI	NC_018345	11149 nt	3	5	06/02/2012	12/21/2012
<i>Haemaphysalis columbae</i>	NC_012448	5968 nt	3	-	04/07/2009	04/07/2009
<i>Haemaphysalis</i> sp. β1.JA27	NC_012423	5970 nt	-	-	03/25/2009	03/25/2009
<i>Haemaphysalis</i> sp. β2.SEA5141	NC_012425	5970 nt	-	-	03/25/2009	03/25/2009
<i>Ichthyophthirius multifiliis</i>	NC_015981	51686 nt	41	11	09/08/2011	10/21/2011
<i>Leucocytozon caulleryi</i>	NC_015304	5959 nt	3	15	04/27/2011	04/27/2011
<i>Leucocytozon fringilliarum</i>	NC_012451	5962 nt	3	-	04/07/2009	04/07/2009
<i>Leucocytozon majoris</i>	NC_012450	5964 nt	3	-	04/07/2009	04/07/2009
<i>Leucocytozon sabrazei</i>	NC_009336	5935 nt	3	-	04/05/2007	04/05/2007
<i>Parafaelempocheus virens</i>	NC_012447	5883 nt	3	-	04/07/2009	04/07/2009
<i>Paramesurus aurelia</i>	NC_001324	40499 nt	46	8	09/12/2008	02/01/2010
<i>Paramesurus caudatum</i>	NC_014262	43660 nt	42	7	06/24/2010	09/17/2011

Figure12: Depicting Organelle resource database of NCBI

Different worm genres were identified and retrieved using their accession numbers. The number of characters or base pairs present in the mitochondrial genome was mentioned in the database.

S no.	Genus	Species
1	<i>Angiostrongylus</i>	<i>Angiostrongylus cantonensis</i> <i>Angiostrongylus costaricensis</i> <i>Angiostrongylus vasorum</i>
2	<i>Diplogonoporus</i>	<i>Diplogonoporus balaenopterae</i> <i>Diplogonoporus balaenopterae</i>
3	<i>Dictyocaulus</i>	<i>Dictyocaulus eckerti</i> <i>Dictyocaulus viviparous</i>
4	<i>Ascaris</i>	<i>Ascaris lumbricoides</i> <i>Ascaris suum</i>
5	<i>Baylisascaris</i>	<i>Baylisascaris ailuri</i> <i>Baylisascaris procyonis</i> <i>Baylisascaris schroederi</i> <i>Baylisascaris schroederi</i>
6	<i>Toxocara</i>	<i>Toxocara canis</i> <i>Toxocara cati</i> <i>Toxocara malaysiensis</i>
7	<i>Taenia</i>	<i>Taenia asiatica</i> <i>Taenia crassiceps</i> <i>Taenia hydatigena</i> <i>Taenia krepkogorski</i> <i>Taenia laticollis</i> <i>Taenia madoquae</i> <i>Taenia martis</i> <i>Taenia multiceps</i> <i>Taenia mustelae</i> <i>Taenia ovis</i> <i>Taenia parva</i> <i>Taenia pisiformis</i> <i>Taenia saginata</i> <i>Taenia serialis</i> <i>Taenia solium</i> <i>Taenia twitchelli</i> <i>Taeniopygia guttata</i>

Table 1 List of different worm genera

Species	Accession	Size (nt)	GC (%)	Map Date	Map Length (nt)	Map Start (nt)	Map End (nt)
Taenia crassiceps	NC_002547	13452	42.1	24-07-2009	13452	1	13452
Taenia hydatigena	NC_012896	13482	42.1	24-04-2013	13482	1	13482
Taenia kruszchowskii mitochondrial DNA	NC_021142	13782	42.1	24-04-2013	13782	1	13782
Taenia laticollis mitochondrial DNA	NC_021140	13483	42.1	24-04-2013	13483	1	13483
Taenia madoquae mitochondrial DNA	NC_021139	13688	42.1	24-04-2013	13688	1	13688
Taenia martis mitochondrial DNA / maten tapeworm	NC_020133	13536	42.1	24-01-12-2013	13536	1	13536
Taenia multiceps	NC_012894	13683	42.1	24-07-2009	13683	1	13683
Taenia mustelae mitochondrial DNA	NC_021143	13682	42.1	24-04-2013	13682	1	13682
Taenia ovis mitochondrial DNA / sheep tapeworm	NC_021138	13784	42.1	24-04-2013	13784	1	13784
Taenia parva mitochondrial DNA	NC_021141	13483	42.1	24-04-2013	13483	1	13483
Taenia psiformis	NC_013844	13387	42.1	24-02-16-2010	13387	1	13387
Taenia saginata / beef tapeworm	NC_009938	13678	42.1	24-10-18-2007	13678	1	13678
Taenia serialis mitochondrial DNA	NC_021457	13688	42.1	24-06-16-2013	13688	1	13688
Taenia solium / pork tapeworm	NC_004022	13788	42.1	24-06-11-2002	13788	1	13788
Taenia taenioides	NC_014768	13647	42.1	24-12-08-2010	13647	1	13647
Taeniopsis cyathophanta / species Taenia solium	NC_021093	13519	42.1	24-04-2013	13519	1	13519
Taeniopygia guttata / zebra finch	NC_007897	18853	42.1	24-03-28-2009	18853	1	18853
Taeniura meyeni / blotched fantail ray	NC_019541	17838	42.1	24-10-03-2012	17838	1	17838
Takifugu chinensis / karasu	NC_011633	16447	42.1	24-12-05-2008	16447	1	16447
Takifugu chrysurus / akamafugu	NC_011624	16448	42.1	24-12-05-2008	16448	1	16448
Takifugu exocentrus / mushfugu	NC_011622	16443	42.1	24-12-05-2008	16443	1	16443
Takifugu fasciatus / obscure pufferfish	NC_013387	16444	42.1	24-03-12-2009	16444	1	16444
Takifugu niphobius / grass puffer	NC_011625	16442	42.1	24-12-05-2008	16442	1	16442
Takifugu oblongus / lattice blaesop	NC_011634	16444	42.1	24-12-05-2008	16444	1	16444
Takifugu obscurus / mefugu	NC_011626	16445	42.1	24-12-05-2008	16445	1	16445
Takifugu ocellatus	NC_011635	16448	42.1	24-12-05-2008	16448	1	16448
Takifugu pardalis / panther puffer	NC_011627	16463	42.1	24-12-05-2008	16463	1	16463
Takifugu poecilonotus / line patterned puffer	NC_011628	16448	42.1	24-12-05-2008	16448	1	16448
Takifugu porphyreus / purple puffer	NC_011628	16447	42.1	24-12-05-2008	16447	1	16447
Takifugu rubripes / torafugu	NC_004299	16447	42.1	24-09-24-2002	16447	1	16447
Takifugu snyderi / atlas-fugu	NC_011630	16450	42.1	24-12-05-2008	16450	1	16450
Takifugu stictonotus / goniafugu	NC_011629	16451	42.1	24-12-05-2008	16451	1	16451
Takifugu vermicularis / pear puffer	NC_011631	16443	42.1	24-12-05-2008	16443	1	16443
Takifugu xanthopterus / yellowfin puffer	NC_011632	16442	42.1	24-12-05-2008	16442	1	16442
Takydromus sedineatus	NC_022703	18943	42.1	24-11-03-2013	18943	1	18943
Taeniocera	NC_008773	18245	42.1	24-01-12-2007	18245	1	18245
Taeniocera	NC_018922	18245	42.1	24-03-03-2012	18245	1	18245

Fig 13: Depicts mitochondrial genome retrieval of *taenia* genus

The fasta sequence of all the species listed above was downloaded from NCBI database. Different folders were made for different genus.

4.2 Extraction of COI gene from the sequences

From whole mitochondrial genome of different worm species, the COI gene sequence was extracted using the COI gene sequence (1527 bp) retrieved from NCBI using EMBL alignment tools.

This was further reconfirmed by aligning with a partial COI sequence (372 bp) retrieved from NCBI database. The alignment files were saved. (Appendix 1)

4.3 Discrimination of species using java program

For discrimination, a java program was developed, to find out the various parameters required to discriminate various pathogenic species. The java code for the program is as mentioned. (Appendix 2)

4.3.1 Oligonucleotide frequency calculation

Dinucleotide and trinucleotide frequencies were found out using the java application “Pratibha” and stored as two .xls files namely dinucleotide frequencies and trinucleotide frequencies. (Appendix 3)



Figure14: Depicting dinucleotide frequencies of Angiostrongylus Costaricensis.

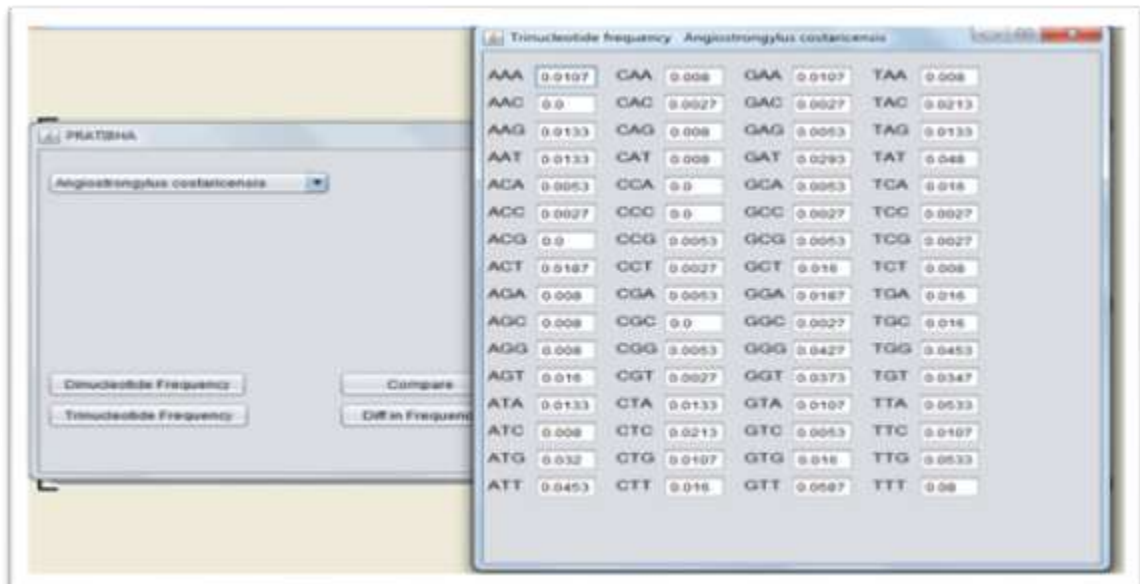


Figure15: Depicting trinucleotide frequencies of Angiostrongylus Costaricensis.

4.3.2 Calculation of variance

The variance of the dinucleotide and trinucleotide frequencies was calculated using the java application and stored in the above mentioned .xls files. (Appendix 3)



Figure16: Depicting variance of oligotide frequency of Angiostrongylus Costaricensis.

4.3.3 Difference in Oligonucleotide frequency

The difference in maximum and minimum dinucleotide and trinucleotide frequency was calculated using the java application and stored .xls file named as "Oligonucleotide frequency difference". (Appendix 3)

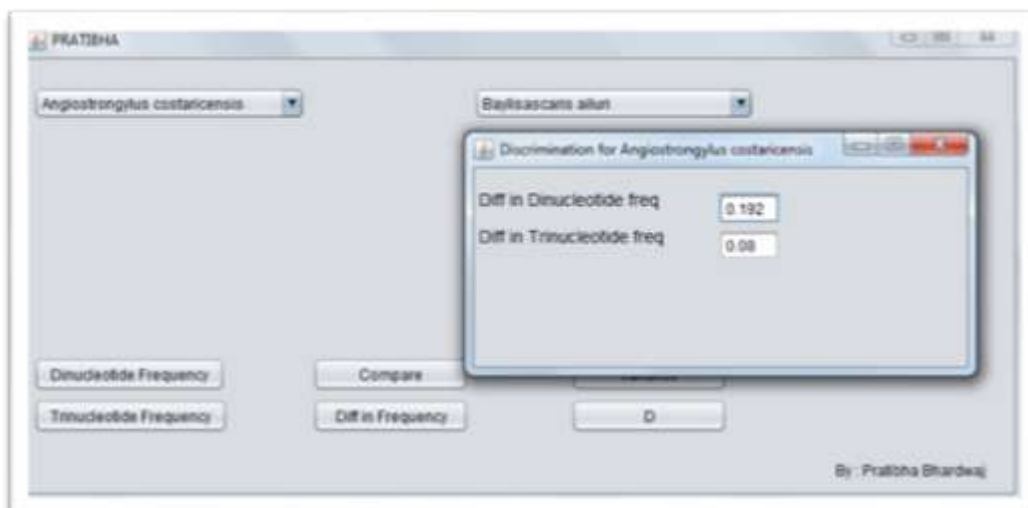


Figure16: Depicting the Oligonucleotide frequency difference for Angiostrongylus Costaricensis

4.3.4 Comparison of Oligonucleotide frequencies

A line graph was plotted between the dinucleotide and trinucleotide frequencies of two species.

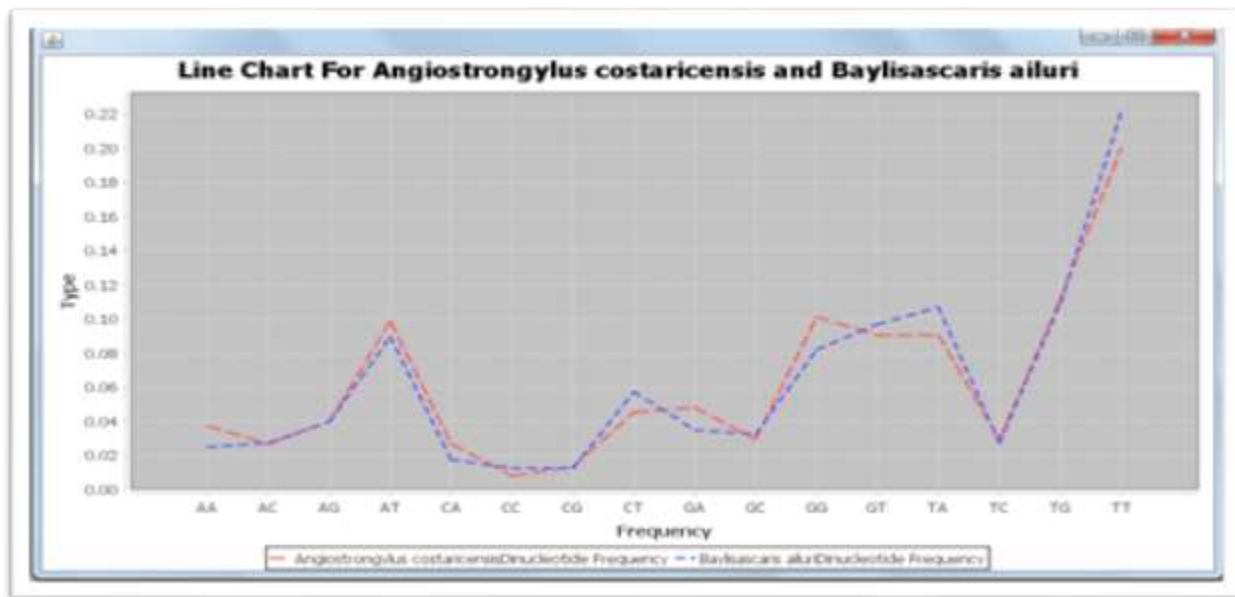


Figure17: Depicting the graph for the comparison of dinucleotide frequencies of the two species namely Angiostrongylus Costaricensis and Baylisascaris Aluri.

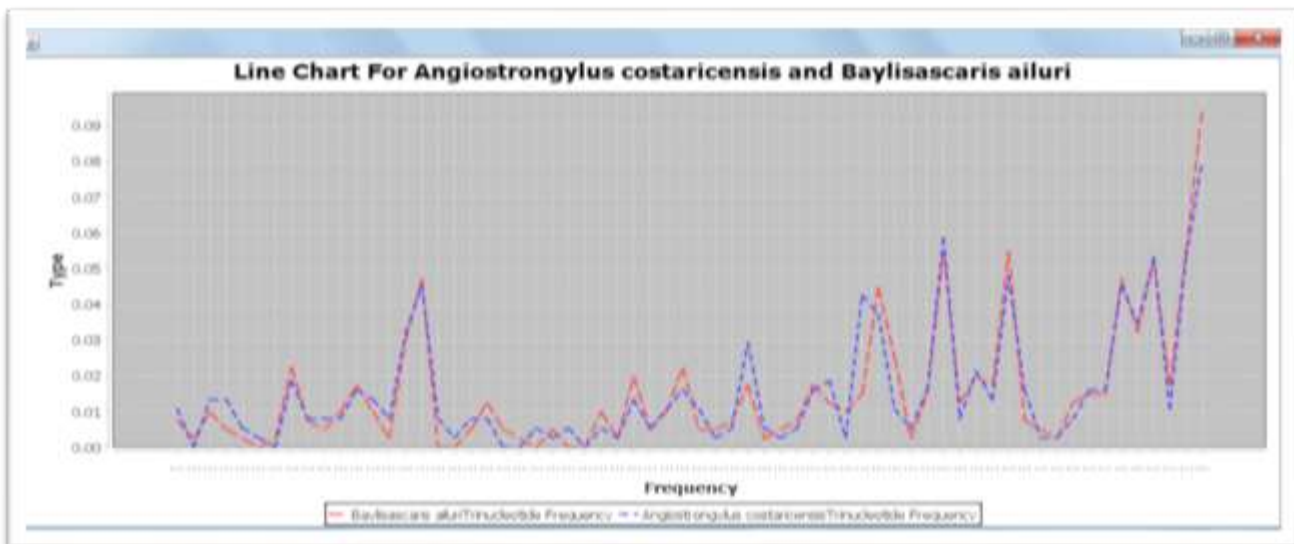


Figure18: Depicting the graph for the comparison of trinucleotide frequencies of the two species namely Angiostrongylus Costaricensis and Baylisascaris Aluri.

4.3.5 Statistical analysis

The Euclidean distance D was calculated using the formula

$$D = \sqrt{\sum_{i=1}^N |F1 - F2|^2}$$

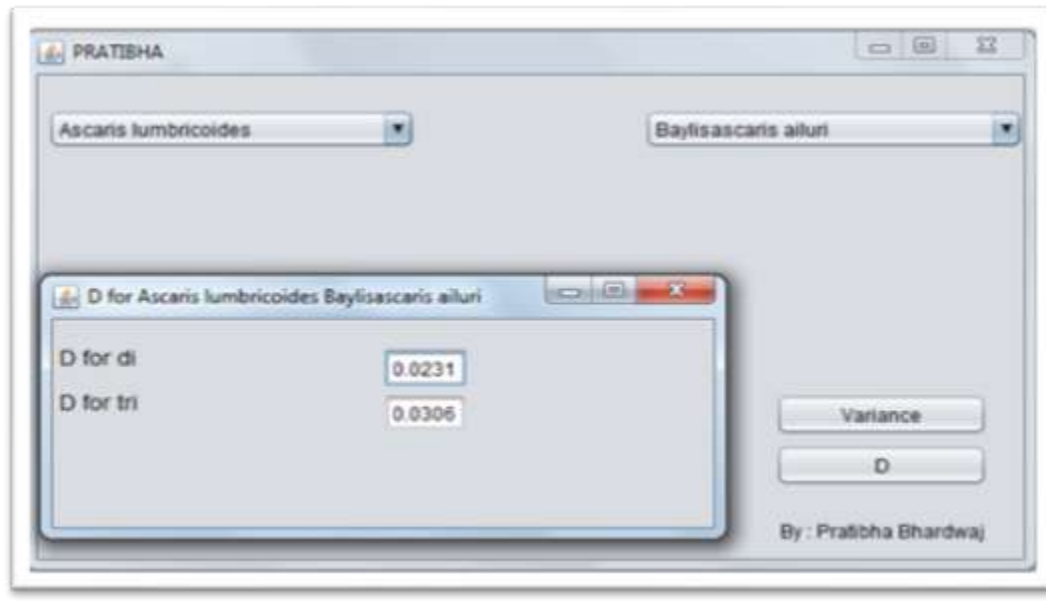


Figure19: Depicting D of Angiostrongylus Costaricensis.

5. DISCUSSION AND FUTURE PERSPECTIVE

The diversity in worms in the tropical region contributes to a wide range of worm borne diseases. According to a report published by NIA, diseases and epidemiological conditions caused by worms are as diverged as the types of worms which are responsible for them. The diseases caused by them varies from malaria to eye infections (Nimir *et al.*, 2012). The wide variety of worms like lungworms, roundworms, fluke worms etc. whose whole genome is available has been studied in this work.

Nowadays, we are more inclined towards gene based diagnostic techniques for better identification with precision, e.g., PCR based diagnostic methods. In a recent study, saliva and urine samples of *Plasmodium falciparum* and *Plasmodium vivax*-infected patients have been found to contain malarial DNA which can be amplified using PCR. However, only trace amounts of malarial DNA has been found in saliva and urine, the amount found is less than that is found in the concurrent blood samples of infected individuals, this has resulted into constrains in their usefulness in diagnosis. *Plasmodium* possess small mitochondrial genomes (mtDNA) of approximately 6 kb with a copy number of approximately 30 to 100 per parasite, the copy number of 18S rRNA is 4 to 8 per parasite nucleus . Therefore, the diagnostic sensitivity of a PCR assay targeting mtDNA is superior to that of an 18S rRNA-based technique. The mtDNA sequences of every malaria species are much conserved, on the other hand variation in sequences occurs between species. The cytochrome *b* gene (*Cytb*) found in mtDNA is used widely to study phylogenetics and evolutionary relationships among plasmodia. So, despite being low abundance, the sequence divergence as compared to 18S rRNA, *Cytb* has a potential role in differentiating malarial species. (Pattakorn *et al.*, 2010). Our aim was to device an *in silico* method to differentiate between the species of these worms based on their genomic variability. The recent trends in these techniques have been the use of DNA barcoding and oligo nucleotide frequency distribution (Tyagi *et al.*, 2010). Our method is based on DNA barcoding using oligo nucleotide frequency distribution techniques. Oligonucleotide frequency range of a barcode locus can discriminate between species. Ability to discriminate species using very short DNA fragments may have wider applications in forensic and conservation studies. (Tyagi *et al.*, 2010). A program was developed to analyse the barcode gene and give outputs in the form of dinucleotide frequencies, trinucleotide frequencies, their comparison and Euclidean distance. The variance between oligonucleotide frequencies is also calculated.

Our results show distinguishable variances for each species. We have been able to identify these species uniquely with the help of these indices. The results are comparable to reported researches in this field on other species like marine metazoan, fish, fungus etc (Bucklin *et al.*, 2010; Becker *et al.*, 2011; Begerow *et al.*, 2011). We have been able to curate all the indices to find out even a slight change in the species arising due to mutation (non-inheritable mutation) which may lead to increase or decrease in their virulence potential. Thus a treatment for such a mutation once diagnosed may be easily targeted. All the data have been included in Appendix II .The data will serve as a starting point to any researchers planning a work on virulence of the worms.

5.1 **Unique Selling Proposition (USP) of our work:**

The uniqueness of our work is the use of the DNA barcoding technique as an *in silico* diagnostic tool. Its originality lies in the fact that no research has been reported till date on bar coding of the worms especially pathogenic ones.

5.2 **Conclusion:**

The results of dinucleotide frequency distribution discriminates have found to discriminate between the species well (Appendix II). However to add more stringency to the process the trinucleotide frequency indices gives us an even more divergence with better resolution. (Chanda et al., 2010)

All *in silico* analysis are subject to a critical statistical test to prove its viability. We have used the popular method of finding out the Euclidian Distance (D) (Tyagi et al., 2010) to facilitate the process of validation of our work. The D values also correspond to our proposed method of finding the divergence.

5.3 **Future milestones:**

- These results can be used for confirmation of PCR diagnostic methods.
- Our tool can be expanded to accommodate most of the diagnostic technique for pathogens. The sequences of other pathogens can be added to the JAVA program and indices for them can be generated and used for disease diagnosis.
- These indices can also be used to trace drug resistivity of the pathogens. The resistivity arising even from point mutations like SNPs can be traced with these indices (Jeanette *et al.*, 2011).

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APPENDIX

Appendix 1: Alignment files

```
NC_013065.1 7751 TTGATTGGAAGAAAAATTCTCTTACATTT-ATATATATAAGAAATATCAA 7799
                .|||||
EU340360.1 1 -----GATTTGATATCT----- 12

NC_013065.1 7800 GGTGGTTTGTGCGTTTTGATTAGAAAGTTCTAATCATAAGGATATTGGTAC 7849
                ||.....| |.....|
EU340360.1 13 --TGATTGTCTCTTTG-----GATCATAAGCGTGTGGTGT 47

NC_013065.1 7850 TCTTTATTTTTTGGTTTATGGTCGGGT--ATGT-TAGGTAAGTCTT 7896
                |.....| |.....| |.....|
EU340360.1 48 TGTTTATATTATCTTGG---AGTGTGGGGTGGATTATAGGTTTAGGTT 94

NC_013065.1 7897 TATCTTTGATTG-TTCGTTTGAATTGTCTAAGCCTGGAATGTTGTTGTC 7945
                ||.....| |.....| |.....|
EU340360.1 95 TAAGTTTG-TTGATACGTTTAAATTTTTGTGATCCT---TATTATAAAC 139

NC_013065.1 7946 TAAT-----GGGCAATTGTATAATTCAATT--ATTACGGCTCATGC 7984
                | | |.....| |.....|
EU340360.1 140 TTATTCCTTGAGG----TATATAATT--ATTTGATAACTAATCACGG 182

NC_013065.1 7985 TTTTTTGGATGATTTTTTTTTATGGTGATGCCTAGTATGATTGGTGGTTTTG 8034
                |.....| |.....| |.....|
EU340360.1 183 TATAGCAATGATTTTTTTTTTTTAATGCCTGTTTAAATAGGGGGTTTTG 232

NC_013065.1 8035 GTAATTGAATAT---TGCCTTTGATGTTGGGGGCTCCGGATATGAG--- 8077
                || | | |.....| |.....|
EU340360.1 233 GTA---AATATCTTCTCCGTTTTTTTTGAG-----TATGAGTGA 269

NC_013065.1 8078 -----TTTTCCTCGTTTGAATAATTTGAGTTTTTG-ATTAT--TACCAA 8118
                ||.....| |.....| |.....|
EU340360.1 270 TTTACCTTTGCCCGTTTAAATCTTTGAGTGTGTTGAATGATGGTTC--- 316

NC_013065.1 8119 CTTCGATGTTT---TTGATTTTATGATTCTTGTGTTTGTGGATATAGGATG 8164
                ||.....| |.....| |.....|
EU340360.1 317 CTCAATATTTTATATGGAATTAAG--TTTGTATTATGGATCT--GGTG 361

NC_013065.1 8165 TGGGACTAGTTGGACTGTTTATCCGCCCTTGAGAAGTTTAGGTCATCCTG 8214
                | |.....| |.....| |.....|
EU340360.1 362 T----TGGTTGGACCTTTTATCCACCTTGTCTTCTTTAGCTACTTCTG 406

NC_013065.1 8215 GTAGAAGG-GTGGATTTGGCGATTTTATGTTTGCATTGTGCTGGACTGAG 8263
                ||.....| |.....| |.....|
EU340360.1 407 GT-GTTGGTGTGGATTACTTAATGTTCTTCTTACATCTTGCTG---GTG 451

NC_013065.1 8264 T-TCTATTTTG---GGGGGATTAATTTTATGTGTACAACGAAGAAT-AT 8308
                |.....| |.....| |.....|
EU340360.1 452 TATCTAGTTGATTGGTTCTATAAATTTTAT---TACTAC-TATAATGTT 497

NC_013065.1 8309 GCGAAGAAGTTC AATTTCTTTGGAACA--TATGAGTTTGTGTTTGTGATC 8356
                ||.....| |.....| |.....|
EU340360.1 498 GCGTCTAAGGTCATGTTCTT----CAGTTATTAG-----ATGATC 533

NC_013065.1 8357 TGTTTTTGTGACTGTTTTTTTGTGGTGTGCTTTACCTGTGTTGGCCG 8406
                |.....| |.....| |.....|
EU340360.1 534 TTATTTATTTACTTCGGTGTGTTATTGTTATCGTTGCCGGTCTTGCTG 583
```



```

NC_013065.1  8775 TTATTTGGTATAAAGATATTGT-----TTCAACCTATTTTAT  8811
      .|||.||  |.|||...|||      |||.|||.|||.|
SMU82262    225 ATATATG---TTAAGTGGTTGTGGGTTGCGTGTTGTTGATCCTGTTGT-T  270

NC_013065.1  8812 TG-TGGGTTTTGGGTTTTATTTTTTTTATTACTATCGGTGGGTAAACGGG  8860
      |||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.
SMU82262    271 TGATGAATTGTTGGTTTTATTTTTTTGTTTACAGTTGGTGGGGTTACTGG  320

NC_013065.1  8861 GGTTATATTGTCTAATTCTAGTTTGGATATTATTTTACATGATACTTATT  8910
      |.|||||  ||  |.|.|||.|||.
SMU82262    321 -----TATAGTTT---TA----TCTGCTTGATCCT----  343

NC_013065.1  8911 ATGTAGTTAGGCATTTTCATTAT----GTTTAAAGTTGGGGGCTGTTT  8955
      |||.|||.|||.|||.|||.|||.  |||.
SMU82262    344 ---TAGATAGTTGTTTCATGATACTTGGTTT-----  372

```

Appendix 2

```
/*  
 * To change this license header, choose License Headers in Project Properties.  
 * To change this template file, choose Tools | Templates  
 * and open the template in the editor.  
 */  
  
package pratibha;  
  
//import java.awt.Dimension;  
import java.awt.BasicStroke;  
import java.awt.Color;  
import java.awt.Dimension;  
import static java.lang.StrictMath.sqrt;  
import java.text.DecimalFormat;  
import javax.swing.JFrame;  
import javax.swing.JLabel;  
import javax.swing.JTextField;  
import org.jfree.chart.ChartFactory;  
import org.jfree.chart.ChartPanel;  
import org.jfree.chart.JFreeChart;  
import org.jfree.chart.axis.NumberAxis;  
import org.jfree.chart.plot.CategoryPlot;  
import org.jfree.chart.plot.PlotOrientation;  
import org.jfree.chart.renderer.category.LineAndShapeRenderer;  
import org.jfree.data.category.CategoryDataset;  
import org.jfree.data.category.DefaultCategoryDataset;  
  
public class aJFrame extends javax.swing.JFrame {  
  
    int a=10;  
    String s="";  
    String q="";
```

```

String t="";

/**
 * Creates new form aJFrame
 */
public aJFrame() {
    initComponents();
}
/**
 * This method is called from within the constructor to initialize the form.
 * WARNING: Do NOT modify this code. The content of this method is always
 * regenerated by the Form Editor.
 */
@SuppressWarnings("unchecked")
// <editor-fold defaultstate="collapsed" desc="Generated Code">
private void initComponents() {

    JFrame1 = new javax.swing.JFrame();
    JFrame2 = new javax.swing.JFrame();
    JColorChooser1 = new javax.swing.JColorChooser();
    JButton6 = new javax.swing.JButton();
    JComboBox1 = new javax.swing.JComboBox();
    JButton1 = new javax.swing.JButton();
    JButton2 = new javax.swing.JButton();
    JComboBox2 = new javax.swing.JComboBox();
    JButton4 = new javax.swing.JButton();
    JLabel2 = new javax.swing.JLabel();
    JButton3 = new javax.swing.JButton();
    JButton5 = new javax.swing.JButton();
    JButton7 = new javax.swing.JButton();

    javax.swing.GroupLayout JFrame1Layout = new javax.swing.GroupLayout(JFrame1.getContentPane());
    JFrame1.getContentPane().setLayout(JFrame1Layout);
    JFrame1Layout.setHorizontalGroup(
        JFrame1Layout.createParallelGroup(javax.swing.GroupLayout.Alignment.LEADING)
            .addGap(0, 400, Short.MAX_VALUE)

```

```

);

jFrame1Layout.setVerticalGroup(

    JFrame1Layout.createParallelGroup(javax.swing.GroupLayout.Alignment.LEADING)

        .addGap(0, 300, Short.MAX_VALUE)

);

javax.swing.GroupLayout jFrame2Layout = new javax.swing.GroupLayout(jFrame2.getContentPane());
jFrame2.getContentPane().setLayout(jFrame2Layout);

jFrame2Layout.setHorizontalGroup(

    JFrame2Layout.createParallelGroup(javax.swing.GroupLayout.Alignment.LEADING)

        .addGap(0, 400, Short.MAX_VALUE)

);

jFrame2Layout.setVerticalGroup(

    JFrame2Layout.createParallelGroup(javax.swing.GroupLayout.Alignment.LEADING)

        .addGap(0, 300, Short.MAX_VALUE)

);

jButton6.setText("jButton6");

setDefaultCloseOperation(javax.swing.WindowConstants.EXIT_ON_CLOSE);

setBackground(new java.awt.Color(102, 0, 255));

setBounds(new java.awt.Rectangle(0, 0, 0, 0));

jComboBox1.setModel(new javax.swing.DefaultComboBoxModel(new String[] { "Select Species", "Angiostrongylus cantonensis",
"Angiostrongylus costaricensis", "Ascaris lumbricoides", "Ascaris suum", "Baylisascaris ailuri", "Baylisascaris procyonis", "Baylisascaris
schroederi", "Baylisascaris transfuga", "Toxocara canis", "Toxocara cati", "Toxocara malaysiensis", "Aelurostrongylus abstrusus",
"Dictyocaulus eckerti", "Dictyocaulus viviparus", "Diplogonoporus balaenopterae", "Diplogonoporus grandis", "Taenia asiatica", "Taenia
crassiceps", "Taenia hydatigena", "Taenia krepkogorski", "Taenia laticollis", "Taenia madoquae", "Taenia martis", "Taenia multiceps",
"Taenia mustelae", "Taenia ovis", "Taenia parva", "Taenia pisiformis", "Taenia saginata", "Taenia serialis", "Taenia solium", "Taenia
twitchelli" }));

jComboBox1.addActionListener(new java.awt.event.ActionListener() {

    public void actionPerformed(java.awt.event.ActionEvent evt) {

        jComboBox1ActionPerformed(evt);

    }

});

jButton1.setText("Dinucleotide Frequency");

jButton1.addActionListener(new java.awt.event.ActionListener() {

```

```

public void actionPerformed(java.awt.event.ActionEvent evt) {

    jButton1ActionPerformed(evt);

}

});

jButton2.setText("Trinucleotide Frequency");

jButton2.addActionListener(new java.awt.event.ActionListener() {

    public void actionPerformed(java.awt.event.ActionEvent evt) {

        jButton2ActionPerformed(evt);

    }

});

jComboBox2.setModel(new javax.swing.DefaultComboBoxModel(new String[] { "Select Species", "Angiostrongylus cantonensis",
"Angiostrongylus costaricensis", "Ascaris lumbricoides", "Ascaris suum", "Baylisascaris ailuri", "Baylisascaris procyonis", "Baylisascaris
schroederi", "Baylisascaris transfuga", "Toxocara canis", "Toxocara cati", "Toxocara malaysiensis", "Aelurostrongylus abstrusus",
"Dictyocauluseckerti", "Dictyocaulus viviparus", "Diplogonoporus balaenopterae", "Diplogonoporus grandis", "Taenia asiatica", "Taenia
crassiceps", "Taenia hydatigena", "Taenia krepkogorski", "Taenia laticollis", "Taenia madoquae", "Taenia martis", "Taenia multiceps",
"Taenia mustelae", "Taenia ovis", "Taenia parva", "Taenia pisiformis", "Taenia saginata", "Taenia serialis", "Taenia solium", "Taenia
twitchelli" }));

jComboBox2.addActionListener(new java.awt.event.ActionListener() {

    public void actionPerformed(java.awt.event.ActionEvent evt) {

        jComboBox2ActionPerformed(evt);

    }

});

jButton4.setText("Compare");

jButton4.addActionListener(new java.awt.event.ActionListener() {

    public void actionPerformed(java.awt.event.ActionEvent evt) {

        jButton4ActionPerformed(evt);

    }

});

jLabel2.setText("By : Pratibha Bhardwaj");

jButton3.setText("Diff in Frequency");

jButton3.addActionListener(new java.awt.event.ActionListener() {

    public void actionPerformed(java.awt.event.ActionEvent evt) {

        jButton3ActionPerformed(evt);

    }

});

```

```

    }
});

jButton5.setText("Variance");

jButton5.addActionListener(new java.awt.event.ActionListener() {
    public void actionPerformed(java.awt.event.ActionEvent evt) {
        jButton5ActionPerformed(evt);
    }
});

jButton7.setText("D");

jButton7.addActionListener(new java.awt.event.ActionListener() {
    public void actionPerformed(java.awt.event.ActionEvent evt) {
        jButton7ActionPerformed(evt);
    }
});

javax.swing.GroupLayout layout = new javax.swing.GroupLayout(getContentPane());
getContentPane().setLayout(layout);

layout.setHorizontalGroup(
    layout.createParallelGroup(javax.swing.GroupLayout.Alignment.LEADING)
        .addGroup(layout.createSequentialGroup()
            .addContainerGap()
            .addComponent(jLabel1, javax.swing.GroupLayout.PREFERRED_SIZE, 128,
                javax.swing.GroupLayout.PREFERRED_SIZE)
            .addGap(19, 19, 19)
            .addGroup(layout.createParallelGroup(javax.swing.GroupLayout.Alignment.LEADING)
                .addComponent(jButton2)
                .addGap(19, 19, 19)
                .addComponent(jButton1))
            .addContainerGap(19, true))
);

```

```

        .addComponent(jComboBox1, javax.swing.GroupLayout.PREFERRED_SIZE, 222,
javax.swing.GroupLayout.PREFERRED_SIZE))

        .addPreferredGap(javax.swing.LayoutStyle.ComponentPlacement.RELATED)

        .addGroup(layout.createParallelGroup(javax.swing.GroupLayout.Alignment.TRAILING)

        .addComponent(jComboBox2, javax.swing.GroupLayout.PREFERRED_SIZE, 229,
javax.swing.GroupLayout.PREFERRED_SIZE)

        .addGroup(layout.createSequentialGroup())

        .addGroup(layout.createParallelGroup(javax.swing.GroupLayout.Alignment.LEADING, false)

        .addComponent(jButton3, javax.swing.GroupLayout.DEFAULT_SIZE, javax.swing.GroupLayout.DEFAULT_SIZE,
Short.MAX_VALUE)

        .addComponent(jButton4, javax.swing.GroupLayout.DEFAULT_SIZE, 128, Short.MAX_VALUE))

        .addGap(83, 83, 83)

        .addGroup(layout.createParallelGroup(javax.swing.GroupLayout.Alignment.TRAILING)

        .addComponent(jButton7, javax.swing.GroupLayout.PREFERRED_SIZE, 128,
javax.swing.GroupLayout.PREFERRED_SIZE)

        .addComponent(jButton5, javax.swing.GroupLayout.PREFERRED_SIZE, 128,
javax.swing.GroupLayout.PREFERRED_SIZE))

        .addGap(22, 22, 22))))))

);

layout.setVerticalGroup(

    layout.createParallelGroup(javax.swing.GroupLayout.Alignment.LEADING)

    .addGroup(layout.createSequentialGroup())

    .addGap(23, 23, 23)

    .addGroup(layout.createParallelGroup(javax.swing.GroupLayout.Alignment.BASELINE)

    .addComponent(jComboBox1, javax.swing.GroupLayout.PREFERRED_SIZE, javax.swing.GroupLayout.DEFAULT_SIZE,
javax.swing.GroupLayout.PREFERRED_SIZE)

    .addComponent(jComboBox2, javax.swing.GroupLayout.PREFERRED_SIZE, javax.swing.GroupLayout.DEFAULT_SIZE,
javax.swing.GroupLayout.PREFERRED_SIZE))

    .addPreferredGap(javax.swing.LayoutStyle.ComponentPlacement.RELATED, 164, Short.MAX_VALUE)

    .addGroup(layout.createParallelGroup(javax.swing.GroupLayout.Alignment.BASELINE)

    .addComponent(jButton4)

    .addComponent(jButton1)

    .addComponent(jButton5))

    .addPreferredGap(javax.swing.LayoutStyle.ComponentPlacement.RELATED)

    .addGroup(layout.createParallelGroup(javax.swing.GroupLayout.Alignment.BASELINE)

    .addComponent(jButton2)

    .addComponent(jButton3)

    .addComponent(jButton7))

```



```

        .addGap(18, 18, 18)

        .addComponent(jLabel2, javax.swing.GroupLayout.PREFERRED_SIZE, 25, javax.swing.GroupLayout.PREFERRED_SIZE)

        .addContainerGap()

    );

    pack();
} // </editor-fold>

private void jButton4ActionPerformed(java.awt.event.ActionEvent evt) {

    ammy asIt = new ammy(s,t);

    CategoryDataset dataset = asIt.GetData1(s,t);

    CategoryDataset dataset1 = asIt.GetData2(s,t);

    asIt.drawchart1(dataset);

    asIt.drawchart1(dataset1);

}

private void jButton1ActionPerformed(java.awt.event.ActionEvent evt) {

    // TODO add your handling code here:

    if("Angiostrongylus cantonensis".equals(s))

    {

        q=
"GCTTTTGGGATTGTTAGACAGTCTACTTTATATTTAACGGGTAAAAAAGAGGTTTTGGTTATTTGGGTATGGTTTATGCTAT
TTTAAAGAATTGGTTTGATTGGTTGTGTGGTTTGGGCTCATCATATATACGGTTGGTATGGATTAGATTCTCGTGCTTATTT
TACTGCGGCTACTATAGTTATTGCGGTTCCCTACGGGAGTGAAGGTTTTTAGGTGGTTGGCAACTTTATTTGGTATAAAGATAT
TGTTTTCAACCTATTTTATTGTGGGTTTTGGGTTTTATTTTTTTATTTACTATCGGTGGGTTAACGGGGTTATATTGTCTAATTC
TAGTTTGGATATTATTTACATGATACTTATTATGTAGTTAGGCATTTTCATTATGTTT";

    }

    else if("Angiostrongylus costaricensis".equals(s))

    {

        q=
"GCTTTTGGGATTATTAGTCAATCTGCTTTGTATTTGTCAGGGAAGAAAGAGGTTTTGGTTATTTAGGGATGGTTTATGCGAT
TTTAAAGAATTGGGTTGATTGGGTGTGTAGTTTGAGCTCATCATATGTATACTGTTGGTATGGATTGGATTCTCGTGCTTACTT
TACTGCAGCTACAATAGTTATTGCGGTTCCCTACTGGGGTTAAAGTGTTTAGTTGGTTGGCTACACTTTATGGGATGAAAATGA
TGTTTCAGCCGATTTTGTGTGGGTTATGGGGTTTTATTTTTTGTTTACTATTGGGGGTTTGACCGGGGTTATGTTATCTAATTC
AAGTTTGGATATTATTTGCATGATACTTATTATGTGGTT";

    }

    else if("Angiostrongylus vasorum".equals(s))

    {

        q=
"GCTTTTGGGATTGTTAGTCAGTCGACTTTATATTTGACTGGGAAGAAGGAGGTGTTTGGTTATTTGGGGATGGTTTATGCGAT
TTTAAAGGATTGGTTTGATTGGTTGTGTGGTGTGAGCTCATCATATGTATACTGTTGGTATAGATTAGATTCTCGTGCTTATTT
TACTGCGGCTACTATGGTGATTGCGGTGCCGACTGGAGTGAAGGTTTTTAGTTGGTTGGCTACTTTGTTGGGATGAAGTATA
GTATTTACAGCCTATTTTGTGTGGGTTATAGGATTTATTTTTTTTTATTTACTATTGGGGGTTTGACGGGTGTGATATTGTCAA
TTCGAGATTGGATATTATTTACATGATACGTATTATGTGGTAAAGTCATTTTCATTATGTGAGGTTGTTTCATGATACTTGGTT
T";

    }

}

```

```

else if("Diplogonoporus balaenopterae".equals(s))
{
    q=
"GGGTTTGGAATGATTAGACATGTTTGTAGTAACTTAGGTTGTTTCATATGATACTTTGGATTTTATGGTTTATTATTTGCTATG
TTTTCTATCGTTTGTCTTGGTAGGGTTGTATGGGGTCATCATATGTTTACGGTAGGTTTAGATGTGAAGACAGCTGTTTTTTT
AGGTCAGTTACTATGATTATAGGGGTGCCTACTGGAATAAAGGTGTTTTCTTGGCTGTATATGATTTTAAAAAGTCGTGTCTC
TTTGCCTGAACCTATATTTTGGTGGGTGTTATCTTTTATCGTGCTGTTTACAATAGGGGGTGTACTGGTATTATACTTTCTGC
TTGTGTTCTTGATAAATATTTTGCATGATACTTGATTT";
}

else if("Diplogonoporus grandis".equals(s))
{
    q=
"GGGTTTGGAATGATTAGACATGTTTGTAGTAACTTAGGTTGTTTCATATGATACTTTTGGATTTTATGGTTTATTATTTGCTATG
TTTTCTATCGTTTGTCTTGGTAGGGTTGTATGGGGTCATCATATGTTTACGGTAGGTTTAGATGTGAAGACAGCTGTTTTTTT
AGGTCAGTTACTATGATTATAGGGGTGCCTACTGGAATAAAGGTGTTTTCTTGGCTGTATATGATTTTAAAAAGTCGTGTCTC
TTTGCCTGAACCTATATTTTGGTGGGTGTTATCTTTTATCGTGCTGTTTACAATAGGGGGTGTACTGGTATTATACTTTCTGC
TTGTGTTCTTGATAAATATTTTGCATGATACTTGATTT";
}

else if("Aelurostrongylus abstrusus".equals(s))
{
    q=
"GCTTTTGGTATTGTTAGTCAGTCTACTTTGTATTTGACGGGGAAGAAGGAAGTTTTTGGTTATTTAGGGATAGTTTATGCTAT
TATAAGTATTGGTTAATTGGTTGTGTTTGGGCTCATCATATATACTGTTGGTATAGATTTGGATTCCTCGTGCTTATTTT
ACGGCGGCTACGATGGTTATTGCTGTGCCAACGGGTGTTAAGGTTTTTAGTTGGTTGGCTACTTTATTTGGAATGAAGATAGT
GTTTCAGCCGGTTTTGTTGTGGGTTTTGGGTTTTATTTTTTGTACTATTGGGGGGTTAACTGGGGTCATGCTTTCGAATTCT
AGTTTGATATTATTTGTCATGATACTTATTATGTGGTTAGTCATTTTCATTATGTGTTGAGTTT";
}

else if("Dictyocaulus eckerti".equals(s))
{
    q=
"GCTTTTGGTATTATTAGTCAGTCAACTTTGTATTTAACTGGTAAAAAGGAGGTTTTTGGTTCTTTGGGTATGGTTTATGCTATT
TTAAGTATTGGTTAATTGGTTGTGTAGTATGAGCACATCATATATACTGTTGGAATAGATTTGGATTCGCGTGCTTATTTT
ACTGCTGCTACTATGGTAATTGCTGTTCCTACGGGTGTAAGGTTTTTAGTTGGTTGGCTACTTTGTATGGTTAAAAATAGTA
TATAATCCTTTGTGTTATGGGTTTTGGGTTTTATTTTTTATTACTATTGGGGGGTTAACTGGAGTTATTTTGTCAAATCTA
GTTTATAGATTTTTGTTACATGATACTTATTATGTTGTAAGGCATTT";
}

else if("Dictyocaulus viviparus".equals(s))
{
    q=
"GCTTTTGGTATTATTAGACAATCTACTTTGTATTTAACTGGTAAAAAGGAGGTTTTTGGTTCTTTGGGTATGGTTTATGCTATT
TTAAGTATTGGTTAATTGGTTGTGTGTGGGCACATCATATGATACTGTTGGGATGGATTTGGATTCGCGTGCTTATTTT
ACTGCTGCTACTATAGTAATTGCTGTTCCTACTGGAGTTAAGGTTTTTAGATGATTGGCTACTTTATATGGATTGAAAATGGTT
TATAATCCTTTGTGTTGTGAGTTTTAGGTTTTATTTTTTGTACTATTGGTGGTTAACTGGTGTATTATTTGTCAAATCTA
GTCTTGATATTTTGTGTCATGATACTTATTAT";
}

else if("Ascaris lumbricoides".equals(s))
{

```

```
q=  
"GCTTTTGGTATTATTAGTCAGAGTAGTTTGTATTTGACTGGTAAAAAGGAGGTTTTTGGGTCCTTGGGTATGGTTTATGCTAT  
TTTAAAGTATTGGTTTGGATTGGTTGTGTTGTTTGGCTCATCATATGTATACTGTGGTATGGATCTTGATTCTCGGGCTTATTTT  
ACTGCTGCAACTATGGTTATTGCTGTTCTACTGGTGTAAAGGTTTTTAGTTGGTTGGCTACCTTGTGGTATAAAAAATGGTT  
TTTCAGCCTTTACTTTTATGAGTTATGGGTTTTATTTTTTTGTTTACTATTGGTGGGTTAACCGGGTTAATACTTTCTAATTCTA  
GTTTGGATATTATCTTGCATGATACTTATTATGTTGTTAGTCATTTTCATTATGTTCTTAGTTT";
```

```
}
```

```
else if("Ascaris suum".equals(s))
```

```
{
```

```
q=  
"GCTTTTGGTATTATTAGTCAGAGTAGTTTGTATCTGACTGGTAAAAAGGAGGTTTTTGGGTCCTTGGGTATGGTTTATGCTAT  
TTTGAGTATTGGTTAATTGGTTGTGTTGTTTGGCTCATCATATGTATACTGTGGTATGGATCTTGACTCTCGGGCTTATTTT  
ACTGCTGCAACTATGGTTATTGCTGTTCTACTGGTGTAAAGGTTTTTAGTTGGTTGGCTACCTTGTGGTATAAAGATGGTT  
TTTCAACCTTTACTTTTATGAGTTATGGGTTTTATTTTTTTGTTTACTATTGGTGGGTTAACCGGGTTATGCTTTCTAATTCTA  
GTTTGGATATTATCTTGCATGATACTTA-TTATGTTGTTAGTCATTTTCATTATGTCCTTAGTTT";
```

```
}
```

```
else if("Baylisascaris ailuri".equals(s))
```

```
{
```

```
q=  
"GCTTTTGGTATTATTAGCCAGAGTAGGTTGTATTTAACTGGTAAAAAGGAAGTTTTTGGTTCCTTGGGTATGGTTTATGCTAT  
TTTGAGTATTGGTTAATTGGTTGTGTTGTTTGGGCTCATCATATGTATACTGTAGGTATGGATTTGGATTCTCGTGCTTATTTT  
ACTGCGGCTACTATGGTTATTGCGGTTCCCTACGGGTGTAAAGGTTTTTAGTTGGTTGGCTACTTTGTGGTATGAAGATGGTG  
TTCCAGCCTTTACTTTTGTGAGTTATGGGTTTTATTTTTTTTACTATTGGCGGATTGACTGGGGTGATGCTTTCTAATTCTA  
GTTTGGATATTATTTGCATGATACTTA-TTATGTTGTTAGACATTTTCATTATGTTCTTAGTTT";
```

```
}
```

```
else if("Baylisascaris procyonis".equals(s))
```

```
{
```

```
q=  
"GCTTTTGGTATTATTAGCCAAAGTAGGTTGTATTTAACTGGTAAGAAGGAAGTTTTTGGTTCCTTGGGAATGGTTTATGCTAT  
TTTGAGTATTGGTTTGGATTGGATGTGTTGTTTGGGCTCATCATATGTATACTGTGGGTATGGATTTGGATTCTCGGGCTTATTT  
TACTGCGGCTACTATGGTTATTGCGGTTCCCTACGGGAGTTAAGGTTTTTAGTTGGTTGGCCACTTTATTTGGTATGAAGATAGT  
GTTTCAGCCTTTGCTTTTGTGGGTTATGGGTTTTATTTTTTTGTTTACTATTGGTGGTTTACTGGGGTTATGCTTTCTAATTCT  
AGTTTGGATATTATTTGCATGATACTTATTATGTTGTTAGGCATTTTCATTATGTTCTTAGTTT";
```

```
}
```

```
else if("Baylisascaris schroederi".equals(s))
```

```
{
```

```
q=  
"GCTTTTGGTATTATTAGTCAGAGTAGGTTGTATCTGACTGGTAAGAAGGAGGTTTTTGGTTCCTTGGGTATGGTTACGCAAT  
TTTGAGTATTGGTTTGGATTGGTTGTGTTGTTTGGCTCATCATATGTATACTGTGGGTATAGATTTGGATTCTCGTGCTTATTTT  
ACTGCGGCTACTATGGTTATCGCAGTTCCCTACGGGTGTAAAGGTTTTTAGTTGGTTGGCTACTTTGTGGTATGAAGATGGTG  
TTTCAGCCTTTGCTTTTGTGGGTTATAGGATTTATTTTTTTGTTTACTATTGGTGGATTGACTGGGGTGATGCTTTCTAATTCTA  
GTTTGGATATTATTTGCATGATACTTA-TTATGTTGTTAGGCATTTTCATTATGTTCTTAGTTT";
```

```
}
```

```
else if("Baylisascaris transfuga".equals(s))
```

```
{
```

```
q=  
"GCTTTTGGTATTATTAGTCAGAGTAGATTGTATTTAACTGGTAAAAAGGAGGTTTTTGGTTCCTTGGGTATGGTTTATGCTAT  
TTTGAGTATTGGTTAATTGGTTGTGTTGTTTGGGCTCATCATATGTATACTGTAGGTATGGATTTGGATTCTCGTGCTTATTTT  
ACTGCGGCTACTATGGTTATTGCGGTTCCCTACAGGTGTAAAGGTTTTTAGTTGGTTGGCCACTTTGTGGTATGAAGATGGTG
```

```

TTCAGCCTTTACTTTTGTGGGTTATGGGGTTATTTTTTTATTTACTATTGGTGGATTGACTGGGGTGATGCTTCTAATTCTA
GTTTGGATATTATTTGCATGATACTTATTATGTTGTTAGGCATTTTCATTATGTTCTTAGTTT";

}

else if("Toxocara canis".equals(s))

{

q=
"GCTTTTGGTATTATTAGGCAAAGTAGTTTGTATTTGACTGGTAAAAAGGAGGTTTTGGTCTTTAGGCATGGTTTTATGCTAT
TTAAGTATTGGTCTGATTGGCTGTGTAGTTGGGCTCACCATATGTATACGGTGGGCATGGATTTGGATTCTCGTGCTTATTT
TACTGCGGCAACGATGGTTATTGCTGTGCCTACGGGGTTAAGGTTTTAGTTGGTTAGCCACTCTTTTGGTATGAAGATGG
TGTTCAACCTTTGCTTTTGTGGGTGCTGGGTTTTATTTTTTTATTTACTATCGGGGGTTGACTGGTGTATGTATCTAATTC
TAGGTTGGACATTATCTTGCATGATACTTATTATGTTGTTAGTCATTTTCATTATGTTT";

}

else if("Toxocara cati".equals(s))

{

q=
"GATTTTTGGGCATCCTGAGGTTATATTTTGATTTTACCTGCCTTTGGTATTATTAGTCAAAGTAGTTTATATTTAACTGGTA
AGAAGGAGGTTTTGGTCTTTGGGCATGGTCTATGCTATTTTGGTATTGGTTGATTGGTTGTGTGGTGTGAGCTCACCACA
TGTATACTGTTGGTATAGACTTGGATTCTCGGGCTATTTTACTGCGGCTACTATGGTTATCGCTGTGCCTACGGGTGTTAAGG
TTTTAGTTGGTTGGCTACTCTTTTGGTATAAAAAATGGTTTTTCAACCTTTGCTTTTGTGAGTGTGGGTTTTATTTTTTGT
ACTATTGGTGGGCTTACTGGAGTTATGCTTTCTAATTCTAGTTTGGATATTATTTGCATGACACCTATTATGTTGTGAGGCAT
TTCCACTATGTTT";

}

else if("Toxocara malaysiensis".equals(s))

{

q=
"GCTTTTGGTATTATTAGTCAGAGTAGTTTGTATTTAACTGGTAAAGAAGGAAGTTTTGGTTCGTTGGGGATGGTTTTATGCTAT
TTAAGTATTGGTTTGGTCTGTGTGGTTTGGGCTCATCATATGTATACCGTGGGTATAGATTGGATTCTCGGGCTTATTT
TACTGCGGCGACTATGGTTATTGCTGTGCCTACTGGTGTAAAGGTTTTAGTTGGTTGGCTACTCTTTTGGTATGAAAATGGT
TTTTAGCCTTTACTTTTATGGGTGTTAGGTTTTATTTCTGTGTTACTATTGGGGCCCTTACTGGTGTGATGCTTCTAATTCT
AGCCTTGATATTATTTGCATGATACTTATTATGTTGTTAGACATTTTCATTATGTTT";

}

else if("Taenia asiatica".equals(s))

{

q=
"GGTTTTGGTATGATTAGTCATATATGTTTAAAGAATAAGTATGTGTCCGGATGCTTTTGGTTTTTATGGTTTGTATTTGCTATG
TTTTCAATAGTATGTTTGGGAGAAGTGTGTGGGGTCATGATATGTTTACGGTTGGATTAGTTGTTAAGACTACTGTGTTTTT
AGTTCCGTTACTATGATAATAGGAGTACCAACAGGAATAAAGGTTTTTACTTGACTTTATATGCTTTTAAATTCTCGTGTA
AAAGAGGGATCCTATATTGTGGTGGATAGTTTCTTTTATAGTGTGTTTACCTTTGGTGGTGTGACTGGTATTGTGTTGCTG
TTGTGATTGGATAAAGTTTTGCATGATACTTGATT";

}

else if("Taenia crassiceps".equals(s))

{

q=
"GGTTTTGGAATTATTAGACATATTTGTTTAAAAATAAGTATGAATTGTGATTCTTTTGGTTTTTATGGATTGTTATTTGCTATG
TTTTCAATAGTTTGGTTAGGTAGGAGTGTGGGGTCATCATATGTTTACGGTTGGTTAGATGTTAAGACTGCTGTTTTTTTT
AGTTCTGTACTATGATTATAGGAGTACCTACAGGTATAAAGGTTTACTTGATTGTATATGCTTTTAAATTCGCGTGTGAA
CAAGAGTGATCCTATATTGTGGTGAATTGTTCTTTTATAGTTTTATTTACGTTTGGTGGTGTACTGGAATAGTATTGTCTGC
TTGTGATTAGATAAAGTTCTTCATGATACTTGATT";

}

}

```

```

else if("Taenia hydatigena".equals(s))
{
    q=
"GGATTTGGAATTATTAGTCATATATGTTTGAGAATAAGTATGAGTCCTGATGCCTTTGGGTTCTATGGATTATTATTTGCTAT
GTTTTCAATAGTCTGTTTGGGTAGAAAGTGTGTGGGGTCATCATATGTTTACTGTTGGGTTAGATGTTAAGACTGCTGTTTTTTT
TAGTTCTGTGACTATGATTATAGGTGTGCCTACTGGTATAAAGGTGTTTACTTGGTTATATATGCCTTTAAACTCTCATGTGAA
TAAGAGTGATCCTGTTGTTTGATGAATTGTTTCTTTTATAGTTTGTACTTTTGGTGGGGTTACTGGTATTGTGTGTCAGCA
TGTGTATTAGATAAAGTCTTCATGATACCTGATT";
}

else if("Taenia krepkogorski".equals(s))
{
    q=
"GGATTTGGTATAATTAGTCATATATGTTTAAAGAATAAGTATGTCTTCTGATGTGTTTGGGTTTTATGGTTTATTATTTGCTATG
TTTTCTATAGTTTGTAGGAAGAAGAGTGTGAGGTCATCACATGTTTACTGTTGGTTTAGATGTTAAGACTGCTGTGTTTTTT
AGCTCAATFACTATGATTATTGGTGTGCCTACTGGGATTAAGGTTTTACATGATTATATATGTTATTAAATGCTCGAGTAAA
AAAGAGTGATCCTGTGTTGTGGTGAATTGTTTCATTTATAATATTGTTTACATTTGGTGGAGTTACTGGTATAGTATTGTCTGC
TTGTGTTTTAGATAAAGTGTACATGATACTTGGTTT";
}

else if("Taenia laticollis".equals(s))
{
    q=
"GGATTTGGTATAATTAGACATATATGTTTAAAGTATTAGTATGTGTTCCGGATGCCTTCGGTTTTATGGTTTATTATTTGCTATG
TTTTCTATTGTTTGTAGGGAGAAGAGTTTGGGGTCATCATATGTTTACAGTTGGGTTAGATGTTAAGACTGCTGTATTTTT
AGTTCTGTAACATGATTATTGGTGTACCTACAGGTATAAAGGTTTTTACATGATTATATATGCCTTTAAATTCGGGTTAAA
AAGAGTGATCCTGTATTATGGTGGATAGTTTCTTTTATAGTTTTGTTTACGTTTGGTGGTGTACAGGAATAGTGTGTCTGCT
TGCGTATTAGATAAAGTATTACATGATACTTGATT";
}

else if("Taenia madoquae".equals(s))
{
    q=
"GGTTTTGGGATAATTAGTCATATATGTTTGAGGATTAGTATGTGTCCTGATGCCTTTGGTTTTTATGGTTTGTATTGCTATG
TTCTCAATAGTGTGTTTGGGAAGGAGTGTATGAGGTCATCACATGTTTACGTTGGATTAGATGTTAAGACTGCTGTATTTTT
TAGTTCCGGTTACTATGATAATAGGAGTACCTACAGGAATAAAGGTTTTTACTTGACTTTATATGCTTTTAAATTCCTGTTGA
ATAAGAGTGATCCTGTGTTATGATGGATAGTTTCTTTTATAGTATTGTTTACTTTTGGTGGTGTAACTGGTATTGTATTATCTG
CTTGTTGATTGGATAATGTTTACATGATACTTGATT";
}

else if("Taenia martis".equals(s))
{
    q=
"GGTTTTGGTATAATTAGACATATTTGTCTAAATATAAGTATGAATTATGATTCTTTTGGTTTTTATGGTTTATTATTTGCTATG
TTTTCTATAGTTTGTGGTAGTAGTGTGTGGGGTCATCATATGTTTACTGTTGGATTAGATGTTAAGACTGCTGTTTTTTTC
AGTTCCAGTTACTATGATAATAGGTGTTCTACGGGTATAAAGGTTTTTACTTGATTATATATGCCTTTAAAATCTCGTGTGA
AAGAGTGATCCTGTATTATGGTGAATTGTTTCTTTTATTATTTGTTTACTTTTGGTGGTGTACTGGTATAGTGTATCTGCAT
GTGTTTTGGATAAAGTCTTCATGATACTTGATT";
}

else if("Taenia multiceps".equals(s))
{

```

```

q=
"GGTTTTGGTATAATTAGTCACATATGTTTAAAGAATAAGCATGTGTCCAGATGCTTTTGGTTTTATGGTTTATTATTTGCTATG
TTTTCAATAGTGTGTTTAGGGAGAAGTGTGTGAGGCCATCATATGTTTACAGTTGGGTTAGATGTTAAGACTGCTGTATTTTT
AGTTCCGGTTACTATGATAATAGGAGTGCCACAGGAATAAAGGTTTTACTTGGCTTTATATGCTTTTAAATTCCTCGTGTA
CAAGAGTGATCCTATACTATGATGAATAGTTCTTTTATAGTATTGTTTACTTTTGGTGGTGAACCTGGGATTGATTGTCTGC
TTGTATTAGATAAAGTTTTACATGATACTTGATT";

}

else if("Taenia mustelae".equals(s))

{

q=
"GGTTTTGGTATTATTGGTCATATATGTTTGAAGTATAAGGATGTGTTCTGATGCTTTTGGGTTTTATGGATTGTTGTTTGTATG
TTTTCTATTGTTTGTCTAGGTAGTAGAGTTTGAAGGCATCATATGTTTACTGTTGGTTTAGATGTTAAGACTGCTGTTTTTTA
GTTCTGTACTATGATTATAGGAGTTCCCTACTGGTATAAAGGTGTTTACTTGGTTGTATATGTTACTGAATTCAGTGTTAACA
AGAGGGATCCTGTGTTGTGATGAATAGTGCATTTATATTTTTGTTTACTTTTGGTGGTGTACTGGTATAGTTTTGTCTGCTT
GTGTATTAGATAATGTTTTGCATGATACTTGATT";

}

else if("Taenia ovis".equals(s))

{

q=
"GGATTTGGTATAATTAGTCATATTTGTTTGAAGATTAGTATGTGTCCAGATGCTTTTGGTTTTATGGCTTATTATTTGCTATG
TTTTCTATAGTATGTTTAGGAAGAAGTGTGTGGGGGCATCATATGTTTACTGTTGGTTGGATGTTAAGACGGCTGTATTTTT
AGTTCCGGTTACTATGATCATAGGTGTGCCTACTGGTATAAAGGTTTTACTTGGCTTTATATGCTTCTGAAATCCTCGTGGAAT
AAGAGTGATCCTATTTTGTGATGGATAGTTCTTTTATAGTATTATTTACTTTTGGAGGTGTGACTGGTATTGTTTTATCTGCTT
GTGTATTGGATAAAGTTCTTCATGATACTTGATT";

}

else if("Taenia parva".equals(s))

{

q=
"GGTTTTGGGATTATAAGACATATATGTTTAAAGAATTAGTATGTGTGATGATGCTTTTGGTTTTATGGTTTATTGTTGCTATGT
TTTTCTATTGTGTTTAGGAAGAAGTGTATGAGGCCATCATATGTTTACTGTAGGTTTAGATGTGAAGACTGCTGTGTTTTTTA
GTTCCAGTAACAATGATTATCGGGGTTCCCTACTGGGATAAAGGTTTTACTTGGATTATATGTTACTTAATTCCTGTTAATA
AGGGTGATCCTGTAATTTGATGAATGTTTCTTTTATAGTTTTATTTACGTTTGGTGGTGTACTGGTATAGTTTTATCAGCTT
GTGTTTTAGATAAAGTTTTGCATGATACTTGATT";

}

else if("Taenia pisiformis".equals(s))

{

q=
"GGGTTTGGTATAATTAGTCATATATGTTTAAAGAATAAGTATGTGTTCAGATGCGTTTGGTTTTATGGTTTATTGTTTGAAT
GTTTTCTATAGTTTGTAGGTAGAAAGTGTATGAGGTCATCATATGTTTACTGTTGGATTAGATGTAAAAGACCGCTGTGTTTTT
TAGTTCAGTAACAATGATAATTGGAGTACCTACTGGAATTAAGGTTTACATGACTTTATATGCTTTTAAATTCCTCGTGTA
AAAAGAGTGATCCTGTGTTGTGGTGAATAATTTCTTTTATAGTCTTATTTACTTTTGGAGGTGAACCTGGTATAGTATTATCTG
CTTGTGTTTTAGATAAAGTTTACATGATACTTGATT";

}

else if("Taenia saginata".equals(s))

{

q=
"GGTTTTGGTATGATTAGTCATATATGTTTAAAGAATAAGTATGTGTCCAGATGCTTTTGGTTTTATGGTTTGTGTTTGTATG
TTTTCAATAGTGTGTTTGGGGAGAAGTGTGTGGGGTCATCATATGTTTACGGTTGGGTTAGATGTTAAGACTGCTGTGTTTTT
AGTTCCGGTTACTATGATAATAGGAGTACCAACAGGAATAAAGGTTTTACTTGACTTTATATGCTTTTAAATTCCTCGTGTA

```

```

TAAGAGTGATCCTATATTGTGGTGAATAGTTTCTTTTATAGTGTGTTTACTTTTGGTGGTGTGACTGGTATTGTGTTGCTGC
TTGCGTATTGGATAAAGTTTTGCATGATACTTGATT";

    }

    else if("Taenia serialis".equals(s))

    {

        q=
"GGTTTTGGTATAATTAGTCATATATGTTTAAAGAATAAGTATGTGTCCAGACGCTTTTGGTTTTATGGTTTTGTTATTTGCTATG
TTCTCAATAGTGTGTTTAGGAAGGAGTGTATGGGGTCATCATATGTTTACAGTTGGGTTAGATGTTAAGACTGCTGTATTTTT
AGTTCAGTTACTATGGTAATAGGAGTACCAACAGGAATAAAGGTTTTTACTTGGCTTTATATGTTATTAATAATCTCGTGTGAA
TAAGAGTGATCCTATATTGTGGTGGATAGTTTCTTTTATAGTATTGTTTACTTTTGGTGGTGTAACTGGGATTGTATTGTCTGC
TTGTGTGTTGGATAAAGTTTTACATGATACTTGTT";

    }

    else if("Taenia solium".equals(s))

    {

        q=
"GGGTTTGGTATAATTAGTCATATATGTTTGAAGTATAAGTATGTGTCTGATGCTTTTGGCTTTTATGGGTTATTGTTTGTATG
TTTTCAATAGTATGTTTAGGAAGAAGTGTGTGAGGACATCATATGTTTACGGTTGGGTTAGATGTTAAGACTGCTGTATTTTT
TAGTTCTGTTACTATGATAATTGGAGTGCCTACGGGGATTAAGGTTTTTACTTGGCTTTATATGCTTTTAAAAATCTCGTGTAA
TAAGAGTGATCCGGTTTTATGATGAATAATTTTCGTTTATAGTATTGTTTACATTTGGTGGTGTAAACCGGTATTATTCTATCTGC
TTGTATTAGATAAAGTTCTTCATGATACTTGTT";

    }

    else if("Taenia twitchelli".equals(s))

    {

        q=
"GGTTTTGGTATAATTAGACATATTTGTTTAAATGTAAGTATGAATTATGATTCTTTTGGATTTTATGGTTTTGTTATTTGCTATG
TTTTCTATAGTTTGTAGGTAGAAAGTGTATGAGGTCATCATATGTTTACTGTTGGATTAGATGTTAAGACTGCTGTTTTTTTT
AGTTCTGTTACTATGATTATAGGGTTCTACAGGTATAAAGGTGTTTACTTGGTTATATATGCTTTTAAAAATCTCGTGTAAAT
AAGAGTGATCCTGTTTATGATGAATTGTGTCTTTTATTATTTGTTTACTTTTGGTGGTGTACTGGTATAGTGTATCTGCGT
GTGTTTTGGATAAAGTTCTTCATGATACTTGTT";

    }

    else if("Taeniopygia guttata".equals(s))

    {

        q=
"GGTTTCGGCATCATCTCCCACGTCGTAACCTACTATTTCAGGTAAAAAAGAACCATTTCGGATATATAGGAATAGTATGAGCTA
TGCTATCCATCGGATTCTTAGGATTCATCGTATGAGCCCACCACATGTTTACAGTAGGAATGGACGTAGACACCCGAGCATA
CTTTACATCCGCCACTATAATCATCGCCATCCCAACCGGCATCAAAGTATTTCAGCTGACTAGCAACTCCACGGAGGCACA
ATCAAGTGAGACCCACCAATACTATGAGCTCTAGGATTTATCTTCTATTCCATCGGAGGCCTAACCGGAATCGTCTGGC
CAACTCCTCACTAGACATCGCCCTACACGACACCTACTACGTAGTAGCCCACTTCCACTACGTCCTATCAATAGGAGCAGTGT
TTGCAATCCTAGCAGGATTCACCCACTGATT";

    }

    double AA=0,AC=0,AG=0,AT=0,CA=0,CC=0,CG=0,CT=0,GA=0,GC=0,GG=0,GT=0,TA=0,TC=0,TG=0,TT=0;

    double length = q.length();

    for(int i=0;i<length-1;i++)

    {

```

```

if(q.charAt(i)=='A')
{
    if(q.charAt(i+1)=='A')
    {
        AA++;
    }
    else if(q.charAt(i+1)=='C')
    {
        AC++;
    }
    else if(q.charAt(i+1)=='G')
    {
        AG++;
    }
    else if(q.charAt(i+1)=='T')
    {
        AT++;
    }
}
else if(q.charAt(i)=='C')
{
    if(q.charAt(i+1)=='A')
    {
        CA++;
    }
    else if(q.charAt(i+1)=='C')
    {
        CC++;
    }
    else if(q.charAt(i+1)=='G')
    {
        CG++;
    }
    else if(q.charAt(i+1)=='T')
    {

```



```
        CT++;
    }
}
else if(q.charAt(i)=='G')
{
    if(q.charAt(i+1)=='A')
    {
        GA++;
    }
    else if(q.charAt(i+1)=='C')
    {
        GC++;
    }
    else if(q.charAt(i+1)=='G')
    {
        GG++;
    }
    else if(q.charAt(i+1)=='T')
    {
        GT++;
    }
}
else if(q.charAt(i)=='T')
{
    if(q.charAt(i+1)=='A')
    {
        TA++;
    }
    else if(q.charAt(i+1)=='C')
    {
        TC++;
    }
    else if(q.charAt(i+1)=='G')
    {
        TG++;
    }
}
```

```
    }  
    else if(q.charAt(i+1)=='T')  
    {  
        TT++;  
    }  
}  
}
```

```
AA=AA/length;
```

```
AC=AC/length;
```

```
AG=AG/length;
```

```
AT=AT/length;
```

```
CA=CA/length;
```

```
CC=CC/length;
```

```
CG=CG/length;
```

```
CT=CT/length;
```

```
GA=GA/length;
```

```
GC=GC/length;
```

```
GT=GT/length;
```

```
GG=GG/length;
```

```
TA=TA/length;
```

```
TC=TC/length;
```

```
TG=TG/length;
```

```
TT=TT/length;
```

```
AA=AA*10000;
```

```
AA=Math.round(AA);
```

```
AA=AA/10000;
```

```
AC=AC*10000;
```

```
AC=Math.round(AC);
```

```
AC=AC/10000;
```

```
AG=AG*10000;
```

```
AG=Math.round(AG);
```

```
AG=AG/10000;
```

```
AT=AT*10000;
```

```
AT=Math.round(AT);
AT=AT/10000;
CA=CA*10000;
CA=Math.round(CA);
CA=CA/10000;
CC=CC*10000;
CC=Math.round(CC);
CC=CC/10000;
CG=CG*10000;
CG=Math.round(CG);
CG=CG/10000;
CT=CT*10000;
CT=Math.round(CT);
CT=CT/10000;
GA=GA*10000;
GA=Math.round(GA);
GA=GA/10000;
GC=GC*10000;
GC=Math.round(GC);
GC=GC/10000;
GG=GG*10000;
GG=Math.round(GG);
GG=GG/10000;
GT=GT*10000;
GT=Math.round(GT);
GT=GT/10000;
TA=TA*10000;
TA=Math.round(TA);
TA=TA/10000;
TC=TC*10000;
TC=Math.round(TC);
TC=TC/10000;
TG=TG*10000;
TG=Math.round(TG);
TG=TG/10000;
```

```

TT=TT*10000;

TT=Math.round(TT);

TT=TT/10000;

    JFrame res= new JFrame("Dinucleotide frequency"+" "+s);

res.setSize(420,200);

res.setLayout(null);

res.setLocationRelativeTo(null);

JLabel f =new JLabel();

f.setText(" AA");

f.setSize(50,50);

f.setFont(f.getFont().deriveFont(14.0f));

JLabel f1 =new JLabel();

f1.setText(" AC");

//f1.setSize(50,50);

f1.setBounds(0,30,50,50);

f1.setFont(f1.getFont().deriveFont(14.0f));

JLabel f2 =new JLabel();

f2.setText(" AG");

f2.setBounds(0,60,50,50);

f2.setSize(50,50);

f2.setFont(f2.getFont().deriveFont(14.0f));

JLabel f3 =new JLabel();

f3.setText(" AT");

f3.setSize(50,50);

f3.setBounds(0,90,50,50);

f3.setFont(f3.getFont().deriveFont(14.0f));

JLabel f4 =new JLabel();

f4.setText(" CA");

f4.setBounds(200,0,50,50);

f4.setSize(50,50);

f4.setFont(f4.getFont().deriveFont(14.0f));

JLabel f5 =new JLabel();

f5.setText(" CC");

f5.setBounds(200,30,50,50);

f5.setSize(50,50);

```

```
f5.setFont(f5.getFont().deriveFont(14.0f));

JLabel f6 =new JLabel();

f6.setBounds(200,60,50,50);

f6.setText(" CG");

f6.setSize(50,50);

f6.setFont(f6.getFont().deriveFont(14.0f));

JLabel f7 =new JLabel();

f7.setText(" CT");

f7.setBounds(200,90,50,50);

f7.setSize(50,50);

f7.setFont(f7.getFont().deriveFont(14.0f));

JLabel f8 =new JLabel();

f8.setText(" GA");

f8.setBounds(100,0,50,50);

f8.setSize(50,50);

f8.setFont(f8.getFont().deriveFont(14.0f));

JLabel f9 =new JLabel();

f9.setText(" GC");

f9.setBounds(100,30,50,50);

f9.setSize(50,50);

f9.setFont(f9.getFont().deriveFont(14.0f));

JLabel f10 =new JLabel();

f10.setText(" GG");

f10.setBounds(100,60,50,50);

f10.setSize(50,50);

f10.setFont(f10.getFont().deriveFont(14.0f));

JLabel f11 =new JLabel();

f11.setText(" GT");

f11.setBounds(100,90,50,50);

f11.setSize(50,50);

f11.setFont(f11.getFont().deriveFont(14.0f));

JLabel f12 =new JLabel();

f12.setText(" TA");

f12.setBounds(300,0,50,50);

f12.setSize(50,50);
```

```

f12.setFont(f12.getFont().deriveFont(14.0f));

JLabel f13 =new JLabel();

f13.setText(" TC");

f13.setBounds(300,30,50,50);

f13.setSize(50,50);

f13.setFont(f13.getFont().deriveFont(14.0f));

JLabel f14 =new JLabel();

f14.setText(" TG");

f14.setBounds(300,60,50,50);

f14.setSize(50,50);

f14.setFont(f14.getFont().deriveFont(14.0f));

JLabel f15 =new JLabel();

f15.setText(" TT");

f15.setBounds(300,90,50,50);

f15.setSize(50,50);

f15.setFont(f15.getFont().deriveFont(14.0f));

String s1 = String.valueOf(AA);

String s2 = String.valueOf(AC);

String s3 = String.valueOf(AG);

String s4 = String.valueOf(AT);

String s5 = String.valueOf(CA);

String s6 = String.valueOf(CC);

String s7 = String.valueOf(CG);

String s8 = String.valueOf(CT);

String s9 = String.valueOf(GA);

String s10 = String.valueOf(GC);

String s11 = String.valueOf(GG);

String s12 = String.valueOf(GT);

String s13 = String.valueOf(TA);

String s14 = String.valueOf(TC);

String s15 = String.valueOf(TG);

String s16 = String.valueOf(TT);

JTextField A1,A2,A3,A4,A5,A6,A7,A8,A9,A10,A11,A12,A13,A14,A15,A16;

A1 = new JTextField(s1);

A1.setBounds(40,15,50,25);

```

```
A1.setEditable(false);

res.add(A1);

A2 = new JTextField(s2);
A2.setBounds(40,45,50,25);
A2.setEditable(false);
res.add(A2);

A3 = new JTextField(s3);
A3.setBounds(40,75,50,25);
A3.setEditable(false);
res.add(A3);

A4 = new JTextField(s4);
A4.setBounds(40,105,50,25);
A4.setEditable(false);
res.add(A4);

A5 = new JTextField(s5);
A5.setBounds(240,15,50,25);
A5.setEditable(false);
res.add(A5);

A6 = new JTextField(s6);
A6.setBounds(240,45,50,25);
A6.setEditable(false);
res.add(A6);

A7 = new JTextField(s7);
A7.setBounds(240,75,50,25);
A7.setEditable(false);
res.add(A7);

A8 = new JTextField(s8);
A8.setBounds(240,105,50,25);
A8.setEditable(false);
res.add(A8);

A9 = new JTextField(s9);
A9.setBounds(140,15,50,25);
A9.setEditable(false);
res.add(A9);

A10 = new JTextField(s10);
```

```
A10.setBounds(140,45,50,25);

A10.setEditable(false);

res.add(A10);

A11 = new JTextField(s11);

A11.setBounds(140,75,50,25);

A11.setEditable(false);

res.add(A11);

A12 = new JTextField(s12);

A12.setBounds(140,105,50,25);

A12.setEditable(false);

res.add(A12);

A13 = new JTextField(s13);

A13.setBounds(340,15,50,25);

A13.setEditable(false);

res.add(A13);

A14 = new JTextField(s14);

A14.setBounds(340,45,50,25);

A14.setEditable(false);

res.add(A14);

A15 = new JTextField(s15);

A15.setBounds(340,75,50,25);

A15.setEditable(false);

res.add(A15);

A16 = new JTextField(s16);

A16.setBounds(340,105,50,25);

A16.setEditable(false);

res.add(A16);

res.add(f);

res.add(f1);

res.add(f2);

res.add(f3);

res.add(f4);

res.add(f5);

res.add(f6);

res.add(f7);
```



```

res.add(f8);

res.add(f9);

res.add(f10);

res.add(f11);

res.add(f12);

res.add(f13);

res.add(f14);

res.add(f15);

res.setVisible(true);
}

```

```

private void jComboBox1ActionPerformed(java.awt.event.ActionEvent evt) {

    // TODO add your handling code here:

    s = (String) jComboBox1.getSelectedItem();

}

```

```

private void jButton2ActionPerformed(java.awt.event.ActionEvent evt) {

    // TODO add your handling code here:

    String q="";

    if("Angiostrongylus cantonensis".equals(s))

    {

        q=
"GCTTTTGGGATTGTTAGACAGTCTACTTTATATTTAACGGGTAAAAAAGAGGTTTTTGGTTATTTGGGTATGGTTTATGCTAT
TTTAAGAATTGGTTTGATTGGTTGTGTGGTTTGGGCTCATCATATATACGGTTGGTATGGATTTAGATTCTCGTGCTTATTT
TACTGCGCTACTATAGTTATTGCGGTTCCCTACGGGAGTGAAGGTTTTTAGGTGGTTGGCAACTTTATTTGGTATAAAGATAT
TGTTTCAACCTATTTTATTGTGGTTTTGGTTTTATTTTTTTATTTACTATCGGTGGGTTAACGGGGTTATATTGTCTAATTC
TAGTTTGGATATTATTTACATGATACTTATTATGTAGTTAGGCATTTTCATTATGTTT";

    }

    else if("Angiostrongylus costaricensis".equals(s))

    {

        q=
"GCTTTTGGGATTATTAGTCAATCTGCTTTGTATTTGTACAGGAAGAAAAGAGGTTTTTGGTTATTTAGGGATGGTTTATGCGAT
TTTAAGAATTGGTTTGATTGGGTGTGTAGTTTGAGCTCATCATATGTATACTGTTGGTATGGATTTGGATTCTCGTGCTTACTT
TACTGACGCTACAATAGTTATTGCGGTTCCCTACTGGGGTTAAAGTGTTTAGTTGGTTGGCTACACTTTATGGGATGAAAATGA
TGTTTCAGCCGATTTTGTGTGGGTTATGGGGTTTTATTTTTTTGTTTACTATTGGGGGTTTGACCGGGGTTATGTTATCTAATTC
AAGTTTGGATATTATTTGCATGATACTTATTATGTGGTT";

    }

    else if("Angiostrongylus vasorum".equals(s))

```

```

{
    q=
"GCTTTTGGGATTGTTAGTCAGTCGACTTTATATTTGACTGGGAAGAAGGAGGTGTTTGGTTATTTGGGGATGGTTTATGCGAT
TTTAAGGATTGGTTTGGATTGGTTGTGTGGTGAGCTCATCATATGTAATACTGTTGGTATAGATTTAGATTCTCGTGCTTATTT
TACTGCCGCTACTATGGTGATTGCCGTGCCGACTGGAGTGAAGGTTTTTAGTTGGTTGGCTACTTTGTTGGGATGAAGTATA
GTATTTACAGCCTATTTTGGTTGGGTTATAGGATTTATTTTTTTTTTATTTACTATTGGGGGTTTACGGGTGTGATATTGTCAA
TTCGAGATTGGATATTATTTTACATGATACGTATTATGTGGTAAGTCATTTTCATTATGTGAGGTTGTTTCATGATACTTGGTT
T";
}

else if("Diplogonoporus balaenopterae".equals(s))
{
    q=
"GGGTTTGGAAATGATTAGACATGTTTGTAGTAACCTAGGTTGTTTCATATGATACTTTTGGATTTTATGGTTTATTATTTGCTATG
TTTTCTATCGTTTGTCTTGGTAGGGTTGTATGGGGTCATCATATGTTTACGGTAGGTTTAGATGTGAAGACAGCTGTTTTTTTT
AGGTCAGTFACTATGATTATAGGGGTGCCTACTGGAATAAAGGTGTTTTCTTGGCTGTATATGATTTTAAAAAGTCGTGTCTC
TTTGGCGTGAACCTATAATTTGGTGGGTGTTATCTTTTATCGTGCTGTTTACAATAGGGGGTGTACTGGTATTATACTTTCTGC
TTGTGTTCTTGATAATATTTTGCATGATACTTGATTT";
}

else if("Diplogonoporus grandis".equals(s))
{
    q=
"GGGTTTGGAAATGATTAGACATGTTTGTAGTAACCTAGGTTGTTTCATATGATACTTTTGGATTTTATGGTTTATTATTTGCTATG
TTTTCTATCGTTTGTCTTGGTAGGGTTGTATGGGGTCATCATATGTTTACGGTAGGTTTAGATGTGAAGACAGCTGTTTTTTTT
AGGTCAGTFACTATGATTATAGGGGTGCCTACTGGAATAAAGGTGTTTTCTTGGCTGTATATGATTTTAAAAAGTCGTGTCTC
TTTGGCGTGAACCTATAATTTGGTGGGTGTTATCTTTTATCGTGCTGTTTACAATAGGGGGTGTACTGGTATTATACTTTCTGC
TTGTGTTCTTGATAATATTTTGCATGATACTTGATTT";
}

else if("Aelurostrongylus abstrusus".equals(s))
{
    q=
"GCTTTTGGTATTGTTAGTCAGTCTACTTTGTATTTGACGGGAAGAAGGAAGTTTTTGGTTATTTAGGGATAGTTTATGCTAT
TATAAGTATTGGTTTAAATTGGTTGTGTGTTTGGGCTCATCATATATACTGTTGGTATAGATTTGGATTCTCGTGCTTATTTT
ACGGCGGCTACGATGGTTATTGCTGTGCCAACGGGTGTTAAGGTTTTTAGTTGGTTGGCTACTTTATTTGGAATGAAGATAGT
GTTTCAGCCGGTTTTGTTGTGGGTTTTGGGTTTTATTTTTTTGTTACTATTGGGGGGTTAACTGGGGTCATGCTTTCGAATTCT
AGTTTGGATATTATTTTGCATGATACTTATTATGTGGTTAGTCATTTTCATTATGTGTTGAGTTT";
}

else if("Dictyocaulus eckerti".equals(s))
{
    q=
"GCTTTTGGTATTATTAGTCAGTCAACTTTGTATTTAACTGGTAAAAAGGAGGTTTTTGGTTCTTTGGGTATGGTTTATGCTATT
TTAAGTATTGGTTTAAATTGGTTGTGTAGTATGAGCACATCATATATACTGTTGGAATAGATTTGGATTTCGCGTGCTTATTTT
ACTGCTGCTACTATGGTAAATTGCTGTTCTACGGGTGTA AAAAGTTTTTAGTTGGTTGGCTACTTTGTATGGTTTAAAAATAGTA
TATAATCCTTTGTGTTATGGGTTTTGGGTTTTATTTTTTTTATTTACTATTGGGGGGTTAACTGGAGTTATTTTGTCAAATTTCTA
GTTTAGATATTTTGTACATGATACTTATTATGTTGTAAGGCATT";
}

else if("Dictyocaulus viviparus".equals(s))
{

```

```
q=  
"GCTTTTGGTATTATTAGACAATCTACTTTGTATTTAACTGGTAAAAAAGAGGTTTTTGGTCTTTGGGTATGGTTTATGCTATT  
TTAAGTATTGGTTTAAATTGGTTGTGTTGTGGGCACATCATATGTATACTGTTGGGATGGATTTGGATTTCGCGTGCTTATTTT  
ACTGCTGCTACTATAGTAATTGCTGTTCTACTGGAGTTAAGGTTTTTAGATGATTGGCTACTTTATATGGATTGAAAATGGTT  
TATAATCCTTTGTTGTTGTGAGTTTTAGGTTTTATTTTTTGTTTACTATTGGTGGTTAACTGGTGTTATTTTGTCAAATTCTA  
GTCTTGATATTTTGTTCATGATACTTATTAT";
```

```
}
```

```
else if("Ascaris lumbricoides".equals(s))
```

```
{
```

```
q=  
"GCTTTTGGTATTATTAGTCAGAGTAGTTTGTATTTGACTGGTAAAAAGGAGGTTTTTGGGCTTTGGGTATGGTTTATGCTAT  
TTTAAAGTATTGGTTTGAATTGGTTGTGTTGTTGAGCTCATCATATGTATACTGTTGGTATGGATCTTGATTCTCGGGCTTATTTT  
ACTGCTGCAACTATGGTTATTGCTGTTCTACTGGTGTTAAGGTTTTAGTTGGTTGGCTACCTGTTTGGTATAAAAATGGTT  
TTTCAGCCTTTACTTTTATGAGTTATGGGTTTTATTTTTTGTTTACTATTGGTGGGTTAACCGGGGTTATACTTTCTAATTCTA  
GTTTGGATATTATCTTGCATGATACTTATTATGTTGTTAGTCATTTTCATTATGTTCTTAGTTT";
```

```
}
```

```
else if("Ascaris suum".equals(s))
```

```
{
```

```
q=  
"GCTTTTGGTATTATTAGTCAGAGTAGTTTGTATCTGACTGGTAAAAAGGAGGTTTTTGGGCTTTGGGTATGGTTTATGCTAT  
TTTGAGTATTGGTTTAAATTGGTTGTGTTGTTGAGCTCATCATATGTATACTGTTGGTATGGATCTTGACTCTCGGGCTTATTTT  
ACTGCTGCAACTATGGTTATTGCTGTTCTACTGGTGTTAAGGTTTTAGTTGGTTGGCTACCTGTTTGGTATAAAGATGGTT  
TTTCAACCTTTACTTTTATGAGTTATGGGTTTTATTTTTTGTTTACTATTGGTGGGTTAACCGGGGTTATGCTTTCTAATTCTA  
GTTTGGATATTATCTTGCATGATACTTA-TTATGTTGTTAGTCATTTTCATTATGTCCTTAGTTT";
```

```
}
```

```
else if("Baylisascaris ailuri".equals(s))
```

```
{
```

```
q=  
"GCTTTTGGTATTATTAGCCAGAGTAGGTTGTATTTAACTGGTAAAAAGGAAGTTTTTGGTCTTTGGGTATGGTTTATGCTAT  
TTTGAGTATTGGTTTAAATTGGTTGTGTTGTTGGGCTCATCATATGTATACTGTAGGTATGGATTTGGATTCTCGTGCTTATTTT  
ACTGCGGCTACTATGGTTATTGCGGTCCTACGGGTGTTAAGGTTTTAGTTGGTTGGCTACTTTGTTTGGTATGAAGATGGTG  
TTCCAGCCTTTACTTTTGTGAGTTATGGGTTTTATTTTTTATTTACTATTGGCGGATTGACTGGGGTGATGCTTTCTAATTCTA  
GTTTGGATATTATTTGCATGATACTTA-TTATGTTGTTAGACATTTTCATTATGTTCTTAGTTT";
```

```
}
```

```
else if("Baylisascaris procyonis".equals(s))
```

```
{
```

```
q=  
"GCTTTTGGTATTATTAGCCAAAGTAGGTTGTATTTAACTGGTAAAGAAGGAAGTTTTTGGTCTTTGGGAATGGTTTATGCTAT  
TTTGAGTATTGGTTTGAATTGGATGTGTGGTTTGGGCTCATCATATGTATACTGTGGGTATGGATTTGGATTCTCGGGCTTATTT  
TACTGCGGCTACTATGGTTATTGCGGTTCTACGGGAGTTAAGGTTTTAGTTGGTTGGCCACTTTATTTGGTATGAAGATAGT  
GTTTCAGCCTTTGCTTTTGTGGGTTATGGGTTTTATTTTTTGTTTACTATTGGTGGTTGACTGGGGTTATGCTTTCTAATTCT  
AGTTTGGATATTATTTGCATGATACTTATTATGTTGTTAGGCATTTTCATTATGTTCTTAGTTT";
```

```
}
```

```
else if("Baylisascaris schroederi".equals(s))
```

```
{
```

```
q=  
"GCTTTTGGTATTATTAGTCAGAGTAGGTTGTATCTGACTGGTAAAGAAGGAGGTTTTTGGTCTTTGGGTATGGTTTACGCAAT  
TTTGAGTATTGGTTTGAATTGGTTGTGTTGTTGAGCTCATCATATGTATACTGTGGGTATAGATTTGGATTCTCGTGCTTATTTT  
ACTGCGGCTACTATGGTTATCGCAGTTCTACGGGTGTTAAGGTTTTAGTTGGTTGGCTACTTTGTTTGGTATGAAGATGGTG
```

```

TTCAGCCTTTGCTTTTGTGGTTATAGGATTTATTTTTTTGTTACTATTGGTGGATTGACTGGGGTGATGCTTCTAATTCTA
GTTTGGATATTATTTGCATGATACTTA-TTATGTTGTTAGGCATTTTCATTATGTTCTTAGTT";

}

else if("Baylisascaris transfuga".equals(s))

{

q=
"GCTTTTGGTATTATTAGTCAGAGTAGATTGTATTTAACTGGTAAAAAGGAGGTTTTTGGTCTTTGGGTATGGTTTATGCTAT
TTTGGATTTGGTTAAATTTGGTTGTGTTGTTGGGCTCATCATATGTATACTGTAGGTATGGATTGGATTCTCGTGCTTATTT
ACTGCGGCTACTATGGTTATTGCGGTTCCACAGGTGTTAAGGTTTTTAGTTGGTTGGCCACTTTGTTGGTATGAAGATGGTG
TTTACGCTTTACTTTTGTGGTTATGGGGTTATTTTTTTTATTACTATTGGTGGATTGACTGGGGTGATGCTTCTAATTCTA
GTTTGGATATTATTTGCATGATACTTATTATGTTGTTAGGCATTTTCATTATGTTCTTAGTT";

}

else if("Toxocara canis".equals(s))

{

q=
"GCTTTTGGTATTATTAGGCAAAGTAGTTTGTATTTGACTGGTAAAAAGGAGGTTTTTGGTCTTTAGGCATGGTTTATGCTAT
TTTAAGTATTGGTCTGATTGGCTGTGATTTGGGCTCACCATATGTATACGGTGGGCATGGATTGGATTCTCGTGCTTATTT
TACTGCGGCAACGATGGTTATTGCTGTGCCTACGGGGGTTAAGGTTTTTAGTTGGTTAGCCACTCTTTTTGGTATGAAGATGG
TGTTTCAACCTTTGCTTTTGTGGGTGCTGGGTTTTATTTTTTTATTTACTATCGGGGGGTTGACTGGTGTATGTTATCTAATTC
TAGGTTGGACATTATCTTGCATGATACTTATTATGTTGTTAGTCATTTTCATTATGTT";

}

else if("Toxocara cati".equals(s))

{

q=
"GATTTTTTGGGCATCCTGAGGTTTATATTTTGATTTTACCTGCCTTTGGTATTATTAGTCAAAGTAGTTTATATTTAACTGGTA
AGAAGGAGGTTTTTGGTCTTTGGGCATGGTCTATGCTATTTGAGTATTGGTTTGGATTGGTTGTGTTGGTGTGAGCTCACCACA
TGTATACTGTTGGTATAGACTTGGATTCTCGGGCTATTTTACTGCGGCTACTATGGTTATCGCTGTGCCTACGGGTGTTAAGG
TTTTTAGTTGGTTGGCTACTCTTTTTGGTATAAAAAATGGTTTTTCAACCTTTGCTTTTGTGAGTGTGGGTTTTATTTTTTGT
ACTATTGGTGGGCTTACTGGAGTTATGCTTCTAATTCTAGTTTGGATATTATTTGCATGACACCTATTATGTTGTGAGGCAT
TTCCACTATGTT";

}

else if("Toxocara malaysiensis".equals(s))

{

q=
"GCTTTTGGTATTATTAGTCAGAGTAGTTTGTATTTAACTGGTAAAGAAGGAAGTTTTTGGTCTGTTGGGATGGTTTATGCTAT
TTTTAGTATTGGTTTGGATTGGCTGTGTTGGTTGGGCTCATCATATGTATACCGTGGGTATAGATTGGATTCTCGGCTTATTT
TACTGCGGCGACTATGGTTATTGCTGTGCCTACTGGTGTAAAGGTTTTTAGTTGGTTGGCTACTCTTTTTGGTATGAAAATGGT
TTTTACGCTTTACTTTTATGGGTGTTAGGTTTTATTTCTTGTTTACTATTGGGGGCCCTTACTGGTGTGATGCTTCTAATTCT
AGCCTTGATATTATTTGCATGATACCTATTATGTTGTTAGACATTTTCATTATGTT";

}

else if("Taenia asiatica".equals(s))

{

q=
"GGTTTTGGTATGATTAGTCATATATGTTTAAAGAATAAGTATGTGTCCGGATGCTTTTGGTTTTTATGGTTTGTATTGCTATG
TTTTCAATAGTATGTTTGGGGAGAAGTGTGTGGGGTCAATGATATGTTTACGGTTGGATTAGTTGTTAAGACTACTGTGTTTTTT
AGTTCCGGTACTATGATAATAGGAGTACCAACAGGAATAAAGGTTTTTACTTGACTTTTATATGCTTTTTAAATTCCTCGTGAAA
TAAGAGGGATCCTATATTGTTGGATAGTTTCTTTTATAGTGTGTTTACCTTTGGTGGTGTGACTGGTATTGTTGTGCTGTC
TTGTGATTGGATAAAGTTTTGCATGATACTTGAATTT";

}

```

```

else if("Taenia crassiceps".equals(s))
{
    q=
"GGTTTTGGAATTATTAGACATATTTGTTTAAAAATAAGTATGAATTGTGATTCTTTTGGTTTTTATGGATTGTTATTTGCTATG
TTTTCAATAGTTTTGTTTAGGTAGGAGTGTGGGGTCATCATATGTTTACGGTTGGTTTAGATGTTAAGACTGCTGTTTTTTTT
AGTTCGTACTATGATTATAGGAGTACCTACAGGTATAAAGGTGTTTACTTTGATTGTATATGCTTTTAAATTCGCGTGTGAA
CAAGAGTGATCCTATATTGTGGTGAATTGTTCTTTTATAGTTTTATTTACGTTTGGTGGTGTACTGGAATAGTATTGTCTGC
TTGTGATTAGATAAAGTTCTTCATGATACTTGATTT";
}

else if("Taenia hydatigena".equals(s))
{
    q=
"GGATTTGGAATTATTAGTCATATATGTTTGAAGAATAAGTATGAGTCCTGATGCTTTTTGGGTTCTATGGATTATTATTTGCTAT
GTTTTCAATAGTCTGTTTGGGTAGAAGTGTGTGGGGTCATCATATGTTTACTGTTGGTTAGATGTTAAGACTGCTGTTTTTTTT
TAGTTCTGTGACTATGATTATAGGTGTGCCTACTGGTATAAAGGTGTTTACTTGGTTATATATGCTTTTAAACTCTCATGTGAA
TAAGAGTGATCCTGTTGTTGATGAATTGTTCTTTTATAGTTTTGTTTACTTTTTGGTGGGGTTACTGGTATTGTGTGTGTCAGCA
TGTGTATTAGATAAAGTTCTTCATGATACCTGATTT";
}

else if("Taenia krepkogorski".equals(s))
{
    q=
"GGATTTGGTATAATTAGTCATATATGTTTAAAGAATAAGTATGCTTCTGATGTGTTTGGGTTTTATGGTTTATTATTTGCTATG
TTTTCTATAGTTTTGTTTAGGAAGAAGAGTGTGAGGTCATCACATGTTTACTGTTGGTTTAGATGTTAAGACTGCTGTGTTTTTT
AGCTCAATTACTATGATTATTGGTGTGCCTACTGGGATTAAGGTTTTTACATGATTATATATGTTATTAATGCTCGAGTAAA
AAAGAGTGATCCTGTGTTGTGGTGAATTGTTTCATTTATAAATTTGTTTACATTTGGTGGAGTTACTGGTATAGTATTGTCTGC
TTGTGTTTTAGATAAAGTGTTACATGATACTTGGTTT";
}

else if("Taenia laticollis".equals(s))
{
    q=
"GGATTTGGTATAATTAGACATATATGTTTAAAGTATTAGTATGTGTTCCGGATGCTTTCGGTTTTTATGGTTTATTATTTGCTATG
TTTTCTATTGTTGTTTAGGAGAAGAGTTTTGGGGTCATCATATGTTTACAGTTGGTTAGATGTTAAGACGGCTGTATTTTTT
AGTTCGTAACTATGATTATTGGTGTACCTACAGGTATAAAGGTTTTTACATGATTATATATGCTTTTAAATTCGCGGTTAAA
AAGAGTGATCCTGTATTATGGTGGATAGTTTCTTTTATAGTTTTGTTTACGTTTGGTGGTGTACAGGAATAGTGTGTCTGCT
TGCATTATTAGATAAAGTATTACATGATACTTGATTT";
}

else if("Taenia madoquae".equals(s))
{
    q=
"GGTTTTGGGATAATTAGTCATATATGTTTGAAGGATTAGTATGTGTCCTGATGCTTTTTGGTTTTTATGGTTTGTATTGCTATG
TTCTCAATAGTGTGTTTGGGAAGGAGTGTATGAGGTATCACATGTTTACGGTTGGATTAGATGTTAAGACTGCTGTATTTTTT
TAGTTCGGTTACTATGATAATAGGAGTACCTACAGGAATAAAGGTTTTTACTTGACTTTATATGCTTTTAAATTCCTCGTGTGA
ATAAGAGTGATCCTGTGTTATGATGGATAGTTTCTTTTATAGTATTGTTTACTTTTTGGTGGTGTAACTGGTATTGTATTATCTG
CTTGTGATTGGATAATGTTTTACATGATACTTGATTT";
}

else if("Taenia martis".equals(s))
{

```

```
q=  
"GGTTTTGGTATAATTAGACATATTTGTCTAAATATAAGTATGAATTATGATTCTTTTGGTTTTATGGTTTATTATTTGCTATG  
TTTTCTATAGTTTGTGGGTAGTAGTGTGGGGTCATCATATGTTTACTGTTGGATTAGATGTTAAGACTGCTGTTTTTTTC  
AGTTCAGTTACTATGATAATAGGTGTTCTACGGGTATAAAGGTTTTTACTTGGATTATATATGCTTTTAAAATCTCGTGTGAAT  
AAGAGTGATCCTGTATTATGGTGAATTGTTCTTTTATTATTTGTTTACTTTTTGGTGGTGTACTGGTATAGTGTATCTGCAT  
GTGTTTTGGATAAAGTTCTTCATGATACTTGATT";
```

```
}
```

```
else if("Taenia multiceps".equals(s))
```

```
{
```

```
q=  
"GGTTTTGGTATAATTAGTCACATATGTTTAAAGAATAAGCATGTGTCAGATGCTTTTTGGTTTTATGGTTTATTATTTGCTATG  
TTTTCAATAGTGTGTTTAGGGAGAAGTGTGTGAGGCCATCATATGTTTACAGTTGGGTTAGATGTTAAGACTGCTGTATTTTT  
AGTTCGGTTACTATGATAATAGGAGTGCCACAGGAATAAAGGTTTTTACTTGGCTTTATATGCTTTTAAAATCTCGTGTAAA  
CAAGAGTGATCCTATACTATGATGAATAGTTCTTTTATAGTATTGTTTACTTTTTGGTGGTGTAACTGGGATTGTATTGTCTGC  
TTGTGTATTAGATAAAGTTTTACATGATACTTGATT";
```

```
}
```

```
else if("Taenia mustelae".equals(s))
```

```
{
```

```
q=  
"GGTTTTGGTATTATTGGTCATATATGTTTGAAGTATAAGGATGTGTTCTGATGCTTTTTGGTTTTATGGATTGTTGTTGCTATG  
TTTTCTATTGTTGTCTAGGTAGTAGAGTTTGAAGGCATCATATGTTTACTGTTGGTTTAGATGTTAAGACTGCTGTTTTTTT  
GTTCTGTTACTATGATTATAGGAGTTCCTACTGGTATAAAGGTGTTTACTTGGTTGTATATGTTACTGAATTCTAGTGTAAACA  
AGAGGGATCCTGTGTTGTGATGAATAGTGCATTTATATTTTTGTTTACTTTTTGGTGGTGTACTGGTATAGTTTTGTCTGCTT  
GTGTATTAGATAATGTTTTGCATGATACTTGATT";
```

```
}
```

```
else if("Taenia ovis".equals(s))
```

```
{
```

```
q=  
"GGATTTGGTATAATTAGTCATATTTGTTTGAAGATTAGTATGTGTCAGATGCTTTTTGGTTTTATGGCTTATTATTTGCTATG  
TTTTCTATAGTATGTTTAGGAAGAAGTGTGTGGGGCATCATATGTTTACTGTTGGGTTGGATGTTAAGACGGCTGTATTTTT  
AGTTCGGTTACTATGATCATAGGTGTGCCTACTGGTATAAAGGTTTTTACTTGGCTTTATATGCTTCTGAAATCTCGTGTGAAT  
AAGAGTGATCCTATTTTGTGATGGATAGTTCTTTTATAGTATTATTTACTTTTTGGAGGTGTGACTGGTATTGTTTTATCTGCTT  
GTGTATTGGATAAAGTTCTTCATGATACTTGATT";
```

```
}
```

```
else if("Taenia parva".equals(s))
```

```
{
```

```
q=  
"GGTTTGGGATTATAAGACATATATGTTTAAAGAATTAGTATGTGTGATGATGCTTTTTGGTTTTATGGTTTATTATTTGCTATG  
TTTTCTATTGTGTGTTTAGGAAGAAGTGTATGAGGCCATCATATGTTTACTGTAGGTTTAGATGTGAAGACTGCTGTGTTTTTT  
GTTTCAGTAACAATGATTATCGGGGTTCTACTGGGATAAAGGTTTTTACTTGGATTATATATGTTACTTAATCTCGTATTAATA  
AGGGTGATCCTGTAATTTGATGAATTGTTCTTTTCATAGTTTTATTTACGTTTGGTGGTGTCACTGGTATAGTTTTATCAGCTT  
GTGTTTTAGATAAAGTTTTGCATGATACTTGATT";
```

```
}
```

```
else if("Taenia pisiformis".equals(s))
```

```
{
```

```
q=  
"GGGTTTTGGTATAATTAGTCATATATGTTTAAAGAATAAGTATGTGTTTCAGATGCGTTTTGGTTTTATGGTTTATTGTTTGAAT  
GTTTTCTATAGTTTGTAGGTAGAAGTGTATGAGGTCATCATATGTTTACTGTTGGATTAGATGTTAAGACCGCTGTGTTTTT  
TAGTTCAGTAACAATGATAATTGGAGTACCTACTGGAATTAAGGTCTTTACATGACTTTATATGCTTTTAAAATCTCGTGTCA
```

```

AAAAGAGTGATCCTGTGTTGGTGAATAATTTCTTTTATAGTCTTATTTACTTTTGGAGGTGTAACCTGGTATAGTATTATCTG
CTTGTGTTTTAGATAAAGTT-TTACATGATACTTGATT";

}

else if("Taenia saginata".equals(s))

{

q=
"GGTTTTGGTATGATTAGTCATATATGTTTAAAGAATAAGTATGTGTCCAGATGCTTTTGGTTTTTATGGTTTTGTTGTTGCTATG
TTTTCAATAGTGTGTTTGGGGAGAAGTGTGTGGGGTCATCATATGTTTACGGTTGGGTAGATGTTAAGACTGCTGTGTTTTTT
AGTTCGGTTACTATGATAAATAGGAGTACCAACAGGAATAAAGGTTTTTACTTGACTTTATATGCTTTTTAAATCTCGTGTA
AAAGAGTGATCCTATATGTGTTGGAATAGTTCTTTTATAGTGTGTTTACTTTTGGTGGTGTGACTGGTATTGTGTTGCTGC
TTGCGTATTGGATAAAGTTTTGCATGATACTTGATT";

}

else if("Taenia serialis".equals(s))

{

q=
"GGTTTTGGTATAATTAGTCATATATGTTTAAAGAATAAGTATGTGTCCAGACGCTTTTGGTTTTTATGGTTTTGTTATTGCTATG
TTCTCAATAGTGTGTTTAGGAAGGAGTGTATGGGGTCATCATATGTTTACAGTTGGGTAGATGTTAAGACTGCTGTATTTTTT
AGTTCAGTTACTATGGTAATAGGAGTACCAACAGGAATAAAGGTTTTTACTTGGCTTTATATGTTATTTAAATCTCGTGTA
AAAGAGTGATCCTATATTGTGTTGGGATAGTTCTTTTATAGTATTGTTTACTTTTGGTGGTGTAACTGGGATTGTATTGCTGC
TTGTGTTGGATAAAGTTTTACATGATACTTGTT";

}

else if("Taenia solium".equals(s))

{

q=
"GGGTTTTGGTATAATTAGTCATATATGTTTGAAGTATAAGTATGTGTCTGATGCTTTTGGCTTTTTATGGGTTATTGTTTGTATG
TTTTCAATAGTATGTTTAGGAAGAAGTGTGTGAGGACATCATATGTTTACGGTTGGGTAGATGTTAAGACTGCTGTATTTTTT
TAGTCTGTTACTATGATAAATTGGAGTGCCTACGGGGATTAAGGTTTTTACTTGGCTTTATATGCTTTTTAAATCTCGTGTA
AAAGAGTGATCCGGTTTTATGATGAATAATTTCTGTTTATAGTATTGTTTACATTTGGTGGTGTAAACCGGATTATTCTATCTGC
TTGTATTAGATAAAGTTCTTCATGATACTTGTT";

}

else if("Taenia twitchelli".equals(s))

{

q=
"GGTTTTGGTATAATTAGACATATTTGTTTAAATGTAAGTATGAATTATGATTCTTTTGGATTTTTATGGTTTTGTTATTGCTATG
TTTTCTATAGTTTGTAGGTAGAAAGTGTATGAGGTCATCATATGTTTACTGTTGGATTAGATGTTAAGACTGCTGTTTTTTTT
AGTTCGTACTATGATTATAGGGTTCCTACAGGTATAAAGGTTTACTTGGTTATATATGCTTTTTAAATCTCGTGTA
AAGAGTGATCCTGTTTTATGATGAATTGTGTCTTTTATTATTTGTTTACTTTTGGTGGTGTACTGGTATAGTGTATCTGCGT
GTGTTTTGGATAAAGTTCTTCATGATACTTGTT";

}

else if("Taeniopygia guttata".equals(s))

{

q=
"GGTTTCGGCATCATCTCCCACGTCGTAACCTACTATTCAGGTAAAAAGAACCATTCCGATATATAGGAATAGTATGAGCTA
TGCTATCCATCGGATTCTAGGATTCATCGTATGAGCCACCACATGTTTACAGTAGGAATGGACGTAGACACCCGAGCATA
CTTTACATCCGCACTATAATCATCGCCATCCCAACCGGCATCAAAGTATTCAGCTGACTAGCAAACTCCACGAGGCACA
ATCAAGTGAGACCCACCAATACTATGAGCTCTAGGATTTATCTTCTATTACCATCGGAGGCCAACCAGGATCGTCTGGC
CAACTCTCACTAGACATCGCCCTACAGCACCTACTACGTAGTAGCCACTTCCACTACGTCCTATCAATAGGAGCAGTGT
TTGCAATCCTAGCAGGATTCACCCACTGATT";

```

```
}
```

```
double
```

```
AAA=0,AAC=0,AAG=0,AAT=0,ACA=0,ACC=0,ACG=0,ACT=0,AGA=0,AGC=0,AGG=0,AGT=0,ATA=0,ATC=0,ATG=0,ATT=0,CAA=0,CAC=0,CAG=0,CAT=0,CCA=0,CCC=0,CCG=0,CCT=0,CGA=0,CGC=0,CGG=0,CGT=0,CTA=0,CTC=0,CTG=0,CTT=0,GAA=0,GAC=0,GAG=0,GAT=0,GCA=0,GCC=0,GCG=0,GCT=0,GGA=0,GGC=0,GGG=0,GGT=0,GTA=0,GTC=0,GTG=0,GTT=0,TAA=0,TAC=0,TAG=0,TAT=0,TCA=0,TCC=0,TCG=0,TCT=0,TGA=0,TGC=0,TGG=0,TGT=0,TTA=0, TTC=0,TTG=0,TTT=0;
```

```
double length = q.length();
```

```
for(int i=0;i<length-2;i++)
```

```
{
```

```
if(q.charAt(i)=='A')
```

```
{
```

```
    if(q.charAt(i+1)=='A')
```

```
    {
```

```
        if(q.charAt(i+2)=='A')
```

```
        AAA++;
```

```
        else if(q.charAt(i+2)=='C')
```

```
        AAC++;
```

```
        else if(q.charAt(i+2)=='G')
```

```
        AAG++;
```

```
        else if(q.charAt(i+2)=='T')
```

```
        AAT++;
```

```
    }
```

```
    else if(q.charAt(i+1)=='C')
```

```
    {
```

```
        if(q.charAt(i+2)=='A')
```

```
        ACA++;
```

```
        else if(q.charAt(i+2)=='C')
```

```
        ACC++;
```

```
        else if(q.charAt(i+2)=='G')
```

```
        ACG++;
```

```
        else if(q.charAt(i+2)=='T')
```

```
        ACT++;
```

```
    }
```

```
    else if(q.charAt(i+1)=='G')
```



```

    {
        if(q.charAt(i+2)=='A')
            AGA++;
        else if(q.charAt(i+2)=='C')
            AGC++;
        else if(q.charAt(i+2)=='G')
            AGG++;
        else if(q.charAt(i+2)=='T')
            AGT++;
    }
else if(q.charAt(i+1)=='T')
{
    if(q.charAt(i+2)=='A')
        ATA++;
    else if(q.charAt(i+2)=='C')
        ATC++;
    else if(q.charAt(i+2)=='G')
        ATG++;
    else if(q.charAt(i+2)=='T')
        ATT++;
}
}
else if(q.charAt(i)=='C')
{
    if(q.charAt(i+1)=='A')
    {
        if(q.charAt(i+2)=='A')
            CAA++;
        else if(q.charAt(i+2)=='C')
            CAC++;
        else if(q.charAt(i+2)=='G')
            CAG++;
        else if(q.charAt(i+2)=='T')
            CAT++;
    }
}

```

```

else if(q.charAt(i+1)=='C')
{
    if(q.charAt(i+2)=='A')
        CCA++;
    else if(q.charAt(i+2)=='C')
        CCC++;
    else if(q.charAt(i+2)=='G')
        CCG++;
    else if(q.charAt(i+2)=='T')
        CCT++;
}
else if(q.charAt(i+1)=='G')
{
    if(q.charAt(i+2)=='A')
        CGA++;
    else if(q.charAt(i+2)=='C')
        CGC++;
    else if(q.charAt(i+2)=='G')
        CGG++;
    else if(q.charAt(i+2)=='T')
        CGT++;
}
else if(q.charAt(i+1)=='T')
{
    if(q.charAt(i+2)=='A')
        CTA++;
    else if(q.charAt(i+2)=='C')
        CTC++;
    else if(q.charAt(i+2)=='G')
        CTG++;
    else if(q.charAt(i+2)=='T')
        CTT++;
}
}
else if(q.charAt(i)=='G')

```

```

{
    if(q.charAt(i+1)=='A')
    {
        if(q.charAt(i+2)=='A')
            GAA++;
        else if(q.charAt(i+2)=='C')
            GAC++;
        else if(q.charAt(i+2)=='G')
            GAG++;
        else if(q.charAt(i+2)=='T')
            GAT++;
    }
    else if(q.charAt(i+1)=='C')
    {
        if(q.charAt(i+2)=='A')
            GCA++;
        else if(q.charAt(i+2)=='C')
            GCC++;
        else if(q.charAt(i+2)=='G')
            GCG++;
        else if(q.charAt(i+2)=='T')
            GCT++;
    }
    else if(q.charAt(i+1)=='G')
    {
        if(q.charAt(i+2)=='A')
            GGA++;
        else if(q.charAt(i+2)=='C')
            GGC++;
        else if(q.charAt(i+2)=='G')
            GGG++;
        else if(q.charAt(i+2)=='T')
            GGT++;
    }
    else if(q.charAt(i+1)=='T')

```

```

    {
        if(q.charAt(i+2)=='A')
            GTA++;
        else if(q.charAt(i+2)=='C')
            GTC++;
        else if(q.charAt(i+2)=='G')
            GTG++;
        else if(q.charAt(i+2)=='T')
            GTT++;
    }
}
else if(q.charAt(i)=='T')
{
    if(q.charAt(i+1)=='A')
    {
        if(q.charAt(i+2)=='A')
            TAA++;
        else if(q.charAt(i+2)=='C')
            TAC++;
        else if(q.charAt(i+2)=='G')
            TAG++;
        else if(q.charAt(i+2)=='T')
            TAT++;
    }
    else if(q.charAt(i+1)=='C')
    {
        if(q.charAt(i+2)=='A')
            TCA++;
        else if(q.charAt(i+2)=='C')
            TCC++;
        else if(q.charAt(i+2)=='G')
            TCG++;
        else if(q.charAt(i+2)=='T')
            TCT++;
    }
}

```

```

else if(q.charAt(i+1)=='G')
{
    if(q.charAt(i+2)=='A')
        TGA++;
    else if(q.charAt(i+2)=='C')
        TGC++;
    else if(q.charAt(i+2)=='G')
        TGG++;
    else if(q.charAt(i+2)=='T')
        TGT++;
}
else if(q.charAt(i+1)=='T')
{
    if(q.charAt(i+2)=='A')
        TTA++;
    else if(q.charAt(i+2)=='C')
        TTC++;
    else if(q.charAt(i+2)=='G')
        TTG++;
    else if(q.charAt(i+2)=='T')
        TTT++;
}
}
}

AAA=AAA/length;
AAC=AAC/length;
AAG=AAG/length;
AAT=AAT/length;
ACA=ACA/length;
ACC=ACC/length;
ACG=ACG/length;
ACT=ACT/length;
AGA=AGA/length;
AGC=AGC/length;
AGG=AGG/length;

```

AGT=AGT/length;

ATA=ATA/length;

ATC=ATC/length;

ATG=ATG/length;

ATT=ATT/length;

CAA=CAA/length;

CAC=CAC/length;

CAG=CAG/length;

CAT=CAT/length;

CCA=CCA/length;

CCC=CCC/length;

CCG=CCG/length;

CCT=CCT/length;

CGA=CGA/length;

CGC=CGC/length;

CGG=CGG/length;

CGT=CGT/length;

CTA=CTA/length;

CTC=CTC/length;

CTG=CTG/length;

CTT=CTT/length;

GAA=GAA/length;

GAC=GAC/length;

GAG=GAG/length;

GAT=GAT/length;

GCA=GCA/length;

GCC=GCC/length;

GCG=GCG/length;

GCT=GCT/length;

GTA=GTA/length;

GTC=GTC/length;

GTG=GTG/length;

GTT=GTT/length;

GGA=GGA/length;

GGC=GGC/length;

GGG=GGG/length;

GGT=GGT/length;

TAA=TAA/length;

TAC=TAC/length;

TAG=TAG/length;

TAT=TAT/length;

TCA=TCA/length;

TCC=TCC/length;

TCG=TCG/length;

TCT=TCT/length;

TGA=TGA/length;

TGC=TGC/length;

TGG=TGG/length;

TGT=TGT/length;

TTA=TTA/length;

TTC=TTC/length;

TTG=TTG/length;

TTT=TTT/length;

AAA=AAA*10000;

AAA=Math.round(AAA);

AAA=AAA/10000;

ACA=ACA*10000;

```
ACA=Math.round(ACA);
ACA=ACA/10000;
AGA=AGA*10000;
AGA=Math.round(AGA);
AGA=AGA/10000;
ATA=ATA*10000;
ATA=Math.round(ATA);
ATA=ATA/10000;
CAA=CAA*10000;
CAA=Math.round(CAA);
CAA=CAA/10000;
CCA=CCA*10000;
CCA=Math.round(CCA);
CCA=CCA/10000;
CGA=CGA*10000;
CGA=Math.round(CGA);
CGA=CGA/10000;
CTA=CTA*10000;
CTA=Math.round(CTA);
CTA=CTA/10000;
GAA=GAA*10000;
GAA=Math.round(GAA);
GAA=GAA/10000;
GCA=GCA*10000;
GCA=Math.round(GCA);
GCA=GCA/10000;
GGA=GGA*10000;
GGA=Math.round(GGA);
GGA=GGA/10000;
GTA=GTA*10000;
GTA=Math.round(GTA);
GTA=GTA/10000;
TAA=TAA*10000;
TAA=Math.round(TAA);
TAA=TAA/10000;
```



```
TCA=TCA*10000;
TCA=Math.round(TCA);
TCA=TCA/10000;
TGA=TGA*10000;
TGA=Math.round(TGA);
TGA=TGA/10000;
TTA=TTA*10000;
TTA=Math.round(TTA);
TTA=TTA/10000;

AAC=AAC*10000;
AAC=Math.round(AAC);
AAC=AAC/10000;
ACC=ACC*10000;
ACC=Math.round(ACC);
ACC=ACC/10000;
AGC=AGC*10000;
AGC=Math.round(AGC);
AGC=AGC/10000;
ATC=ATC*10000;
ATC=Math.round(ATC);
ATC=ATC/10000;
CAC=CAC*10000;
CAC=Math.round(CAC);
CAC=CAC/10000;
CCC=CCC*10000;
CCC=Math.round(CCC);
CCC=CCC/10000;
CGC=CGC*10000;
CGC=Math.round(CGC);
CGC=CGC/10000;
CTC=CTC*10000;
CTC=Math.round(CTC);
CTC=CTC/10000;
GAC=GAC*10000;
```

```
GAC=Math.round(GAC);
GAC=GAC/10000;
GCC=GCC*10000;
GCC=Math.round(GCC);
GCC=GCC/10000;
GGC=GGC*10000;
GGC=Math.round(GGC);
GGC=GGC/10000;
GTC=GTC*10000;
GTC=Math.round(GTC);
GTC=GTC/10000;
TAC=TAC*10000;
TAC=Math.round(TAC);
TAC=TAC/10000;
TCC=TCC*10000;
TCC=Math.round(TCC);
TCC=TCC/10000;
TGC=TGC*10000;
TGC=Math.round(TGC);
TGC=TGC/10000;
TTC=TTC*10000;
TTC=Math.round(TTC);
TTC=TTC/10000;

AAG=AAG*10000;
AAG=Math.round(AAG);
AAG=AAG/10000;
ACG=ACG*10000;
ACG=Math.round(ACG);
ACG=ACG/10000;
AGG=AGG*10000;
AGG=Math.round(AGG);
AGG=AGG/10000;
ATG=ATG*10000;
ATG=Math.round(ATG);
```

ATG=ATG/10000;
CAG=CAG*10000;
CAG=Math.round(CAG);
CAG=CAG/10000;
CCG=CCG*10000;
CCG=Math.round(CCG);
CCG=CCG/10000;
CGG=CGG*10000;
CGG=Math.round(CGG);
CGG=CGG/10000;
CTG=CTG*10000;
CTG=Math.round(CTG);
CTG=CTG/10000;
GAG=GAG*10000;
GAG=Math.round(GAG);
GAG=GAG/10000;
GCG=GCG*10000;
GCG=Math.round(GCG);
GCG=GCG/10000;
GGG=GGG*10000;
GGG=Math.round(GGG);
GGG=GGG/10000;
GTG=GTG*10000;
GTG=Math.round(GTG);
GTG=GTG/10000;
TAG=TAG*10000;
TAG=Math.round(TAG);
TAG=TAG/10000;
TCG=TCG*10000;
TCG=Math.round(TCG);
TCG=TCG/10000;
TGG=TGG*10000;
TGG=Math.round(TGG);
TGG=TGG/10000;
TTG=TTG*10000;

```
TTG=Math.round(TTG);
TTG=TTG/10000;

AAT=AAT*10000;
AAT=Math.round(AAT);
AAT=AAT/10000;
ACT=ACT*10000;
ACT=Math.round(ACT);
ACT=ACT/10000;
AGT=AGT*10000;
AGT=Math.round(AGT);
AGT=AGT/10000;
ATT=ATT*10000;
ATT=Math.round(ATT);
ATT=ATT/10000;
CAT=CAT*10000;
CAT=Math.round(CAT);
CAT=CAT/10000;
CCT=CCT*10000;
CCT=Math.round(CCT);
CCT=CCT/10000;
CGT=CGT*10000;
CGT=Math.round(CG T);
CGT=CGT/10000;
CTT=CTT*10000;
CTT=Math.round(CTT);
CTT=CTT/10000;
GAT=GAT*10000;
GAT=Math.round(GAT);
GAT=GAT/10000;
GCT=GCT*10000;
GCT=Math.round(GCT);
GCT=GCT/10000;
GGT=GGT*10000;
GGT=Math.round(GGT);
```

```

GGT=GGT/10000;

GTT=GTT*10000;

GTT=Math.round(GTT);

GTT=GTT/10000;

TAT=TAT*10000;

TAT=Math.round(TAT);

TAT=TAT/10000;

TCT=TCT*10000;

TCT=Math.round(TCT);

TCT=TCT/10000;

TGT=TGT*10000;

TGT=Math.round(TGT);

TGT=TGT/10000;

TTT=TTT*10000;

TTT=Math.round(TTT);

TTT=TTT/10000;

    JFrame res= new JFrame("Trinucleotide frequency"+" "+s);

res.setSize(500,600);

res.setLayout(null);

    JLabel f =new JLabel();

f.setText(" AAA");

f.setSize(50,50);

f.setFont(f.getFont().deriveFont(14.0f));

    JLabel f1 =new JLabel();

f1.setText(" AAC");

f1.setBounds(0,30,50,50);

f1.setSize(50,50);

f1.setFont(f1.getFont().deriveFont(14.0f));

    JLabel f2 =new JLabel();

f2.setText(" AAG");

f2.setSize(50,50);

f2.setFont(f1.getFont().deriveFont(14.0f));

```

```
f2.setBounds(0,60,50,50);
```

```
JLabel f15 =new JLabel();
```

```
f15.setText(" AAT");
```

```
f15.setSize(50,50);
```

```
f15.setFont(f15.getFont().deriveFont(14.0f));
```

```
f15.setBounds(0,90,50,50);
```

```
JLabel f3 =new JLabel();
```

```
f3.setText(" ACA");
```

```
f3.setSize(50,50);
```

```
f3.setFont(f3.getFont().deriveFont(14.0f));
```

```
f3.setBounds(0,120,50,50);
```

```
JLabel f4 =new JLabel();
```

```
f4.setText(" ACC");
```

```
f4.setSize(50,50);
```

```
f4.setFont(f4.getFont().deriveFont(14.0f));
```

```
f4.setBounds(0,150,50,50);
```

```
JLabel f5 =new JLabel();
```

```
f5.setText(" ACG");
```

```
f5.setSize(50,50);
```

```
f5.setFont(f5.getFont().deriveFont(14.0f));
```

```
f5.setBounds(0,180,50,50);
```

```
JLabel f6 =new JLabel();
```

```
f6.setText(" ACT");
```

```
f6.setSize(50,50);
```

```
f6.setFont(f6.getFont().deriveFont(14.0f));
```

```
f6.setBounds(0,210,50,50);
```

```
JLabel f7 =new JLabel();
```

```
f7.setText(" AGA");
```

```
f7.setSize(50,50);

f7.setFont(f7.getFont().deriveFont(14.0f));

f7.setBounds(0,240,50,50);

    JLabel f8 =new JLabel();

f8.setText(" AGC");

f8.setSize(50,50);

f8.setFont(f8.getFont().deriveFont(14.0f));

f8.setBounds(0,270,50,50);

    JLabel f9 =new JLabel();

f9.setText(" AGG");

f9.setSize(50,50);

f9.setFont(f9.getFont().deriveFont(14.0f));

f9.setBounds(0,300,50,50);

    JLabel f10 =new JLabel();

f10.setText(" AGT");

f10.setSize(50,50);

f10.setFont(f10.getFont().deriveFont(14.0f));

f10.setBounds(0,330,50,50);

    JLabel f11 =new JLabel();

f11.setText(" ATA");

f11.setSize(50,50);

f11.setFont(f11.getFont().deriveFont(14.0f));

f11.setBounds(0,360,50,50);

    JLabel f12 =new JLabel();

f12.setText(" ATC");

f12.setSize(50,50);

f12.setFont(f12.getFont().deriveFont(14.0f));

f12.setBounds(0,390,50,50);

    JLabel f13 =new JLabel();
```

```
f13.setText(" ATG");  
  
f13.setSize(50,50);  
  
f13.setFont(f13.getFont().deriveFont(14.0f));  
  
f13.setBounds(0,420,50,50);
```

```
        JLabel f14 =new JLabel();  
  
f14.setText(" ATT");  
  
f14.setSize(50,50);  
  
f14.setFont(f14.getFont().deriveFont(14.0f));  
  
f14.setBounds(0,450,50,50);
```

```
        JLabel g =new JLabel();  
  
g.setText(" CAA");  
  
g.setSize(50,50);  
  
g.setFont(g.getFont().deriveFont(14.0f));  
  
g.setBounds(100,0,50,50);
```

```
        JLabel g1 =new JLabel();  
  
g1.setText(" CAC");  
  
g1.setBounds(100,30,50,50);  
  
g1.setSize(50,50);  
  
g1.setFont(g1.getFont().deriveFont(14.0f));
```

```
        JLabel g2 =new JLabel();  
  
g2.setText(" CAG");  
  
g2.setSize(50,50);  
  
g2.setFont(g1.getFont().deriveFont(14.0f));  
  
g2.setBounds(100,60,50,50);
```

```
        JLabel g15 =new JLabel();  
  
g15.setText(" CAT");  
  
g15.setSize(50,50);  
  
g15.setFont(g15.getFont().deriveFont(14.0f));  
  
g15.setBounds(100,90,50,50);
```



```
JLabel g3 =new JLabel();  
g3.setText(" CCA");  
g3.setSize(50,50);  
g3.setFont(g3.getFont().deriveFont(14.0f));  
g3.setBounds(100,120,50,50);
```

```
JLabel g4 =new JLabel();  
g4.setText(" CCC");  
g4.setSize(50,50);  
g4.setFont(g4.getFont().deriveFont(14.0f));  
g4.setBounds(100,150,50,50);
```

```
JLabel g5 =new JLabel();  
g5.setText(" CCG");  
g5.setSize(50,50);  
g5.setFont(g5.getFont().deriveFont(14.0f));  
g5.setBounds(100,180,50,50);
```

```
JLabel g6 =new JLabel();  
g6.setText(" CCT");  
g6.setSize(50,50);  
g6.setFont(g6.getFont().deriveFont(14.0f));  
g6.setBounds(100,210,50,50);
```

```
JLabel g7 =new JLabel();  
g7.setText(" CGA");  
g7.setSize(50,50);  
g7.setFont(g7.getFont().deriveFont(14.0f));  
g7.setBounds(100,240,50,50);
```

```
JLabel g8 =new JLabel();  
g8.setText(" CGC");  
g8.setSize(50,50);  
g8.setFont(g8.getFont().deriveFont(14.0f));
```

```
g8.setBounds(100,270,50,50);
```

```
    JLabel g9 =new JLabel();
```

```
g9.setText(" CGG");
```

```
g9.setSize(50,50);
```

```
g9.setFont(g9.getFont().deriveFont(14.0f));
```

```
g9.setBounds(100,300,50,50);
```

```
    JLabel g10 =new JLabel();
```

```
g10.setText(" CGT");
```

```
g10.setSize(50,50);
```

```
g10.setFont(g10.getFont().deriveFont(14.0f));
```

```
g10.setBounds(100,330,50,50);
```

```
    JLabel g11 =new JLabel();
```

```
g11.setText(" CTA");
```

```
g11.setSize(50,50);
```

```
g11.setFont(g11.getFont().deriveFont(14.0f));
```

```
g11.setBounds(100,360,50,50);
```

```
    JLabel g12 =new JLabel();
```

```
g12.setText(" CTC");
```

```
g12.setSize(50,50);
```

```
g12.setFont(g12.getFont().deriveFont(14.0f));
```

```
g12.setBounds(100,390,50,50);
```

```
    JLabel g13 =new JLabel();
```

```
g13.setText(" CTG");
```

```
g13.setSize(50,50);
```

```
g13.setFont(g13.getFont().deriveFont(14.0f));
```

```
g13.setBounds(100,420,50,50);
```

```
    JLabel g14 =new JLabel();
```

```
g14.setText(" CTT");
```

```
g14.setSize(50,50);
```

```
g14.setFont(g14.getFont().deriveFont(14.0f));

g14.setBounds(100,450,50,50);

    JLabel h =new JLabel();

h.setText(" GAA");

h.setSize(50,50);

h.setFont(h.getFont().deriveFont(14.0f));

    h.setBounds(200,0,50,50);

    JLabel h1 =new JLabel();

    h1.setText(" GAC");

    h1.setBounds(200,30,50,50);

h1.setSize(50,50);

h1.setFont(h1.getFont().deriveFont(14.0f));

    JLabel h2 =new JLabel();

    h2.setText(" GAG");

h2.setSize(50,50);

h2.setFont(h1.getFont().deriveFont(14.0f));

    h2.setBounds(200,60,50,50);

    JLabel h15 =new JLabel();

h15.setText(" GAT");

h15.setSize(50,50);

h15.setFont(h15.getFont().deriveFont(14.0f));

h15.setBounds(200,90,50,50);

    JLabel h3 =new JLabel();

h3.setText(" GCA");

h3.setSize(50,50);

h3.setFont(h3.getFont().deriveFont(14.0f));

h3.setBounds(200,120,50,50);

    JLabel h4 =new JLabel();

h4.setText(" GCC");

h4.setSize(50,50);
```

```
h4.setFont(h4.getFont().deriveFont(14.0f));
```

```
h4.setBounds(200,150,50,50);
```

```
    JLabel h5 =new JLabel();
```

```
h5.setText(" GCG");
```

```
h5.setSize(50,50);
```

```
h5.setFont(h5.getFont().deriveFont(14.0f));
```

```
h5.setBounds(200,180,50,50);
```

```
    JLabel h6 =new JLabel();
```

```
h6.setText(" GCT");
```

```
h6.setSize(50,50);
```

```
h6.setFont(h6.getFont().deriveFont(14.0f));
```

```
h6.setBounds(200,210,50,50);
```

```
    JLabel h7 =new JLabel();
```

```
h7.setText(" GGA");
```

```
h7.setSize(50,50);
```

```
h7.setFont(h7.getFont().deriveFont(14.0f));
```

```
h7.setBounds(200,240,50,50);
```

```
    JLabel h8 =new JLabel();
```

```
h8.setText(" GGC");
```

```
h8.setSize(50,50);
```

```
h8.setFont(h8.getFont().deriveFont(14.0f));
```

```
h8.setBounds(200,270,50,50);
```

```
    JLabel h9 =new JLabel();
```

```
h9.setText(" GGG");
```

```
h9.setSize(50,50);
```

```
h9.setFont(h9.getFont().deriveFont(14.0f));
```

```
h9.setBounds(200,300,50,50);
```

```
    JLabel h10 =new JLabel();
```

```
h10.setText(" GGT");  
h10.setSize(50,50);  
h10.setFont(h10.getFont().deriveFont(14.0f));  
h10.setBounds(200,330,50,50);
```

```
    JLabel h11 =new JLabel();  
h11.setText(" GTA");  
h11.setSize(50,50);  
h11.setFont(h11.getFont().deriveFont(14.0f));  
h11.setBounds(200,360,50,50);
```

```
    JLabel h12 =new JLabel();  
h12.setText(" GTC");  
h12.setSize(50,50);  
h12.setFont(h12.getFont().deriveFont(14.0f));  
h12.setBounds(200,390,50,50);
```

```
    JLabel h13 =new JLabel();  
h13.setText(" GTG");  
h13.setSize(50,50);  
h13.setFont(h13.getFont().deriveFont(14.0f));  
h13.setBounds(200,420,50,50);
```

```
    JLabel h14 =new JLabel();  
h14.setText(" GTT");  
h14.setSize(50,50);  
h14.setFont(h14.getFont().deriveFont(14.0f));  
h14.setBounds(200,450,50,50);
```

```
    JLabel l =new JLabel();  
l.setText(" TAA");  
l.setSize(50,50);  
l.setFont(l.getFont().deriveFont(14.0f));  
    l.setBounds(300,0,50,50);
```

```
JLabel l1 =new JLabel();

l1.setText(" TAC");

l1.setBounds(300,30,50,50);

l1.setSize(50,50);

l1.setFont(l1.getFont().deriveFont(14.0f));

JLabel l2 =new JLabel();

l2.setText(" TAG");

l2.setSize(50,50);

l2.setFont(l1.getFont().deriveFont(14.0f));

l2.setBounds(300,60,50,50);

JLabel l15 =new JLabel();

l15.setText(" TAT");

l15.setSize(50,50);

l15.setFont(l15.getFont().deriveFont(14.0f));

l15.setBounds(300,90,50,50);

JLabel l3 =new JLabel();

l3.setText(" TCA");

l3.setSize(50,50);

l3.setFont(l3.getFont().deriveFont(14.0f));

l3.setBounds(300,120,50,50);

JLabel l4 =new JLabel();

l4.setText(" TCC");

l4.setSize(50,50);

l4.setFont(l4.getFont().deriveFont(14.0f));

l4.setBounds(300,150,50,50);

JLabel l5 =new JLabel();

l5.setText(" TCG");

l5.setSize(50,50);

l5.setFont(l5.getFont().deriveFont(14.0f));

l5.setBounds(300,180,50,50);

JLabel l6 =new JLabel();

l6.setText(" TCT");

l6.setSize(50,50);

l6.setFont(l6.getFont().deriveFont(14.0f));

l6.setBounds(300,210,50,50);
```

```
JLabel l7 =new JLabel();

l7.setText(" TGA");

l7.setSize(50,50);

l7.setFont(l7.getFont().deriveFont(14.0f));

l7.setBounds(300,240,50,50);

JLabel l8 =new JLabel();

l8.setText(" TGC");

l8.setSize(50,50);

l8.setFont(l8.getFont().deriveFont(14.0f));

l8.setBounds(300,270,50,50);

JLabel l9 =new JLabel();

l9.setText(" TGG");

l9.setSize(50,50);

l9.setFont(l9.getFont().deriveFont(14.0f));

l9.setBounds(300,300,50,50);

JLabel l10 =new JLabel();

l10.setText(" TGT");

l10.setSize(50,50);

l10.setFont(l10.getFont().deriveFont(14.0f));

l10.setBounds(300,330,50,50);

JLabel l11 =new JLabel();

l11.setText(" TTA");

l11.setSize(50,50);

l11.setFont(l11.getFont().deriveFont(14.0f));

l11.setBounds(300,360,50,50);

JLabel l12 =new JLabel();

l12.setText(" TTC");

l12.setSize(50,50);

l12.setFont(l12.getFont().deriveFont(14.0f));

l12.setBounds(300,390,50,50);

JLabel l13 =new JLabel();

l13.setText(" TTG");

l13.setSize(50,50);

l13.setFont(l13.getFont().deriveFont(14.0f));

l13.setBounds(300,420,50,50);
```

```
JLabel l14 =new JLabel();  
l14.setText(" TTT");  
l14.setSize(50,50);  
l14.setFont(l14.getFont().deriveFont(14.0f));  
l14.setBounds(300,450,50,50);
```

```
String s1 = String.valueOf(AAA);
```

```
String s2 = String.valueOf(AAC);
```

```
String s3 = String.valueOf(AAG);
```

```
String s4 = String.valueOf(AAT);
```

```
String s5 = String.valueOf(ACA);
```

```
String s6 = String.valueOf(ACC);
```

```
String s7 = String.valueOf(ACG);
```

```
String s8 = String.valueOf(ACT);
```

```
String s9 = String.valueOf(AGA);
```

```
String s10 = String.valueOf(AGC);
```

```
String s11 = String.valueOf(AGG);
```

```
String s12 = String.valueOf(AGT);
```

```
String s13 = String.valueOf(ATA);
```

```
String s14 = String.valueOf(ATC);
```

```
String s15 = String.valueOf(ATG);
```

```
String s16 = String.valueOf(ATT);
```

```
String s17 = String.valueOf(CAA);
```

```
String s18 = String.valueOf(CAC);
```

```
String s19 = String.valueOf(CAG);
```

```
String s20 = String.valueOf(CAT);
```

```
String s21 = String.valueOf(CCA);
```

```
String s22 = String.valueOf(CCC);
```

```
String s23 = String.valueOf(CCG);
```

```
String s24 = String.valueOf(CCT);
```

```
String s25 = String.valueOf(CGA);
```

```
String s26 = String.valueOf(CGC);
```

```
String s27 = String.valueOf(CGG);
```

```
String s28 = String.valueOf(CGT);
```



```
String s29 = String.valueOf(CTA);

    String s30 = String.valueOf(CTC);

    String s31 = String.valueOf(CTG);
String s32 = String.valueOf(CTT);

    String s33 = String.valueOf(GAA);
String s34 = String.valueOf(GAC);
String s35 = String.valueOf(GAG);
String s36 = String.valueOf(GAT);
String s37 = String.valueOf(GCA);
String s38 = String.valueOf(GCC);
String s39 = String.valueOf(GCG);
String s40 = String.valueOf(GCT);

    String s41 = String.valueOf(GGA);
String s42 = String.valueOf(GGC);
String s43 = String.valueOf(GGG);
String s44 = String.valueOf(GGT);
String s45 = String.valueOf(GTA);
String s46 = String.valueOf(GTC);
String s47 = String.valueOf(GTG);
String s48 = String.valueOf(GTT);

    String s49 = String.valueOf(TAA);
String s50 = String.valueOf(TAC);

    String s51 = String.valueOf(TAG);
String s52 = String.valueOf(TAT);
String s53 = String.valueOf(TCA);
String s54 = String.valueOf(TCC);
String s55 = String.valueOf(TCG);
String s56 = String.valueOf(TCT);
String s57 = String.valueOf(TGA);
String s58 = String.valueOf(TGC);
String s59 = String.valueOf(TGG);
String s60 = String.valueOf(TGT);
String s61 = String.valueOf(TTA);
```

```
String s62 = String.valueOf(TTC);  
String s63 = String.valueOf(TTG);  
String s64 = String.valueOf(TTT);  
JTextField A1,A2,A3,A4,A5,A6,A7,A8,A9,A10,A11,A12,A13,A14,A15,A16,  
        B1,B2,B3,B4,B5,B6,B7,B8,B9,B10,B11,B12,B13,B14,B15,B16,  
        C1,C2,C3,C4,C5,C6,C7,C8,C9,C10,C11,C12,C13,C14,C15,C16,  
        D1,D2,D3,D4,D5,D6,D7,D8,D9,D10,D11,D12,D13,D14,D15,D16;
```

```
A1 = new JTextField(s1);  
A1.setBounds(40,15,50,25);  
A1.setEditable(false);  
res.add(A1);  
A2 = new JTextField(s2);  
A2.setBounds(40,45,50,25);  
A2.setEditable(false);  
res.add(A2);  
A3 = new JTextField(s3);  
A3.setBounds(40,75,50,25);  
A3.setEditable(false);  
res.add(A3);  
A4 = new JTextField(s4);  
A4.setBounds(40,105,50,25);  
A4.setEditable(false);  
res.add(A4);  
A5 = new JTextField(s5);  
A5.setBounds(40,135,50,25);  
A5.setEditable(false);  
res.add(A5);  
A6 = new JTextField(s6);  
A6.setBounds(40,165,50,25);  
A6.setEditable(false);  
res.add(A6);  
A7 = new JTextField(s7);  
A7.setBounds(40,195,50,25);
```

```
A7.setEditable(false);

res.add(A7);

A8 = new JTextField(s8);
A8.setBounds(40,225,50,25);

A8.setEditable(false);

res.add(A8);

A9 = new JTextField(s9);
A9.setBounds(40,255,50,25);

A9.setEditable(false);

res.add(A9);

A10 = new JTextField(s10);
A10.setBounds(40,285,50,25);

A10.setEditable(false);

res.add(A10);

A11 = new JTextField(s11);
A11.setBounds(40,315,50,25);

A11.setEditable(false);

res.add(A11);

A12 = new JTextField(s12);
A12.setBounds(40,345,50,25);

A12.setEditable(false);

res.add(A12);

A13 = new JTextField(s13);
A13.setBounds(40,375,50,25);

A13.setEditable(false);

res.add(A13);

A14 = new JTextField(s14);
A14.setBounds(40,405,50,25);

A14.setEditable(false);

res.add(A14);

A15 = new JTextField(s15);
A15.setBounds(40,435,50,25);

A15.setEditable(false);

res.add(A15);

A16 = new JTextField(s16);
```

```
A16.setBounds(40,465,50,25);
```

```
A16.setEditable(false);
```

```
res.add(A16);
```

```
    B1 = new JTextField(s17);
```

```
B1.setBounds(140,15,50,25);
```

```
B1.setEditable(false);
```

```
res.add(B1);
```

```
    B2 = new JTextField(s18);
```

```
B2.setBounds(140,45,50,25);
```

```
B2.setEditable(false);
```

```
res.add(B2);
```

```
    B3 = new JTextField(s19);
```

```
B3.setBounds(140,75,50,25);
```

```
B3.setEditable(false);
```

```
res.add(B3);
```

```
    B4 = new JTextField(s20);
```

```
B4.setBounds(140,105,50,25);
```

```
B4.setEditable(false);
```

```
res.add(B4);
```

```
    B5 = new JTextField(s21);
```

```
B5.setBounds(140,135,50,25);
```

```
B5.setEditable(false);
```

```
res.add(B5);
```

```
    B6 = new JTextField(s22);
```

```
B6.setBounds(140,165,50,25);
```

```
B6.setEditable(false);
```

```
res.add(B6);
```

```
    B7 = new JTextField(s23);
```

```
B7.setBounds(140,195,50,25);
```

```
B7.setEditable(false);
```

```
res.add(B7);
```

```
    B8 = new JTextField(s24);
```

```
B8.setBounds(140,225,50,25);
```

```
B8.setEditable(false);
```

```
res.add(B8);

B9 = new JTextField(s25);
B9.setBounds(140,255,50,25);
B9.setEditable(false);
res.add(B9);

B10 = new JTextField(s26);
B10.setBounds(140,285,50,25);
B10.setEditable(false);
res.add(B10);

B11 = new JTextField(s27);
B11.setBounds(140,315,50,25);
B11.setEditable(false);
res.add(B11);

B12 = new JTextField(s28);
B12.setBounds(140,345,50,25);
B12.setEditable(false);
res.add(B12);

B13 = new JTextField(s29);
B13.setBounds(140,375,50,25);
B13.setEditable(false);
res.add(B13);

B14 = new JTextField(s50);
B14.setBounds(140,405,50,25);
B14.setEditable(false);
res.add(B14);

B15 = new JTextField(s31);
B15.setBounds(140,435,50,25);
B15.setEditable(false);
res.add(B15);

B16 = new JTextField(s32);
B16.setBounds(140,465,50,25);
B16.setEditable(false);
res.add(B16);

C1 = new JTextField(s33);
```

```
C1.setBounds(240,15,50,25);

C1.setEditable(false);

res.add(C1);

C2 = new JTextField(s34);

C2.setBounds(240,45,50,25);

C2.setEditable(false);

res.add(C2);

C3 = new JTextField(s35);

C3.setBounds(240,75,50,25);

C3.setEditable(false);

res.add(C3);

C4 = new JTextField(s36);

C4.setBounds(240,105,50,25);

C4.setEditable(false);

res.add(C4);

C5 = new JTextField(s37);

C5.setBounds(240,135,50,25);

C5.setEditable(false);

res.add(C5);

C6 = new JTextField(s38);

C6.setBounds(240,165,50,25);

C6.setEditable(false);

res.add(C6);

C7 = new JTextField(s39);

C7.setBounds(240,195,50,25);

C7.setEditable(false);

res.add(C7);

C8 = new JTextField(s40);

C8.setBounds(240,225,50,25);

C8.setEditable(false);

res.add(C8);

C9 = new JTextField(s41);

C9.setBounds(240,255,50,25);

C9.setEditable(false);

res.add(C9);
```

```
C10 = new JTextField(s42);
C10.setBounds(240,285,50,25);
C10.setEditable(false);
res.add(C10);

C11 = new JTextField(s43);
C11.setBounds(240,315,50,25);
C11.setEditable(false);
res.add(C11);

C12 = new JTextField(s44);
C12.setBounds(240,345,50,25);
C12.setEditable(false);
res.add(C12);

C13 = new JTextField(s45);
C13.setBounds(240,375,50,25);
C13.setEditable(false);
res.add(C13);

C14 = new JTextField(s46);
C14.setBounds(240,405,50,25);
C14.setEditable(false);
res.add(C14);

C15 = new JTextField(s47);
C15.setBounds(240,435,50,25);
C15.setEditable(false);
res.add(C15);

C16 = new JTextField(s48);
C16.setBounds(240,465,50,25);
C16.setEditable(false);
res.add(C16);

D1 = new JTextField(s49);
D1.setBounds(340,15,50,25);
D1.setEditable(false);
res.add(D1);

D2 = new JTextField(s50);
D2.setBounds(340,45,50,25);
```

```
D2.setEditable(false);

res.add(D2);

D3 = new JTextField(s51);
D3.setBounds(340,75,50,25);

D3.setEditable(false);

res.add(D3);

D4 = new JTextField(s52);
D4.setBounds(340,105,50,25);

D4.setEditable(false);

res.add(D4);

D5 = new JTextField(s53);
D5.setBounds(340,135,50,25);

D5.setEditable(false);

res.add(D5);

D6 = new JTextField(s54);
D6.setBounds(340,165,50,25);

D6.setEditable(false);

res.add(D6);

D7 = new JTextField(s55);
D7.setBounds(340,195,50,25);

D7.setEditable(false);

res.add(D7);

D8 = new JTextField(s56);
D8.setBounds(340,225,50,25);

D8.setEditable(false);

res.add(D8);

D9 = new JTextField(s57);
D9.setBounds(340,255,50,25);

D9.setEditable(false);

res.add(D9);

D10 = new JTextField(s58);
D10.setBounds(340,285,50,25);

D10.setEditable(false);

res.add(D10);

D11 = new JTextField(s59);
```



```
D11.setBounds(340,315,50,25);

D11.setEditable(false);

res.add(D11);

D12 = new JTextField(s60);

D12.setBounds(340,345,50,25);

D12.setEditable(false);

res.add(D12);

D13 = new JTextField(s61);

D13.setBounds(340,375,50,25);

D13.setEditable(false);

res.add(D13);

D14 = new JTextField(s62);

D14.setBounds(340,405,50,25);

D14.setEditable(false);

res.add(D14);

D15 = new JTextField(s63);

D15.setBounds(340,435,50,25);

D15.setEditable(false);

res.add(D15);

D16 = new JTextField(s64);

D16.setBounds(340,465,50,25);

D16.setEditable(false);

res.add(D16);

res.add(f);

res.add(f1);

res.add(f2);

res.add(f3);

res.add(f4);

res.add(f5);

res.add(f6);

res.add(f7);

res.add(f8);

res.add(f9);

res.add(f10);

res.add(f11);
```

```
res.add(f12);  
res.add(f13);  
res.add(f14);  
res.add(f15);  
    res.add(g);  
res.add(g1);  
res.add(g2);  
res.add(g3);  
res.add(g4);  
res.add(g5);  
res.add(g6);  
res.add(g7);  
res.add(g8);  
res.add(g9);  
res.add(g10);  
res.add(g11);  
res.add(g12);  
res.add(g13);  
res.add(g14);  
res.add(g15);  
    res.add(h);  
res.add(h1);  
res.add(h2);  
res.add(h3);  
res.add(h4);  
res.add(h5);  
res.add(h6);  
res.add(h7);  
res.add(h8);  
res.add(h9);  
res.add(h10);  
res.add(h11);  
res.add(h12);  
res.add(h13);  
res.add(h14);
```

```
res.add(h15);

res.add(l);

res.add(l1);

res.add(l2);

res.add(l3);

res.add(l4);

res.add(l5);

res.add(l6);

res.add(l7);

res.add(l8);

res.add(l9);

res.add(l10);

res.add(l11);

res.add(l12);

res.add(l13);

res.add(l14);

res.add(l15);

res.setLocationRelativeTo(null);

res.setVisible(true);
}

private void jComboBox2ActionPerformed(java.awt.event.ActionEvent evt) {

    // TODO add your handling code here:

    t = (String) jComboBox2.getSelectedItem();

}

@SuppressWarnings("empty-statement")

private void jButton3ActionPerformed(java.awt.event.ActionEvent evt)

{

    // TODO add your handling code here:

    ammy diff;
```

```
diff = new ammy(s);

double [] x1 = diff.calcDifreq(s);

double [] x2 = diff.calcTrifreq(s);

double max1= x1[0];

double max2= x2[0];

double min1= x1[0];

double min2= x2[0];

for (int i=0;i<x1.length;i++)

{

    if(x1[i]>max1)

        max1=x1[i];

    else;

}

for (int i=0;i<x1.length;i++)

{

    if(x1[i]<min1)

        min1=x1[i];

}
```

```
        else;

    }

    for (int i=0;i<x2.length;i++)

    {

        if(x2[i]>max2)

            max2=x2[i];

        else;

    }

    for (int i=0;i<x2.length;i++)

    {

        if(x2[i]<min2)

            min2=x2[i];

        else;

    }

    double diffe1= max1-min1;

    double diffe2= max2-min2;

    diffe1=diffe1*10000;

    diffe1=Math.round(diffe1);

    diffe1=diffe1/10000;
```

```

diffe2=diffe2*10000;

diffe2=Math.round(diffe2);

diffe2=diffe2/10000;

JFrame res= new JFrame("Discrimination for "+s);

res.setSize(420,200);

res.setLayout(null);

res.setLocationRelativeTo(null);

JLabel f =new JLabel();

f.setText(" Diff in Dinucleotide freq");

f.setSize(300,50);

f.setFont(f.getFont().deriveFont(14.0f));

JLabel f1 =new JLabel();

f1.setText(" Diff in Trinucleotide freq");

//f1.setSize(300,50);

f1.setBounds(0,30,300,50);

f1.setFont(f1.getFont().deriveFont(14.0f));

res.add(f);

res.add(f1);

String s1 = String.valueOf(diffe1);

String s2 = String.valueOf(diffe2);

JTextField A1,A2;

A1 = new JTextField(s1);

A1.setBounds(200,20,50,25);

A1.setEditable(false);

res.add(A1);

A2 = new JTextField(s2);

A2.setBounds(200,50,50,25);

A2.setEditable(false);

res.add(A2);

res.setVisible(true);

}

```

```
private void jButton5ActionPerformed(java.awt.event.ActionEvent evt)
```

```
{
    // TODO add your handling code here:

    ammy diff;

    diff = new ammy(s);

    double [] x1 = diff.calcDifreq(s);

    double [] x2 = diff.calcTrifreq(s);

    double [] m1= new double[x1.length];

    double [] m2 =new double[x2.length];

    double sum1 = 0;

    double sum2 = 0;

    double avg1;

    double avg2;

    for(int i=0;i<x1.length;i++)

    {

        sum1+=x1[i];

    }

    avg1=sum1/x1.length;

    for(int i=0;i<x2.length;i++)
```

```
{  
  
sum2+=x2[i];  
  
}  
  
avg2=sum2/x2.length;  
  
for(int i=0;i<x1.length;i++)  
  
{  
  
m1[i]=x1[i]-avg1;  
  
}  
  
for(int i=0;i<x2.length;i++)  
  
{  
  
m2[i]=x2[i]-avg2;  
  
}  
  
for(int i=0;i<x1.length;i++)  
  
{  
  
m1[i]*=m1[i];  
  
}  
  
for(int i=0;i<x2.length;i++)  
  
{
```



```
m2[i]*=m2[i];

}

double summate1=0;

double summate2=0;

for(int i=0;i<m1.length;i++)

{

summate1+=m1[i];

}

for(int i=0;i<m2.length;i++)

{

summate2+=m2[i];

}

double var1=summate1/m1.length;

double var2=summate2/m2.length;

var1=var1*10000;

var1=Math.round(var1);

var1=var1/10000;
```

```

var2=var2*10000;

var2=Math.round(var2);

var2=var2/10000;
System.out.println(var1+",");

    JFrame res= new JFrame("Variance for "+s);
    res.setSize(420,200);
    res.setLayout(null);
    res.setLocationRelativeTo(null);
    JLabel f =new JLabel();
    f.setText(" Variance for Dinucleotide freq");
    f.setSize(300,50);
    f.setFont(f.getFont().deriveFont(14.0f));
    JLabel f1 =new JLabel();
    f1.setText(" Variance for Trinucleotide freq");
    //f1.setSize(300,50);
    f1.setBounds(0,30,300,50);
    f1.setFont(f1.getFont().deriveFont(14.0f));
    res.add(f);
    res.add(f1);

    String s1 = String.valueOf(var1);
    String s2 = String.valueOf(var2);
    JTextField A1,A2;
    A1 = new JTextField(s1);
    A1.setBounds(200,20,50,25);
    A1.setEditable(false);
    res.add(A1);
    A2 = new JTextField(s2);
    A2.setBounds(200,50,50,25);
    A2.setEditable(false);
    res.add(A2);
    res.setVisible(true);

```

```

    }

private void jButton7ActionPerformed(java.awt.event.ActionEvent evt)
{
    // TODO add your handling code here:

    ammy diff;

    diff = new ammy(s,t);

    double [] x1 = diff.calcDifreq(s);

    double [] x2 = diff.calcTrifreq(s);

    double [] y1 = diff.calcDifreq(t);

    double [] y2 = diff.calcTrifreq(t);

    for(int i=0;i<x1.length;i++)

    {

        x1[i]=x1[i]-y1[i];

        x1[i]*=x1[i];

    }

    for(int i=0;i<x2.length;i++)

    {

        x2[i]=x2[i]-y2[i];

```

```
        x2[i]*=x2[i];

    }

    double su1=0;

    for(int i=0;i<x1.length;i++)

    {

        su1+=x1[i];

    }

    double su2=0;

    for(int i=0;i<x2.length;i++)

    {

        su2+=x2[i];

    }

    su1=sqrt(su1);

    su2=sqrt(su2);

    su1=su1*10000;

    su1=Math.round(su1);

    su1=su1/10000;
```

```

    su2=su2*10000;

    su2=Math.round(su2);

    su2=su2/10000;

    JFrame res= new JFrame("D for "+s+" "+t);

    res.setSize(420,200);

    res.setLayout(null);

    res.setLocationRelativeTo(null);

    JLabel f =new JLabel();

    f.setText(" D for di ");

    f.setSize(300,50);

    f.setFont(f.getFont().deriveFont(14.0f));

    JLabel f1 =new JLabel();

    f1.setText(" D for tri ");

    //f1.setSize(300,50);

    f1.setBounds(0,30,300,50);

    f1.setFont(f1.getFont().deriveFont(14.0f));

    res.add(f);

    res.add(f1);

    String s1 = String.valueOf(su1);

    String s2 = String.valueOf(su2);

    JTextField A1,A2;

    A1 = new JTextField(s1);

    A1.setBounds(200,20,50,25);

    A1.setEditable(false);

    res.add(A1);

    A2 = new JTextField(s2);

    A2.setBounds(200,50,50,25);

    A2.setEditable(false);

    res.add(A2);

    res.setVisible(true);

}

/**

```

```

* @param args the command line arguments
*/

public static void main(String args[]) {

    /* Set the Nimbus look and feel */

    //<editor-fold defaultstate="collapsed" desc=" Look and feel setting code (optional) ">

    /* If Nimbus (introduced in Java SE 6) is not available, stay with the default look and feel.
    * For details see http://download.oracle.com/javase/tutorial/uiswing/lookandfeel/plaf.html
    */

    try {

        for (javax.swing.UIManager.LookAndFeelInfo info : javax.swing.UIManager.getInstalledLookAndFeels()) {

            if ("Nimbus".equals(info.getName())) {

                javax.swing.UIManager.setLookAndFeel(info.getClassName());

                break;

            }

        }

    } catch (ClassNotFoundException ex) {

        java.util.logging.Logger.getLogger(aJFrame.class.getName()).log(java.util.logging.Level.SEVERE, null, ex);

    } catch (InstantiationException ex) {

        java.util.logging.Logger.getLogger(aJFrame.class.getName()).log(java.util.logging.Level.SEVERE, null, ex);

    } catch (IllegalAccessException ex) {

        java.util.logging.Logger.getLogger(aJFrame.class.getName()).log(java.util.logging.Level.SEVERE, null, ex);

    } catch (javax.swing.UnsupportedLookAndFeelException ex) {

        java.util.logging.Logger.getLogger(aJFrame.class.getName()).log(java.util.logging.Level.SEVERE, null, ex);

    }

    //</editor-fold>

    /* Create and display the form */

    java.awt.EventQueue.invokeLater(new Runnable() {

        public void run() {

            aJFrame f=new aJFrame();

            f.setTitle("PRATIBHA");

            f.setVisible(true);

            f.setLocationRelativeTo(null);

            f.setBackground(Color.green);

        }

    }

```

```

    });
}

// Variables declaration - do not modify

private javax.swing.JButton jButton1;
private javax.swing.JButton jButton2;
private javax.swing.JButton jButton3;
private javax.swing.JButton jButton4;
private javax.swing.JButton jButton5;
private javax.swing.JButton jButton6;
private javax.swing.JButton jButton7;
private javax.swing.JColorChooser jColorChooser1;
private javax.swing.JComboBox jComboBox1;
private javax.swing.JComboBox jComboBox2;
private javax.swing.JFrame jFrame1;
private javax.swing.JFrame jFrame2;
private javax.swing.JLabel jLabel2;

// End of variables declaration
}

```

```

class ammy {
    String a="",b="";
    ammy(String a)
    {
        this.a=a;
    }
    ammy(String a, String b)
    {
        this.a=a;
        this.b=b;
    }
    double[] calcDifreq(String s)

```

```

{
String q="";

if("Angiostrongylus cantonensis".equals(s))
{
q=
"GCTTTTGGGATTGTTAGACAGTCTACTTTATATTTAACGGGTAAAAAAGAGGTTTTTGGTTATTGGGTATGGTTTATGCTAT
TTTAAGAATTGGTTTGATTGGTTGTGTGGTTTGGGCTCATCATATATACGGTTGGTATGGATTAGATTCTCGTGCTTATT
TACTGCGGCTACTATAGTTATTGCGGTTCTACGGGAGTGAAGGTTTTAGGTGGTTGGCAACTTTATTGGTATAAAGATAT
TGTTTCAACCTATTTTATTGTGGGTTTTGGGTTTTATTTTTTTTACTATCGGTGGGTTAACGGGGTTATATTGTCTAATTC
TAGTTTGGATATTATTTACATGATACTTATTATGTAGTTAGGCATTTTCATTATGTTT";
}

else if("Angiostrongylus costaricensis".equals(s))
{
q=
"GCTTTTGGGATTATTAGTCAATCTGCTTTGTATTTGTCAGGGAAGAAAGAGGTTTTTGGTTATTTAGGGATGGTTTATGCGAT
TTTAAGAATTGGGTTGATTGGGTGTGTAGTTTGAGCTCATCATATGTATACTGTTGGTATGGATTGGATTCTCGTGCTTACTT
TACTGCAGCTACAATAGTTATTGCGGTTCTACTGGGTTAAAGTGTTAGTTGGTTGGCTACACTTTATGGGATGAAAATGA
TGTTTCAGCCGATTTTGTGTGGGTTATGGGGTTTATTTTTTGTACTATTGGGGGTTTGACCGGGGTTATGTTATCTAATTC
AAGTTTGGATATTATTTGCATGATACTTATTATGTGGTT";
}

else if("Angiostrongylus vasorum".equals(s))
{
q=
"GCTTTTGGGATTGTTAGTCAGTCGACTTTATATTTGACTGGGAAGAAGGAGGTGTTTGGTTATTTGGGGATGGTTTATGCGAT
TTTAAGGATTGGTTTGATTGGTTGTGTGGTGTGAGCTCATCATATGTATACTGTTGGTATAGATTAGATTCTCGTGCTTATT
TACTGCGGCTACTATGGTGATTGCGGTGCCGACTGGAGTGAAGGTTTTTAGTTGGTTGGCTACTTTGTTGGGATGAAGTATA
GTATTTACAGCCTATTTTGTGTGGGTTATAGGATTTATTTTTTTTACTATTGGGGGTTTGACCGGTGTGATATTGTCAA
TTCGAGATTGGATATTATTTACATGATACGTATTATGTGGTAAGTCATTTTCATTATGTGAGGTTGTTTCATGATACTTGGTT
T";
}

else if("Diplogonoporus balaenopterae".equals(s))
{
q=
"GGGTTTGGGAATGATTAGACATGTTTGTAGTAACTTAGGTTGTTTCATATGATACTTTTGGATTTTATGGTTTATTATTTGCTATG
TTTTCTATCGTTTGTCTTGGTAGGGTTGTATGGGGTCATCATATGTTTACGGTAGGTTTAGATGTGAAGACAGCTGTTTTTTT
AGGTCAGTFACTATGATTATAGGGGTGCCTACTGGAATAAAGGTGTTTTCTTGGCTGTATATGATTTTAAAAAGTCGTGTCTC
TTTGCCTGAACCTATATTTGGTGGGTGTTATCTTTTATCGTGCTGTTTACAATAGGGGGTGTACTGGTATTATACTTTCTGC
TTGTGTTCTTGATAATATTTTGCATGATACTTGATTT";
}

else if("Diplogonoporus grandis".equals(s))
{
q=
"GGGTTTGGGAATGATTAGACATGTTTGTAGTAACTTAGGTTGTTTCATATGATACTTTTGGATTTTATGGTTTATTATTTGCTATG
TTTTCTATCGTTTGTCTTGGTAGGGTTGTATGGGGTCATCATATGTTTACGGTAGGTTTAGATGTGAAGACAGCTGTTTTTTT
AGGTCAGTFACTATGATTATAGGGGTGCCTACTGGAATAAAGGTGTTTTCTTGGCTGTATATGATTTTAAAAAGTCGTGTCTC
TTTGCCTGAACCTATATTTGGTGGGTGTTATCTTTTATCGTGCTGTTTACAATAGGGGGTGTACTGGTATTATACTTTCTGC
TTGTGTTCTTGATAATATTTTGCATGATACTTGATTT";
}

```



```

}

else if("Aelurostrongylus abstrusus".equals(s))

{

    q=
"GCTTTTGGTATTGTTAGTCAGTCTACTTTGTATTTGACGGGAAGAAGGAAGTTTTTGGTTATTTAGGGATAGTTTATGCTAT
TATAAGTATTGGTTAATTGGTTGTGTTGGGCTCATCATATATACTGTTGGTATAGATTTGGATTCTCGTGCTTATTTT
ACGGCGGCTACGATGGTTATTGCTGTGCCAACGGGTGTTAAGGTTTTTAGTTGGTTGGCTACTTTATTGGAATGAAGATAGT
GTTTCAGCCGGTTTTGTTGTGGGTTTTGGGTTTTATTTTTTTGTTACTATTGGGGGGTTAACTGGGGTCATGCTTTCGAATTCT
AGTTTGGATATTATTTGCATGATACTTATTATGTGGTTAGTCATTTTCATTATGTGTTGAGTTT";

}

else if("Dictyocaulus eckerti".equals(s))

{

    q=
"GCTTTTGGTATTATTAGTCAGTCAACTTTGTATTTAACTGGTAAAAAGGAGGTTTTTGGTTCCTTGGGTATGGTTTATGCTATT
TTAAGTATTGGTTAATTGGTTGTGTAGTATGAGCACATCATATATACTGTTGGAATAGATTTGGATTTCGCGTGCTTATTTT
ACTGCTGCTACTATGGTAATTGCTGTTCTACGGGTGTA AAAAGTTTTTAGTTGGTTGGCTACTTTGTATGGTTAAAAATAGTA
TATAATCCTTTGTTGTTATGGGTTTTGGGTTTTATTTTTTTATTACTATTGGGGGGTTAACTGGAGTTATTTTGTCAAATTCTA
GTTTAGATATTTTGTACATGATACTTATTATGTTGTAAGGCATT";

}

else if("Dictyocaulus viviparus".equals(s))

{

    q=
"GCTTTTGGTATTATTAGACAATCTACTTTGTATTTAACTGGTAAAAAGGAGGTTTTTGGTTCCTTGGGTATGGTTTATGCTATT
TTAAGTATTGGTTAATTGGTTGTGTGTGGGCACATCATATGTATACTGTTGGGATGGATTTGGATTTCGCGTGCTTATTTT
ACTGCTGCTACTATAGTAATTGCTGTTCTACTGGAGTTAAGGTTTTTAGATGATTGGCTACTTTATATGGATTGAAAATGGTT
TATAATCCTTTGTTGTTGTGAGTTTTAGGTTTTATTTTTTTGTTACTATTGGTGGTTAACTGGTGTATTTTGTCAAATTCTA
GTCTTGATATTTTGTGCATGATACTTATTAT";

}

else if("Ascaris lumbricoides".equals(s))

{

    q=
"GCTTTTGGTATTATTAGTCAGAGTAGTTTGTATTTGACTGGTAAAAAGGAGGTTTTTGGGTCTTTGGGTATGGTTTATGCTAT
TTTAAAGTATTGGTTGATTGGTTGTGTTGTTTGGAGCTCATCATATGTATACTGTTGGTATGGATCTTGATTCTCGGGCTTATTTT
ACTGCTGCAACTATGGTTATTGCTGTTCTACTGGTGTAAAGGTTTTTAGTTGGTTGGCTACCTTGTTTGGTATAAAAATGGTT
TTTCAGCCTTTACTTTTATGAGTTATGGGTTTTATTTTTTTGTTACTATTGGTGGGTTAAACCGGGGTTATACTTTCTAATTCTA
GTTTGGATATTATCTTGCATGATACTTATTATGTTGTTAGTCATTTTCATTATGTTCTTAGTTT";

}

else if("Ascaris suum".equals(s))

{

    q=
"GCTTTTGGTATTATTAGTCAGAGTAGTTTGTATCTGACTGGTAAAAAGGAGGTTTTTGGGTCTTTGGGTATGGTTTATGCTAT
TTTGAAGTATTGGTTAATTGGTTGTGTTGTTTGGAGCTCATCATATGTATACTGTTGGTATGGATCTTGACTCTCGGGCTTATTTT
ACTGCTGCAACTATGGTTATTGCTGTTCTACTGGTGTAAAGGTTTTTAGTTGGTTGGCTACCTTGTTTGGTATAAAGATGGTT
TTTCAACCTTTACTTTTATGAGTTATGGGTTTTATTTTTTTGTTACTATTGGTGGGTTAAACCGGGGTTATGCTTTCTAATTCTA
GTTTGGATATTATCTTGCATGATACTTAA-TTATGTTGTTAGTCATTTTCATTATGTCCTTAGTTT";

}

else if("Baylisascaris ailuri".equals(s))

```

```

{

    q=
"GCTTTTGGTATTATTAGCCAGAGTAGGTTGTATTTAACTGGTAAAAAGGAAGTTTTTGGTCTTTGGGTATGGTTTATGCTAT
TTTGAGTATTGGTTTAATTGGTTGTGTTGTTGGGCTCATCATATGTATACTGTAGGTATGGATTGGATTCTCGTGCTTATTT
ACTGCGGCTACTATGGTTATTGCGGTCCCTACGGGTGTTAAGGTTTTTAGTTGGTTGGCTACTTTGTTGGTATGAAGATGGTG
TTCCAGCCTTTACTTTTGTGAGTTATGGGTTTTATTTTTTTTATTACTATTGGCGGATTGACTGGGGTGATGCTTCTAATTCTA
GTTTGGATATTATTTGCATGATACTTA-TTATGTTGTTAGACATTTTCATTATGTTCTTAGTTT";

}

else if("Baylisascaris procyonis".equals(s))

{

    q=
"GCTTTTGGTATTATTAGCCAAAGTAGGTTGTATTTAACTGGTAAGAAGGAAGTTTTTGGTCTTTGGGAATGGTTTATGCTAT
TTTGAGTATTGGTTTGGATTGGATGTGTGGTTTGGGCTCATCATATGTATACTGTGGGTATGGATTGGATTCTCGGGCTTATTT
TACTGCGGCTACTATGGTTATTGCGGTTCCTACGGGAGTTAAGGTTTTTAGTTGGTTGGCCACTTTATTTGGTATGAAGATAGT
GTTTCAGCCTTTGCTTTTGTGGGTTATGGGTTTTATTTTTTTGTTTACTATTGGTGGTTGACTGGGGTTATGCTTCTAATTCT
AGTTTGGATATTATTTGCATGATACTTATTATGTTGTTAGGCATTTTCATTATGTTCTTAGTTT";

}

else if("Baylisascaris schroederi".equals(s))

{

    q=
"GCTTTTGGTATTATTAGTCAGAGTAGGTTGTATCTGACTGGTAAGAAGGAGGTTTTTGGTCTTTGGGTATGGTTTACGCAAT
TTTGAGTATTGGTTTGGATTGGTTGTGTTGTTTGGGCTCATCATATGTATACTGTGGGTATAGATTGGATTCTCGTGCTTATTTT
ACTGCGGCTACTATGGTTATCGCAGTTCCTACGGGTGTTAAGGTTTTTAGTTGGTTGGCCACTTTGTTGGTATGAAGATGGTG
TTTCAGCCTTTGCTTTTGTGGGTTATAGGATTTATTTTTTTGTTTACTATTGGTGGATTGACTGGGGTGATGCTTCTAATTCTA
GTTTGGATATTATTTGCATGATACTTA-TTATGTTGTTAGGCATTTTCATTATGTTCTTAGTTT";

}

else if("Baylisascaris transfuga".equals(s))

{

    q=
"GCTTTTGGTATTATTAGTCAGAGTAGATTGTATTTAACTGGTAAAAAGGAGGTTTTTGGTCTTTGGGTATGGTTTATGCTAT
TTTGAGTATTGGTTTAATTGGTTGTGTTGTTTGGGCTCATCATATGTATACTGTAGGTATGGATTGGATTCTCGTGCTTATTTT
ACTGCGGCTACTATGGTTATTGCGGTTCCTACAGGTGTTAAGGTTTTTAGTTGGTTGGCCACTTTGTTGGTATGAAGATGGTG
TTTCAGCCTTTACTTTTGTGGGTTATGGGTTTTATTTTTTTTATTACTATTGGTGGATTGACTGGGGTGATGCTTCTAATTCTA
GTTTGGATATTATTTGCATGATACTTATTATGTTGTTAGGCATTTTCATTATGTTCTTAGTTT";

}

else if("Toxocara canis".equals(s))

{

    q=
"GCTTTTGGTATTATTAGCCAAAGTAGTTTGTATTTGACTGGTAAAAAGGAGGTTTTTGGTCTTTAGGCATGGTTTATGCTAT
TTTAAGTATTGGTCTGATTGGCTGTGTAGTTTGGGCTCACCATATGTATACGGTGGGCATGGATTGGATTCTCGTGCTTATTT
TACTGCGGCAACGATGGTTATTGCTGTGCCTACGGGGGTTAAGGTTTTTAGTTGGTTAGCCACTCTTTTGGTATGAAGATGG
TGTTTCAACCTTTGCTTTTGTGGGTTGCTGGGTTTTATTTTTTTTATTACTATCGGGGGGTTGACTGGTGTATGTTATCTAATTC
TAGGTTGGACATTATCTTGCATGATACTTATTATGTTGTTAGTCATTTTCATTATGTTT";

}

else if("Toxocara cati".equals(s))

{

    q=
"GATTTTTTGGGCATCCTGAGGTTTATATTTTGATTTTACCTGCCTTGGTATTATTAGTCAAAGTAGTTTATATTTAACTGGTA

```

AGAAGGAGGTTTTGGTCTTTGGGCATGGTCTATGCTATTTGAGTATTGGTTGATTGGTTGTGGTGTGAGCTCACCACA
TGTATACTGTTGGTATAGACTTGGATTCTCGGGCTTATTTACTGCGGCTACTATGGTTATCGCTGTGCCTACGGGTGTTAAGG
TTTTAGTTGGTTGGCTACTCTTTTGGTATAAAAAATGGTTTTTCAACCTTTGCTTTTGTGAGTGTGGGTTTTATTTTTTGT
ACTATTGGTGGGCTTACTGGAGTTATGCTTTCTAATTCTAGTTGGATATTATTTGCATGACACCTATTATGTTGTGAGGCAT
TTCCACTATGTTT";

}else if("Toxocara malaysiensis".equals(s))

{

q=

"GCTTTTGGTATTATTAGTCAGAGTAGTTTGTATTTAACTGGTAAGAAGGAAGTTTTTGGTTCGTTGGGGATGGTTTTATGCTAT
TTTAAGTATTGGTTGATTGGCTGTGTGGTTTGGGCTCATCATATGTATACCGTGGGTATAGATTGGATTCTCGGGCTTATTT
TACTGCGGCGACTATGGTTATTGCTGTGCCTACTGGTGTAAAGGTTTTAGTTGGTTGGCTACTCTTTTGGTATGAAAATGGT
TTTTACAGCTTTACTTTTTATGGGTGTTAGGTTTTATTTCTTGTTTACTATTGGGGGCCCTTACTGGTGTGATGCTTTCTAATTCT
AGCCTTGATATTATTTGCATGATACCTATTATGTTGTTAGACATTTTCATTATGTTT";

}

else if("Taenia asiatica".equals(s))

{

q=

"GGTTTTGGTATGATTAGTCATATATGTTTAAAGAATAAGTATGTGTCCGGATGCTTTTGGTTTTATGGTTTGTATTGCTATG
TTTTCAATAGTATGTTTGGGGAGAAGTGTGTGGGGTCATGATATGTTTACGGTTGGATTAGTTGTTAAGACTACTGTGTTTTTT
AGTTCCGGTACTATGATAATAGGAGTACCAACAGGAATAAAGGTTTTTACTTGACTTTATATGCTTTTAAATTCCTCGTGTA
AAAGAGGGATCCTATATTGTGGTGGATAGTTTCTTTTATAGTGTGTTTACCTTTGGTGGTGTGACTGGTATTGTGTTGTCCTGC
TTGTGATTGGATAAAGTTTTGCATGATACTTGATT";

}

else if("Taenia crassiceps".equals(s))

{

q=

"GGTTTTGGAATTATTAGACATATTTGTTTAAAATAAGTATGAATTGTGATTCTTTTGGTTTTTATGGATTGTTATTGCTATG
TTTTCAATAGTTTGTAGGTAGGAGTGTGGGGTCATCATATGTTTACGGTTGGTTTAGATGTTAAGACTGCTGTTTTTTTT
AGTTCTGTTACTATGATTATAGGAGTACCTACAGGTATAAAGGTGTTTACTTGATTGTATATGCTTTTAAATTCGCGTGTGAA
CAAGAGTGATCCTATATTGTGGTGAATTGTTTCTTTTATAGTTTTATTTACGTTTGGTGGTGTACTGGAATAGTATTGTCCTGC
TTGTGATTAGATAAAGTTCTTCATGATACTTGATT";

}

else if("Taenia hydatigena".equals(s))

{

q=

"GGATTTGGAATTATTAGTCATATATGTTTGAAGAATAAGTATGAGTCCTGATGCTTTTGGGTTCTATGGATTATTATTGCTAT
GTTTTCAATAGTCTGTTTGGGTAGAAGTGTGTGGGGTCATCATATGTTTACTGTTGGGTTAGATGTTAAGACTGCTGTTTTTTTT
TAGTTCTGTGACTATGATTATAGGTGTGCCTACTGGTATAAAGGTGTTTACTTGGTTATATATGCTTTTAAACTCTCATGTGAA
TAAGAGTGATCCTGTTGTTGATGAATTGTTTCTTTTATAGTTTTGTTTACTTTTGGTGGGTTACTGGTATTGTGTTGTCAGCA
TGTGATTAGATAAAGTTCTTCATGATACTTGATT";

}

else if("Taenia krepkogorski".equals(s))

{

q=

"GGATTTGGTATAATTAGTCATATATGTTTAAAGAATAAGTATGTCTTCTGATGTGTTTGGGTTTTATGGTTTATTATTGCTATG
TTTTCTATAGTTTGTAGGAAGAAGAGTGTGAGGTCATCACATGTTTACTGTTGGTTTAGATGTTAAGACTGCTGTGTTTTTT
AGCTCAATTACTATGATTATTGGTGTGCCTACTGGGATTAAGGTTTTTACATGATTATATATGTTATTAAATGCTCGAGTAAA
AAAGAGTGATCCTGTGTTGTGGTGAATTGTTTCAATTATAATATTGTTTACATTTGGTGGAGTTACTGGTATAGTATTGTCCTGC
TTGTGTTTTAGATAAAGTTTACATGATACTTGTTT";

```

}

else if("Taenia laticollis".equals(s))

{

    q=
"GGATTTGGTATAATTAGACATATATGTTTAAAGTATTAGTATGTGTTCCGGATGCTTTCGGTTTTTATGGTTTATTATTTGCTATG
TTTTCTATTGTTTGTAGGGAGAAGAGTTTGGGGTCATCATATGTTTACAGTTGGGTTAGATGTTAAGACGGCTGTATTTTT
AGTTCGTAACATGATTATTGGTGTACCTACAGGTATAAAGGTTTTTACATGATTATATATGCTTTTAAATTCCTCGGGTAAA
AAGAGTGATCCTGTATTATGGTGGATAGTTTCTTTTATAGTTTTGTTTACGTTTGGTGGTGTACAGGAATAGTGTGTCTGCT
TGGTATTAGATAAAGTATTACATGATACTTGATTT";

}

else if("Taenia madoquae".equals(s))

{

    q=
"GGTTTTGGGATAATTAGTCATATATGTTTGAGGATTAGTATGTGTCCTGATGCTTTTGGTTTTTATGGTTTGTATTGCTATG
TTCTCAATAGTGTGTTTGGGAAGGAGTGTATGAGGTATCACATGTTTACGTTGGATTAGATGTTAAGACTGCTGTATTTTT
TAGTTCGGTTACTATGATAATAGGAGTACCTACAGGAATAAAGGTTTTTACTTGACTTTATATGCTTTTAAATTCCTGTGTA
ATAAGAGTGATCCTGTGTTATGATGGATAGTTCTTTTATAGTATTGTTTACTTTTGGTGGTGTAACTGGTATTGTATTATCTG
CTTGTGTATTGGATAATGTTTTACATGATACTTGATTT";

}

else if("Taenia martis".equals(s))

{

    q=
"GGTTTTGGTATAATTAGACATATTTGCTAAATATAAGTATGAATTATGATTCCTTTTGGTTTTTATGGTTTATTATTTGCTATG
TTTTCTATAGTTTGTGGTAGTAGTGTGTTGGGGTCATCATATGTTTACTGTTGGATTAGATGTTAAGACTGCTGTTTTTTTC
AGTTCAGTTACTATGATAATAGGAGTTCCTACGGGTATAAAGGTTTTTACTTGATTATATATGCTTTTAAATTCCTGTGTAAT
AAGAGTGATCCTGTATTATGGTGAATTGTTTCTTTTATTATTTGTTTACTTTTGGTGGTGTACTGGTATAGTGTATCTGCAT
GTGTTTTGGATAAAGTTCCTCATGATACTTGATTT";

}

else if("Taenia multiceps".equals(s))

{

    q=
"GGTTTTGGTATAATTAGTCACATATGTTTAAAGAATAAGCATGTGTCAGATGCTTTTGGTTTTTATGGTTTATTATTTGCTATG
TTTTCAATAGTGTGTTTAGGGAGAAGTGTGTGAGGCCATCATATGTTTACAGTTGGGTTAGATGTTAAGACTGCTGTATTTTTT
AGTTCGGTTACTATGATAATAGGAGTCCCCACAGGAATAAAGGTTTTTACTTGCTTTATATGCTTTTAAATTCCTGTGTA
CAAGAGTGATCCTATACTATGATGAATAGTTTCTTTTATAGTATTGTTTACTTTTGGTGGTGTAACTGGGATTGTATTGCTG
TTGTGTATTAGATAAAGTTTTACATGATACTTGATTT";

}

else if("Taenia mustelae".equals(s))

{

    q=
"GGTTTTGGTATTATTGGTCATATATGTTTGAAGTATAAGGATGTGTTCTGATGCTTTTGGGTTTTATGGATTGTTGTTTGTATG
TTTTCTATTGTTTGTCTAGGTAGTAGAGTTTGAAGGCATCATATGTTTACTGTTGGTTTAGATGTTAAGACTGCTGTTTTTTTT
GTTCTGTTACTATGATTATAGGAGTTCCTACTGGTATAAAGGTTTACTTGTTGTATATGTTACTGAATTCAGTGTAAACA
AGAGGGATCCTGTGTTGTGATGAATAGTGCATTTATATTTTTGTTTACTTTTGGTGGTGTACTGGTATAGTTTTGCTGCTT
GTGTATTAGATAATGTTTTGCATGATACTTGATTT";

}

else if("Taenia ovis".equals(s))

```

```

{

    q=
"GGATTGGTATAATTAGTCATATTTGTTGAGGATTAGTATGTGTCCAGATGCTTTTGGTTTTATGGCTTATTATTTGCTATG
TTTTCTATAGTATGTTTAGGAAGAAGTGTGTGGGGGCATCATATGTTTACTGTTGGGTTGGATGTTAAGACGCTGTATTTTT
AGTTCGGTFACTATGATCATAGGTGTGCCTACTGGTATAAAGGTTTTTACTTGGCTTTATATGCTTCTGAAATCTCGTGTGAAT
AAGAGTGATCCTATTTTGTGATGGATAGTTCTTTTATAGTATTATTTACTTTTGGAGGTGTGACTGGTATTGTTTTATCTGCTT
GTGTATTGGATAAAGTTCTTCATGATACTTGATTT";

}

else if("Taenia parva".equals(s))

{

    q=
"GGTTTGGGATTATAAGACATATATGTTTAAGAATTAGTATGTGTGATGATGCTTTTGGTTTTTATGGTTTGTATTGCTATGT
TTTTCTATTGTGTTTTAGGAAGAAGTGTATGAGGCCATCATATGTTTACTGTAGGTTTAGATGTGAAGACTGCTGTGTTTTTA
GTTTCAGTAACAATGATTATCGGGGTTCCCTACTGGGATAAAGGTTTTTACTTGGATTATATGTTACTTAATTCTCGTATTAATA
AGGGTGATCCTGTAATTTGATGAATTGTTCTTTCATAGTTTTTACGTTTGGTGGTGTCACTGGTATAGTTTTATCAGCTT
GTGTTTTAGATAAAGTTTTGCATGATACTTGATTT";

}

else if("Taenia pisiformis".equals(s))

{

    q=
"GGGTTTGGTATAATTAGTCATATATGTTTAAGAATAAGTATGTGTTCAGATGCGTTTGGTTTTTATGGTTTATTGTTTGAAT
GTTTTCTATAGTTTGTAGGTAGAAGTGTATGAGGTCATCATATGTTTACTGTGGATTAGATGTAAGACCGCTGTGTTTTT
TAGTTCAGTAACAATGATAATTGGAGTACCTACTGGAATTAAGGTTTACATGACTTTATATGCTTTTAAATTCTCGTGCA
AAAAGAGTGATCCTGTGTTGTGGTGAATAATTTCTTTTATAGTCTTATTTACTTTTGGAGGTGTAAGTGGTATAGTATTATCTG
CTTGTGTTTTAGATAAAGTT-TTACATGATACTTGATTT";

}

else if("Taenia saginata".equals(s))

{

    q=
"GGTTTGGTATGATTAGTCATATATGTTTAAGAATAAGTATGTGTCCAGATGCTTTTGGTTTTTATGGTTTGTGTTTGTATG
TTTTCAATAGTGTGTTTGGGGAGAAGTGTGTGGGGTCATCATATGTTTACGGTTGGGTTAGATGTTAAGACTGCTGTGTTTTT
AGTTCGGTFACTATGATAATAGGAGTACCAACAGGAATAAAGGTTTTTACTTGGCTTTATATGCTTTTAAATTCTCGTGAAA
TAAGAGTGATCCTATATTGTGGTGAATAGTTCTTTTATAGTGTGTTTACTTTTGGTGGTGTGACTGGTATTGTGTTGTCTGC
TTGCGTATTGGATAAAGTTTTGCATGATACTTGATTT";

}

else if("Taenia serialis".equals(s))

{

    q=
"GGTTTTGGTATAATTAGTCATATATGTTTAAGAATAAGTATGTGTCCAGACGCTTTTGGTTTTTATGGTTTGTATTGCTATG
TTCTCAATAGTGTGTTTAGGAAGGAGTGTATGGGGTCATCATATGTTTACAGTTGGGTTAGATGTTAAGACTGCTGTATTTTT
AGCTCAGTFACTATGGTAATAGGAGTACCAACAGGAATAAAGGTTTTTACTTGGCTTTATATGTTATTAAATTCTCGTGTGAA
TAAGAGTGATCCTATATTGTGGTGGATAGTTCTTTTATAGTATTGTTTACTTTTGGTGGTGTAACTGGGATTGTATTGTCTGC
TTGTGTGTTGGATAAAGTTTTACATGATACTTGATTT";

}

else if("Taenia solium".equals(s))

{

    q=
"GGGTTTGGTATAATTAGTCATATATGTTTGAAGTATAAGTATGTGTTCTGATGCTTTTGGCTTTTATGGGTTATTGTTGCTATG

```

```
TTTTCAATAGTATGTTTAGGAAGAAGTGTGTGAGGACATCATATGTTTACGGTTGGGTTAGATGTTAAGACGGCTGTATTTTT
TAGTTCTGTTACTATGATAAATTGGAGTGCCTACGGGGATTAAGGTTTTTACTTGGCTTTATATGCTTTTAAAAATCTCGTGTTAA
TAAGAGTGATCCGGTTTTATGATGAATAATTTTCGTTTATAGTATTGTTTACATTTGGTGGTGTAAACCGGTATTATTCTATCTGC
TTGTGTATTAGATAAAGTTCTTCATGATACTTGGTTT";
```

```
}
```

```
else if("Taenia twitchelli".equals(s))
```

```
{
```

```
q=
```

```
"GGTTTTGGTATAATTAGACATATTTGTTTAAATGTAAGTATGAATTATGATTCTTTTGGATTTTATGGTTTGTTATTTGCTATG
TTTTCTATAGTTTGTAGGTAGAAAGTGTATGAGGTCATCATATGTTTACTGTTGGATTAGATGTTAAGACTGCTGTTTTTTTT
AGTTCTGTTACTATGATTATAGGGTTCCTACAGGTATAAAGGTGTTTACTTGGTTATATATGCTTTTAAAAATCTCGTGAAAT
AAGAGTGATCCTGTTTTATGATGAATTGTGTCTTTTATTATTTTGTACTTTTGGTGGTGTACTGGTATAGTGTATCTGCGT
GTGTTTTGGATAAAGTTCTTCATGATACTTGGTTT";
```

```
}
```

```
else if("Taeniopygia guttata".equals(s))
```

```
{
```

```
q=
```

```
"GGTTTCGGCATCATCTCCCACGTCGTAACCTACTATTCAGGTAAAAAAGAACCATTCCGATATATAGGAATAGTATGAGCTA
TGCTATCCATCGGATTCCTAGGATTCATCGTATGAGCCCACCACATGTTTACAGTAGGAATGGACGTAGACACCCGAGCATA
CTTTACATCCGCCACTATAATCATCGCCATCCCAACCGGCATCAAAGTATTCAGCTGACTAGCAACACTCCACGGAGGCACA
ATCAAGTGAGACCCACCAATACTATGAGCTCTAGGATTTATCTTCTATTACCATCGGAGGCCTAACCGGAATCGTCCTGGC
CAACTCCTACTAGACATCGCCCTACACGACACCTACTACGTAGTAGCCCACCTCCACTACGTCCTATCAATAGGAGCAGTGT
TTGCAATCCTAGCAGGATTCACCCACTGATT";
```

```
}
```

```
double AA=0,AC=0,AG=0,AT=0,CA=0,CC=0,CG=0,CT=0,GA=0,GC=0,GG=0,GT=0,TA=0,TC=0,TG=0,TT=0;
```

```
int length = q.length();
```

```
for(int i=0;i<length-1;i++)
```

```
{
```

```
if(q.charAt(i)=='A')
```

```
{
```

```
if(q.charAt(i+1)=='A')
```

```
{
```

```
AA++;
```

```
}
```

```
else if(q.charAt(i+1)=='C')
```

```
{
```

```
AC++;
```

```
}
```

```
else if(q.charAt(i+1)=='G')
```

```

    {
        AG++;
    }
else if(q.charAt(i+1)=='T')
    {
        AT++;
    }
}
else if(q.charAt(i)=='C')
    {
        if(q.charAt(i+1)=='A')
            {
                CA++;
            }
        else if(q.charAt(i+1)=='C')
            {
                CC++;
            }
        else if(q.charAt(i+1)=='G')
            {
                CG++;
            }
        else if(q.charAt(i+1)=='T')
            {
                CT++;
            }
    }
else if(q.charAt(i)=='G')
    {
        if(q.charAt(i+1)=='A')
            {
                GA++;
            }
        else if(q.charAt(i+1)=='C')
            {

```

```

        GC++;
    }
    else if(q.charAt(i+1)=='G')
    {
        GG++;
    }
    else if(q.charAt(i+1)=='T')
    {
        GT++;
    }
}
else if(q.charAt(i)=='T')
{
    if(q.charAt(i+1)=='A')
    {
        TA++;
    }
    else if(q.charAt(i+1)=='C')
    {
        TC++;
    }
    else if(q.charAt(i+1)=='G')
    {
        TG++;
    }
    else if(q.charAt(i+1)=='T')
    {
        TT++;
    }
}
}
AA=AA/length;
AC=AC/length;
AG=AG/length;
AT=AT/length;

```


CA=CA/length;

CC=CC/length;

CG=CG/length;

CT=CT/length;

GA=GA/length;

GC=GC/length;

GT=GT/length;

GG=GG/length;

TA=TA/length;

TC=TC/length;

TG=TG/length;

TT=TT/length;

AA=AA*10000;

AA=Math.round(AA);

AA=AA/10000;

AC=AC*10000;

AC=Math.round(AC);

AC=AC/10000;

AG=AG*10000;

AG=Math.round(AG);

AG=AG/10000;

AT=AT*10000;

AT=Math.round(AT);

AT=AT/10000;

CA=CA*10000;

CA=Math.round(CA);

CA=CA/10000;

CC=CC*10000;

CC=Math.round(CC);

CC=CC/10000;

CG=CG*10000;

CG=Math.round(CG);

CG=CG/10000;

CT=CT*10000;

```

CT=Math.round(CT);

CT=CT/10000;

GA=GA*10000;

GA=Math.round(GA);

GA=GA/10000;

GC=GC*10000;

GC=Math.round(GC);

GC=GC/10000;

GG=GG*10000;

GG=Math.round(GG);

GG=GG/10000;

GT=GT*10000;

GT=Math.round(GT);

GT=GT/10000;

TA=TA*10000;

TA=Math.round(TA);

TA=TA/10000;

TC=TC*10000;

TC=Math.round(TC);

TC=TC/10000;

TG=TG*10000;

TG=Math.round(TG);

TG=TG/10000;

TT=TT*10000;

TT=Math.round(TT);

TT=TT/10000;

double[] c={AA,AC,AG,AT,CA,CC,CG,CT,GA,GC,GG,GT,TA,TC,TG,TT};

    return c;
}

double[] calcTrifreq(String s)

{
String q="";

```

```

if("Angiostrongylus cantonensis".equals(s))
{
    q=
"GCTTTTGGGATTGTTAGACAGTCTACTTTATATTTAACGGGTAAAAAAGAGGTTTTGGTTATTTGGGTATGGTTTATGCTAT
TTAAGAATTGGTTTGATTGGTTGTGTGGTTTGGGCTCATCATATATACGGTTGGTATGGATTAGATTCTCGTGCTTATT
TACTGCGGCTACTATAGTTATTGCGGTTCTACGGGAGTGAAGGTTTTAGGTGGTTGGCAACTTTATTGGTATAAAGATAT
TGTTTCAACCTATTTTATTGTGGTTTTGGTTTTATTTTTTATTTACTATCGGTGGGTTAACGGGGTTATATTGTCTAATTC
TAGTTTGGATATTTTACATGATACTTATTATGTAGTTAGGCATTTTCATTATGTTT";
}

else if("Angiostrongylus costaricensis".equals(s))
{
    q=
"GCTTTTGGGATTATTAGTCAATCTGCTTTGTATTTGTACAGGAAGAAAGAGGTTTTGGTTATTTAGGGATGGTTTATGCGAT
TTAAGAATTGGGTTGATTGGGTGTGTAGTTTGTAGCTCATCATATGTATACTGTTGGTATGGATTGGATTCTCGTGCTTACTT
TACTGCAGCTACAATAGTTATTGCGGTTCTACTGGGGTAAAGTGTTTGTGGTTGGCTACACTTTATGGGATGAAAATGA
TGTTTCAGCCGATTTTGTGTGGGTTATGGGGTTATTTTTTGTACTATTGGGGGTTTGACCGGGGTTATGTTATCTAATTC
AAGTTTGGATATTTTGCATGATACTTATTATGTGGTT";
}

else if("Angiostrongylus vasorum".equals(s))
{
    q=
"GCTTTTGGGATTGTTAGTCAGTCGACTTTATATTTGACTGGGAAGAAGGAGGTGTTTGGTTATTTGGGGATGGTTTATGCGAT
TTAAGGATTGGTTTGATTGGTTGTGTGGTGTGAGCTCATCATATGTATACTGTTGGTATAGATTAGATTCTCGTGCTTATT
TACTGCGGCTACTATGGTGATTGCGGTGCCGACTGGAGTGAAGGTTTTTGTGGTTGGCTACTTTGTTGGGATGAAGTATA
GTATTTACAGCCTATTTTGTGTGGGTTATAGGATTTATTTTTTTTTTACTATTGGGGGTTTGACCGGGTGTGATATTGTCAA
TTCGAGATTGGATATTTTACATGATACGTATTATGTGGTAAGTCATTTTCATTATGTGAGGTTGTTTCATGATACTTGGTT
T";
}

else if("Diplogonoporus balaenopterae".equals(s))
{
    q=
"GGGTTTGGAAATGATTAGACATGTTTGTAGTAACCTAGGTTGTTTCATATGATACTTTTGGATTTTATGGTTTATTATTGCTATG
TTTTCTATCGTTTGTCTTGGTAGGGTTGTATGGGGTCATCATATGTTTACGGTAGGTTTAGATGTGAAGACAGCTGTTTTTTTT
AGGTCAGTTACTATGATTATAGGGGTGCCACTGGAATAAAGGTGTTTTCTTGGCTGTATATGATTTTAAAAAGTCGTGTCTC
TTTGGCGTGAACCTATATTTTGGTGGGTGTTATCTTTTATCGTGCTGTTTACAATAGGGGGTGTACTGGTATTATACTTTCTGC
TTGTGTTCTTGATAATATTTTGCATGATACTTGATTT";
}

else if("Diplogonoporus grandis".equals(s))
{
    q=
"GGGTTTGGAAATGATTAGACATGTTTGTAGTAACCTAGGTTGTTTCATATGATACTTTTGGATTTTATGGTTTATTATTGCTATG
TTTTCTATCGTTTGTCTTGGTAGGGTTGTATGGGGTCATCATATGTTTACGGTAGGTTTAGATGTGAAGACAGCTGTTTTTTTT
AGGTCAGTTACTATGATTATAGGGGTGCCACTGGAATAAAGGTGTTTTCTTGGCTGTATATGATTTTAAAAAGTCGTGTCTC
TTTGGCGTGAACCTATATTTTGGTGGGTGTTATCTTTTATCGTGCTGTTTACAATAGGGGGTGTACTGGTATTATACTTTCTGC
TTGTGTTCTTGATAATATTTTGCATGATACTTGATTT";
}

else if("Aelurostrongylus abstrusus".equals(s))

```

```

{

q=
"GCTTTTGGTATTGTTAGTCAGTCTACTTTGTATTTGACGGGGAAGAAGGAAGTTTTTGGTATTAGGGATAGTTTTATGCTAT
TATAAGTATTGGTTAATTGGTTGTGTTGGGCTCATCATATATACTGTTGGTATAGATTGGATTCTCGTGCTTATTTT
ACGGCGGCTACGATGGTTATTGCTGTGCCAACGGGTGTTAAGGTTTTTAGTTGGTTGGCTACTTTATTGGAATGAAGATAGT
GTTTCAGCCGGTTTTGTTGTGGGTTTTGGGTTTTATTTTTTTGTTACTATTGGGGGGTTAACTGGGGTCATGCTTTCGAATTCT
AGTTTGGATATTATTTGCATGATACTTATTATGTGGTTAGTCATTTTCATTATGTGTTGAGTTT";

}

else if("Dictyocaulus eckerti".equals(s))

{

q=
"GCTTTTGGTATTATTAGTCAGTCAACTTTGTATTTAACTGGTAAAAAGGAGGTTTTTGGTCTTTGGGTATGGTTTATGCTATT
TTAAGTATTGGTTAATTGGTTGTGTAGTATGAGCACATCATATATACTGTTGGAATAGATTGGATTTCGCGTGCTTATTTT
ACTGCTGCTACTATGGTAATTGCTGTTCTACGGGTGTAAGGTTTTTAGTTGGTTGGCTACTTTGTATGGTTAAAAATAGTA
TATAATCCTTTGTTGTTATGGGTTTTGGGTTTTATTTTTTTTACTATTGGGGGGTTAACTGGAGTTATTTTGTCAAATTCTA
GTTTAGATATTTTGTACATGATACTTATTATGTTGTAAGGCATT";

}

else if("Dictyocaulus viviparus".equals(s))

{

q=
"GCTTTTGGTATTATTAGACAATCTACTTTGTATTTAACTGGTAAAAAGGAGGTTTTTGGTCTTTGGGTATGGTTTATGCTATT
TTAAGTATTGGTTAATTGGTTGTGTGTGGGCACATCATATGTATACTGTTGGGATGGATTGGATTTCGCGTGCTTATTTT
ACTGCTGCTACTATAGTAATTGCTGTTCTACTGGAGTTAAGGTTTTTAGATGATTGGCTACTTTATATGGATTGAAAATGGTT
TATAATCCTTTGTTGTTGTGAGTTTTAGGTTTTATTTTTTTGTTACTATTGGTGGTTAACTGGTGTATTTTGTCAAATTCTA
GTCTTGATATTTTGTGTCATGATACTTATTAT";

}

else if("Ascaris lumbricoides".equals(s))

{

q=
"GCTTTTGGTATTATTAGTCAGAGTAGTTTGTATTTGACTGGTAAAAAGGAGGTTTTTGGGCTTTGGGTATGGTTTATGCTAT
TTTAAAGTATTGGTTGATTGGTTGTGTTGTTGAGCTCATCATATGTATACTGTTGGTATGGATCTTGATTCTCGGGCTTATTTT
ACTGCTGCAACTATGGTTATTGCTGTTCTACTGGTGTTAAGGTTTTTAGTTGGTTGGCTACCTGTTTGGTATAAAAAATGGTT
TTTCAGCCTTACTTTTATGAGTTATGGGTTTTATTTTTTTGTTACTATTGGTGGGTTAACCGGGGTTATACTTTCTAATTCTA
GTTTGGATATTATCTGTCATGATACTTATTATGTTGTTAGTCATTTTCATTATGTTCTTAGTTT";

}

else if("Ascaris suum".equals(s))

{

q=
"GCTTTTGGTATTATTAGTCAGAGTAGTTTGTATCTGACTGGTAAAAAGGAGGTTTTTGGGCTTTGGGTATGGTTTATGCTAT
TTTGAGTATTGGTTAATTGGTTGTGTTGTTGAGCTCATCATATGTATACTGTTGGTATGGATCTTGACTCTCGGGCTTATTTT
ACTGCTGCAACTATGGTTATTGCTGTTCTACTGGTGTTAAGGTTTTTAGTTGGTTGGCTACCTGTTTGGTATAAAGATGGTT
TTTCAACCTTACTTTTATGAGTTATGGGTTTTATTTTTTTGTTACTATTGGTGGGTTAACCGGGGTTATGCTTTCTAATTCTA
GTTTGGATATTATCTGTCATGATACTTATTATGTTGTTAGTCATTTTCATTATGTCCTTAGTTT";

}

else if("Baylisascaris ailuri".equals(s))

{

q=
"GCTTTTGGTATTATTAGCCAGAGTAGGTTGTATTTAACTGGTAAAAAGGAAGTTTTTGGTCTTTGGGTATGGTTTATGCTAT

```

```
TTTGAGTATTGGTTAATTGGTTGTGTTGTTGGGCTCATCATATGTATACTGTAGGTATGGATTGGATTCTCGTGCTTATTT
ACTGCGGCTACTATGGTTATTGCGGTCCTACGGGTGTTAAGGTTTTAGTTGGTTGGCTACTTTGTTGGTATGAAGATGGTG
TTCCAGCCTTTACTTTTGTGAGTTATGGGTTTTATTTTTTTTACTATTGGCGGATTGACTGGGGTGATGCTTCTAATTCTA
GTTTGGATATTATTTGCATGATACTTA-TTATGTTGTTAGACATTTTCATTATGTTCTTAGTTT";
```

```
}
```

```
else if("Baylisascaris procyonis".equals(s))
```

```
{
```

```
q=
```

```
"GCTTTTGGTATTATTAGCCAAAGTAGGTTGTATTTAACTGGTAAGAAGGAAGTTTTTGGTTCCTTGGGAATGGTTATGCTAT
TTTGAGTATTGGTTGATTGGATGTGTGGTTTGGGCTCATCATATGTATACTGTGGGTATGGATTGGATTCTCGGGCTTATTT
TACTGCGGCTACTATGGTTATTGCGGTTCTACGGGAGTTAAGGTTTTAGTTGGTTGGCCACTTTATTTGGTATGAAGATAGT
GTTTCAGCCTTTGCTTTTGTGGGTTATGGGGTTTTATTTTTTGTACTATTGGTGGTTGACTGGGGTTATGCTTCTAATTCT
AGTTTGGATATTATTTGCATGATACTTATTATGTTGTTAGGCATTTTCATTATGTTCTTAGTTT";
```

```
}
```

```
else if("Baylisascaris schroederi".equals(s))
```

```
{
```

```
q=
```

```
"GCTTTTGGTATTATTAGTCAGAGTAGGTTGTATCTGACTGGTAAGAAGGAGGTTTTTGGTTCCTTGGGTATGGTTTACGCAAT
TTTGAGTATTGGTTGATTGGTTGTGTTGTTGAGCTCATCATATGTATACTGTGGGTATAGATTGGATTCTCGTGCTTATTTT
ACTGCGGCTACTATGGTTATCGCAGTTCCTACGGGTGTTAAGGTTTTAGTTGGTTGGCTACTTTGTTGGTATGAAGATGGTG
TTTCAGCCTTTGCTTTTGTGGGTTATAGGATTTATTTTTTGTACTATTGGTGGATTGACTGGGGTGATGCTTCTAATTCTA
GTTTGGATATTATTTGCATGATACTTA-TTATGTTGTTAGGCATTTTCATTATGTTCTTAGTTT";
```

```
}
```

```
else if("Baylisascaris transfuga".equals(s))
```

```
{
```

```
q=
```

```
"GCTTTTGGTATTATTAGTCAGAGTAGATTGTATTTAACTGGTAAAAAGGAGGTTTTTGGTTCCTTGGGTATGGTTTATGCTAT
TTTGAGTATTGGTTAATTGGTTGTGTTGTTTGGGCTCATCATATGTATACTGTAGGTATGGATTGGATTCTCGTGCTTATTTT
ACTGCGGCTACTATGGTTATTGCGGTTCTACAGGTGTTAAGGTTTTAGTTGGTTGGCCACTTTGTTGGTATGAAGATGGTG
TTTCAGCCTTTACTTTTGTGGGTTATGGGGTTTTATTTTTTACTATTGGTGGATTGACTGGGGTGATGCTTCTAATTCTA
GTTTGGATATTATTTGCATGATACTTATTATGTTGTTAGGCATTTTCATTATGTTCTTAGTTT";
```

```
}
```

```
else if("Toxocara canis".equals(s))
```

```
{
```

```
q=
```

```
"GCTTTTGGTATTATTAGCCAAAGTAGTTTGTATTTGACTGGTAAAAAGGAGGTTTTTGGTTCCTTAGGCATGGTTTATGCTAT
TTTAAAGTATTGGTCTGATTGGCTGTGTAGTTTGGGCTCACCATATGTATACGGTGGGCATGGATTGGATTCTCGTGCTTATTT
TACTGCGCAACGATGGTTATTGCTGTGCCTACGGGGGTTAAGGTTTTAGTTGGTTAGCCACTTTTTGGTATGAAGATGG
TGTTTCAACCTTTGCTTTTGTGGGTGCTGGGTTTTATTTTTTACTATCGGGGGTTGACTGGTGTATGTTATCTAATTC
TAGGTTGGACATTATCTTGCATGATACTTATTATGTTGTTAGTCATTTTCATTATGTTT";
```

```
}
```

```
else if("Toxocara cati".equals(s))
```

```
{
```

```
q=
```

```
"GATTTTTTGGGCATCCTGAGGTTTATATTTGATTTTACCTGCCTTGGTATTATTAGTCAAAGTAGTTTATATTTAACTGGTA
AGAAGGAGGTTTTTGGTTCCTTGGGCATGGTCTATGCTATTTTGGTATTGGTTGATTGGTTGTGTGGTGTGAGCTCACCACA
TGTATACTGTTGGTATAGACTTGGATTCTCGGGCTATTTTACTGCGGCTACTATGGTTATCGCTGTGCCTACGGGTGTTAAGG
TTTTAGTTGGTTGGCTACTCTTTTGGTATAAAAATGGTTTTTCAACCTTGTCTTTGTGAGTGTGGGTTTTATTTTTTGT
```

```

ACTATTGGTGGGCTTACTGGAGTTATGCTTTCTAATTCTAGTTTGGATATTATTTGCATGACACCTATTATGTTGTGAGGCAT
TTCCACTATGTTT";

    }else if("Toxocara malaysiensis".equals(s))

    {

        q=
"GCTTTTGGTATTATTAGTCAGAGTAGTTTGTATTTAACTGGTAAGAAGGAAGTTTTGGTTCGTTGGGGATGGTTTATGCTAT
TTTAAAGTATTGGTTTGATTGGCTGTGTGGTTTGGGCTCATCATATGTATAACCGTGGGTATAGATTGGATTCTCGGGCTTATTT
TACTGCGGCGACTATGGTTATTGCTGTGCCTACTGGTGTAAAGGTTTTAGTTGGTTGGCTACTCTTTTTGGTATGAAAATGGT
TTTTACGCCCTTACTTTTTATGGGTGTTAGGTTTTATTTCTTGTTTACTATTGGGGGCCCTACTGGTGTGATGCTTTCTAATTCT
AGCCTTGATATTATTTGCATGATACCTATTATGTTGTTAGACATTTTCATTATGTTT";

    }

    else if("Taenia asiatica".equals(s))

    {

        q=
"GGTTTTGGTATGATTAGTCATATATGTTTAAAGAATAAGTATGTGTCCGGATGCTTTTTGGTTTTTATGGTTTGTATTGCTATG
TTTTCAATAGTATGTTTGGGGAGAAGTGTGTGGGGTCATGATATGTTTACGGTTGGATTAGTTGTTAAGACTACTGTGTTTTTT
AGTTCGGTTACTATGATAATAGGAGTACCAACAGGAATAAAGGTTTTACTTGACTTTATATGCTTTTTAAATTCCTCGTGTA
AAAGAGGGATCCTATATTGTGGTGGATAGTTTCTTTTATAGTGTGTTTACCTTTGGTGGTGTGACTGGTATTGTGTTGTCTGC
TTGTGATTGGATAAAGTTTTGCATGATACTTGATT";

    }

    else if("Taenia crassiceps".equals(s))

    {

        q=
"GGTTTTGGAATTATTAGACATATTTGTTTAAAATAAGTATGAATTGTGATTCTTTTGGTTTTTATGGATTGTTATTGCTATG
TTTTCAATAGTTTTGTTTAGGTAGGAGTGTGTGGGGTCATCATATGTTTACGGTTGGTTTAGATGTTAAGACTGCTGTTTTTTTT
AGTTCGTGTTACTATGATTATAGGAGTACCTACAGGTATAAAGGTGTTTACTTGATTGTATATGCTTTTTAAATTCGCGTGTGAA
CAAGAGTGATCCTATATTGTGGTGAATTGTTCTTTTATAGTTTTATTTACGTTTGGTGGTGTACTGGAATAGTATTGTCTGC
TTGTGATTAGATAAAGTTCTTCATGATACTTGATT";

    }

    else if("Taenia hydatigena".equals(s))

    {

        q=
"GGATTTGGAAATTATTAGTCATATATGTTTGAAGAATAAGTATGAGTCCTGATGCTTTTTGGGTTCTATGGATTATTATTGCTAT
GTTTTCAATAGTCTGTTTGGGTAGAAAGTGTGTGGGGTCATCATATGTTTACTGTTGGGTTAGATGTTAAGACTGCTGTTTTTTTT
TAGTTCTGTGACTATGATTATAGGTGTGCCTACTGGTATAAAGGTGTTTACTTGGTTATATATGCTTTTTAAACTCTCATGTGAA
TAAGAGTGATCCTGTTGTTGATGAATTGTTCTTTTATAGTTTTGTTTACTTTTTGGTGGGTTACTGGTATTGTGTTGTCTGCA
TGTGTATTAGATAAAGTTCTTCATGATACCTGATT";

    }

    else if("Taenia krepkogorski".equals(s))

    {

        q=
"GGATTTGGTATAATTAGTCATATATGTTTAAAGAATAAGTATGTCCTCTGATGTGTTTGGGTTTTATGGTTTATTATTGCTATG
TTTTCTATAGTTTTGTTTAGGAAGAAGAGTGTGAGGTCATCACATGTTTACTGTTGGGTTTAGATGTTAAGACTGCTGTGTTTTTT
AGTCAATTACTATGATTATTGGTGTGCCTACTGGGATTAAGGTTTTTACATGATTATATATGTTATTAAATGCTCGAGTAAA
AAAGAGTGATCCTGTGTTGTGGTGAATTGTTTCAATTATAAATATTGTTTACATTTGGTGGAGTTACTGGTATAGTATTGTCTGC
TTGTGTTTTAGATAAAGTGTACATGATACTTGTT";

    }

    else if("Taenia laticollis".equals(s))

```

```

{

    q=
"GGATTTGGTATAATTAGACATATATGTTAAGTATTAGTATGTGTTCCGGATGCTTTCCGGTTTTATGGTTTTATTATTTGCTATG
TTTTCTATTGTTTGTAGGGAGAAGAGTTTGGGGTCATCATATGTTTACAGTTGGGTTAGATGTTAAGACGGCTGTATTTTT
AGTTCGTAACTATGATTATTGGTGTACCTACAGGTATAAAGGTTTTTACATGATTATATATGCTTTTAAATTCCTCGGGTAAA
AAGAGTGATCCTGTATTATGGTGGATAGTTCTTTTATAGTTTTGTTTACGTTTGGTGGTGTACAGGAATAGTGTGTCTGCT
TGCCTATTAGATAAAGTATTACATGATACTTGATTT";

}

else if("Taenia madoquae".equals(s))

{

    q=
"GGTTTTGGGATAATTAGTCATATATGTTTGGAGATTAGTATGTGCTCCTGATGCTTTTGGTTTTATGGTTTTGTTATTTGCTATG
TTCTCAATAGTGTGTTTGGGAAGGAGTGTATGAGGTCATCACATGTTTACGGTTGGATTAGATGTTAAGACTGCTGTATTTTT
TAGTTCGGTTACTATGATAATAGGAGTACCTACAGGAATAAAGGTTTTTACTTGACTTTATATGCTTTTAAATTCCTCGTGTGA
ATAAGAGTGATCCTGTGTTATGATGGATAGTTCTTTTATAGTATTGTTTACTTTTGGTGGTGTAACTGGTATTGTATTATCTG
CTTGTGATTGGATAATGTTTTACATGATACTTGATTT";

}

else if("Taenia martis".equals(s))

{

    q=
"GGTTTTGGTATAATTAGACATATTTGTCTAAATATAAGTATGAATTATGATTCTTTTGGTTTTATGGTTTTATTATTTGCTATG
TTTTCTATAGTTTGTGGGTAGTAGTGTGTTGGGTCATCATATGTTTACTGTTGGATTAGATGTTAAGACTGCTGTTTTTTTC
AGTTCAGTTACTATGATAATAGGTGTTCTACGGGTATAAAGGTTTTTACTTGATTATATATGCTTTTAAAATCCTCGTGTGAAT
AAGAGTGATCCTGTATTATGGTGAATTGTTCTTTTATTATTTGTTTACTTTTGGTGGTGTACTGGTATAGTGTATCTGCAT
GTGTTTTGGATAAAGTCTTCATGATACTTGATTT";

}

else if("Taenia multiceps".equals(s))

{

    q=
"GGTTTTGGTATAATTAGTCACATATGTTTAAAGAATAAGCATGTGTCAGATGCTTTTGGTTTTATGGTTTTATTATTTGCTATG
TTTTCAATAGTGTGTTTAGGGAGAAGTGTGTGAGGCCATCATATGTTTACAGTTGGGTTAGATGTTAAGACTGCTGTATTTTTT
AGTTCGGTTACTATGATAATAGGAGTGCCACAGGAATAAAGGTTTTTACTTGGCTTTATATGCTTTTAAATTCCTCGTGTAAA
CAAGAGTGATCCTATACTATGATGAATAGTTCTTTTATAGTATTGTTTACTTTTGGTGGTGTAACTGGGATTGTATTGTCTGC
TTGTATTAGATAAAGTTTTACATGATACTTGATTT";

}

else if("Taenia mustelae".equals(s))

{

    q=
"GGTTTTGGTATTATTGGTCATATATGTTTGGAGTATAAGGATGTGTTCTGATGCTTTTGGGTTTTATGGATTGTTGTTTGTCTATG
TTTTCTATTGTTTGTCTAGGTAGTAGAGTTTGGGGCATCATATGTTTACTGTTGGTTTAGATGTTAAGACTGCTGTTTTTTTTT
GTTCTGTTACTATGATTATAGGAGTTCTACTGGTATAAAGGTTTACTTGGTTGTATATGTTACTGAATTCAGTGTAAACA
AGAGGGATCCTGTGTTGTGATGAATAGTGCATTTATATTTTTGTTTACTTTTGGTGGTGTACTGGTATAGTTTTGTCTGCTT
GTGTATTAGATAAAGTTTTGCATGATACTTGATTT";

}

else if("Taenia ovis".equals(s))

{

    q=
"GGATTTGGTATAATTAGTCATATTTGTTTGGAGATTAGTATGTGTCAGATGCTTTTGGTTTTATGGCTTATTATTTGCTATG

```

```
TTTTCTATAGTATGTTTAGGAAGAAGTGTGTGGGGGCATCATATGTTTACTGTTGGGTTGGATGTTAAGACGGCTGTATTTTT
AGTTCGGTFACTATGATCATAGGTGTGCTACTGGTATAAAGGTTTTACTTGGCTTTATATGCTTCTGAAATCTCGTGTGAAT
AAGAGTGATCCTATTTTGTGATGGATAGTTTCTTTTATAGTATTATTTACTTTTGGAGGTGTGACTGGTATTGTTTTATCTGCTT
GTGTATTGGATAAAGTTCTTCATGATACTTGATTT";
```

```
}
```

```
else if("Taenia parva".equals(s))
```

```
{
```

```
q=
```

```
"GGTTTGGGATTATAAGACATATATGTTTAAAGAATTAGTATGTGTGATGATGCTTTTGGTTTTTATGGTTTGTATTGCTATGT
TTTTCTATTGTGTGTTTAGGAAGAAGTGTATGAGGCCATCATATGTTTACTGTAGGTTTAGATGTGAAGACTGCTGTGTTTTTA
GTTTCAGTAACAATGATTATCGGGGTTCTACTGGGATAAAGGTTTTACTTGGATTATATGTTACTTAATTCTCGTATTAATA
AGGGTGATCCTGTAATTTGATGAATTGTTCTTTTCATAGTTTTATTTACGTTTGGTGGTGCCTACTGGTATAGTTTTATCAGCTT
GTGTTTTAGATAAAGTTTTGCATGATACTTGATTT";
```

```
}
```

```
else if("Taenia pisiformis".equals(s))
```

```
{
```

```
q=
```

```
"GGGTTTGGTATAATTAGTCATATATGTTTAAAGAATAAGTATGTGTTTCAGATGCGTTTTGGTTTTTATGGTTTATTGTTTGAAT
GTTTTCTATAGTTTGTAGGTAGAAAGTGTATGAGGTATCATATGTTTACTGTTGGATTAGATGTTAAAGACCGCTGTGTTTTT
TAGTTTCAGTAACAATGATAATTGGAGTACCTACTGGAATTAAGGCTTTTACATGACTTTTATGCTTTTAAATTCTCGTGCA
AAAAGAGTGATCCTGTGTTGTGGTGAATAATTTCTTTTATAGTCTTATTTACTTTTGGAGGTGTAAGTGGTATAGTATTATCTG
CTTGTGTTTTAGATAAAGTTTACATGATACTTGATTT";
```

```
}
```

```
else if("Taenia saginata".equals(s))
```

```
{
```

```
q=
```

```
"GGTTTGGTATGATTAGTCATATATGTTTAAAGAATAAGTATGTGTCAGATGCTTTTGGTTTTTATGGTTTGTGTTTGTCTATG
TTTTCAATAGTGTGTTTGGGGAGAAGTGTGTGGGGTCATCATATGTTTACGGTTGGGTTAGATGTTAAGACTGCTGTGTTTTTT
AGTTCGGTFACTATGATAATAGGAGTACCAACAGGAATAAAGGTTTTACTTGGCTTTATATGCTTTTAAATTCTCGTGTA
AAAGAGTGATCCTATATTGTGGTGAATAGTTTCTTTTATAGTGTGTTTACTTTTGGTGGTGTGACTGGTATTGTGTTGCTGC
TTGCGTATTGGATAAAGTTTTGCATGATACTTGATTT";
```

```
}
```

```
else if("Taenia serialis".equals(s))
```

```
{
```

```
q=
```

```
"GGTTTGGTATAATTAGTCATATATGTTTAAAGAATAAGTATGTGTCAGACGCTTTTGGTTTTTATGGTTTGTATTGCTATG
TTCTCAATAGTGTGTTTAGGAAGGAGTGTATGGGGTCATCATATGTTTACAGTTGGGTTAGATGTTAAGACTGCTGTATTTTTT
AGCTCAGTFACTATGGTAATAGGAGTACCAACAGGAATAAAGGTTTTACTTGGCTTTATATGTTATTTAAATTCTCGTGTA
AAAGAGTGATCCTATATTGTGGTGGATAGTTTCTTTTATAGTATTGTTTACTTTTGGTGGTGTAACTGGGATTGATTGCTG
TTGTGTTGGATAAAGTTTTACATGATACTTGATTT";
```

```
}
```

```
else if("Taenia solium".equals(s))
```

```
{
```

```
q=
```

```
"GGGTTTGGTATAATTAGTCATATATGTTTGAAGTATAAGTATGTGTTCTGATGCTTTTGGCTTTTATGGGTTATTGTTTGTCTATG
TTTTCAATAGTATGTTTAGGAAGAAGTGTGTGAGGACATCATATGTTTACGGTTGGGTTAGATGTTAAGACGGCTGTATTTTT
TAGTTCTGTTACTATGATAATTGGAGTGCCTACGGGGATTAAGGTTTTACTTGGCTTTATATGCTTTTAAATCTCGTGTTAA
AAAGAGTGATCCGGTTTTATGATGAATAATTCGTTTATAGTATTGTTTACATTTGGTGGTGTAAACGGTATTATTCTATCTGC
TTGTGATTAGATAAAGTTCTTCATGATACTTGATTT";
```



```

    }

    else if("Taenia twitchelli".equals(s))

    {

        q=
"GGTTTTGGTATAATTAGACATATTTGTTTAAATGTAAGTATGAATTATGATTCTTTTGGATTTTATGGTTTGTATTGCTATG
TTTTCTATAGTTTGTAGGTAGAAAGTGTATGAGGTCATCATATGTTTACTGTTGGATTAGATGTTAAGACTGCTGTTTTTTT
AGTTCGTACTATGATTATAGGGTTCCTACAGGTATAAAGGTGTTTACTTGGTTATATATGCTTTTAAAATCTCGTGAAAT
AAGAGTGATCCTGTTTTATGATGAATTGTGTCTTTTATTATTTTGTACTTTTGGTGGTGTACTGGTATAGTGTATCTGCGT
GTGTTTTGGATAAAGTCTTCATGATACTTGGTTT";

    }

    else if("Taeniopygia guttata".equals(s))

    {

        q=
"GGTTTCGGCATCATCTCCCACGTCGTAACCTACTATTTCAGGTAAAAAAGAACCATTTCGGATATATAGGAATAGTATGAGCTA
TGCTATCCATCGGATTCTAGGATTCATCGTATGAGCCACCACATGTTTACAGTAGGAATGGACGTAGACACCCGAGCATA
CTTTACATCCGCCACTATAATCATCGCCATCCCAACCGGCATCAAAGTATTTCAGCTGACTAGCAACACTCCACGGAGGCACA
ATCAAGTGAGACCCACCAATACTATGAGCTCTAGGATTTATCTTCTATTCCACATCGGAGGCCTAACCGGAATCGTCCTGGC
CAACTCCTCACTAGACATCGCCCTACAGCACCTACTACGTAGTAGCCCACTTCCACTACGTCTCTATCAATAGGAGCAGTGT
TTGCAATCCTAGCAGGATTCACCCACTGATT";

    }

double
AAA=0,AAC=0,AAG=0,AAT=0,ACA=0,ACC=0,ACG=0,ACT=0,AGA=0,AGC=0,AGG=0,AGT=0,ATA=0,ATC=0,ATG=0,ATT=0,CA
A=0,CAC=0,CAG=0,CAT=0,CCA=0,CCC=0,CCG=0,CCT=0,CGA=0,CGC=0,CGG=0,CGT=0,CTA=0,CTC=0,CTG=0,CTT=0,GAA=0,G
AC=0,GAG=0,GAT=0,GCA=0,GCC=0,GCG=0,GCT=0,GGA=0,GGC=0,GGG=0,GGT=0,GTA=0,GTC=0,GTG=0,GTT=0,TAA=0,TAC=
0,TAG=0,TAT=0,TCA=0,TCC=0,TCG=0,TCT=0,TGA=0,TGC=0,TGG=0,TGT=0,TTA=0,TTC=0,TTG=0,TTT=0;

int length = q.length();

for(int i=0;i<length-2;i++)

{

if(q.charAt(i)=='A')

{

    if(q.charAt(i+1)=='A')

    {

        if(q.charAt(i+2)=='A')

        AAA++;

        else if(q.charAt(i+2)=='C')

        AAC++;

        else if(q.charAt(i+2)=='G')

        AAG++;

        else if(q.charAt(i+2)=='T')

        AAT++;

    }

}

}

```

```

}
else if(q.charAt(i+1)=='C')
{
    if(q.charAt(i+2)=='A')
        ACA++;
    else if(q.charAt(i+2)=='C')
        ACC++;
    else if(q.charAt(i+2)=='G')
        ACG++;
    else if(q.charAt(i+2)=='T')
        ACT++;
}
else if(q.charAt(i+1)=='G')
{
    if(q.charAt(i+2)=='A')
        AGA++;
    else if(q.charAt(i+2)=='C')
        AGC++;
    else if(q.charAt(i+2)=='G')
        AGG++;
    else if(q.charAt(i+2)=='T')
        AGT++;
}
else if(q.charAt(i+1)=='T')
{
    if(q.charAt(i+2)=='A')
        ATA++;
    else if(q.charAt(i+2)=='C')
        ATC++;
    else if(q.charAt(i+2)=='G')
        ATG++;
    else if(q.charAt(i+2)=='T')
        ATT++;
}
}

```

```

}
else if(q.charAt(i)=='C')
{
    if(q.charAt(i+1)=='A')
    {
        if(q.charAt(i+2)=='A')
            CAA++;
        else if(q.charAt(i+2)=='C')
            CAC++;
        else if(q.charAt(i+2)=='G')
            CAG++;
        else if(q.charAt(i+2)=='T')
            CAT++;
    }
    else if(q.charAt(i+1)=='C')
    {
        if(q.charAt(i+2)=='A')
            CCA++;
        else if(q.charAt(i+2)=='C')
            CCC++;
        else if(q.charAt(i+2)=='G')
            CCG++;
        else if(q.charAt(i+2)=='T')
            CCT++;
    }
    else if(q.charAt(i+1)=='G')
    {
        if(q.charAt(i+2)=='A')
            CGA++;
        else if(q.charAt(i+2)=='C')
            CGC++;
        else if(q.charAt(i+2)=='G')
            CGG++;
        else if(q.charAt(i+2)=='T')
            CGT++;
    }
}

```

```

    }
else if(q.charAt(i+1)=='T')
{
    if(q.charAt(i+2)=='A')
        CTA++;
    else if(q.charAt(i+2)=='C')
        CTC++;
    else if(q.charAt(i+2)=='G')
        CTG++;
    else if(q.charAt(i+2)=='T')
        CTT++;
}
}
else if(q.charAt(i)=='G')
{
    if(q.charAt(i+1)=='A')
    {
        if(q.charAt(i+2)=='A')
            GAA++;
        else if(q.charAt(i+2)=='C')
            GAC++;
        else if(q.charAt(i+2)=='G')
            GAG++;
        else if(q.charAt(i+2)=='T')
            GAT++;
    }
    else if(q.charAt(i+1)=='C')
    {
        if(q.charAt(i+2)=='A')
            GCA++;
        else if(q.charAt(i+2)=='C')
            GCC++;
        else if(q.charAt(i+2)=='G')
            GCG++;
        else if(q.charAt(i+2)=='T')

```

```

        GCT++;
    }
    else if(q.charAt(i+1)=='G')
    {
        if(q.charAt(i+2)=='A')
            GGA++;
        else if(q.charAt(i+2)=='C')
            GGC++;
        else if(q.charAt(i+2)=='G')
            GGG++;
        else if(q.charAt(i+2)=='T')
            GGT++;
    }
    else if(q.charAt(i+1)=='T')
    {
        if(q.charAt(i+2)=='A')
            GTA++;
        else if(q.charAt(i+2)=='C')
            GTC++;
        else if(q.charAt(i+2)=='G')
            GTG++;
        else if(q.charAt(i+2)=='T')
            GTT++;
    }
}
else if(q.charAt(i)=='T')
{
    if(q.charAt(i+1)=='A')
    {
        if(q.charAt(i+2)=='A')
            TAA++;
        else if(q.charAt(i+2)=='C')
            TAC++;
        else if(q.charAt(i+2)=='G')
            TAG++;
    }
}

```

```

        else if(q.charAt(i+2)=='T')
            TAT++;
    }
    else if(q.charAt(i+1)=='C')
    {
        if(q.charAt(i+2)=='A')
            TCA++;
        else if(q.charAt(i+2)=='C')
            TCC++;
        else if(q.charAt(i+2)=='G')
            TCG++;
        else if(q.charAt(i+2)=='T')
            TCT++;
    }
    else if(q.charAt(i+1)=='G')
    {
        if(q.charAt(i+2)=='A')
            TGA++;
        else if(q.charAt(i+2)=='C')
            TGC++;
        else if(q.charAt(i+2)=='G')
            TGG++;
        else if(q.charAt(i+2)=='T')
            TGT++;
    }
    else if(q.charAt(i+1)=='T')
    {
        if(q.charAt(i+2)=='A')
            TTA++;
        else if(q.charAt(i+2)=='C')
            TTC++;
        else if(q.charAt(i+2)=='G')
            TTG++;
        else if(q.charAt(i+2)=='T')
            TTT++;
    }

```

```
    }  
  }  
}
```

AAA=AAA/length;

AAC=AAC/length;

AAG=AAG/length;

AAT=AAT/length;

ACA=ACA/length;

ACC=ACC/length;

ACG=ACG/length;

ACT=ACT/length;

AGA=AGA/length;

AGC=AGC/length;

AGG=AGG/length;

AGT=AGT/length;

ATA=ATA/length;

ATC=ATC/length;

ATG=ATG/length;

ATT=ATT/length;

CAA=CAA/length;

CAC=CAC/length;

CAG=CAG/length;

CAT=CAT/length;

CCA=CCA/length;

CCC=CCC/length;

CCG=CCG/length;

CCT=CCT/length;

CGA=CGA/length;

CGC=CGC/length;

CGG=CGG/length;

CGT=CGT/length;

CTA=CTA/length;

CTC=CTC/length;

CTG=CTG/length;

CTT=CTT/length;

GAA=GAA/length;

GAC=GAC/length;

GAG=GAG/length;

GAT=GAT/length;

GCA=GCA/length;

GCC=GCC/length;

GCG=GCG/length;

GCT=GCT/length;

GTA=GTA/length;

GTC=GTC/length;

GTG=GTG/length;

GTT=GTT/length;

GGA=GGA/length;

GGC=GGC/length;

GGG=GGG/length;

GGT=GGT/length;

TAA=TAA/length;

TAC=TAC/length;

TAG=TAG/length;

TAT=TAT/length;

TCA=TCA/length;

TCC=TCC/length;

TCG=TCG/length;

TCT=TCT/length;


```
TGA=TGA/length;
```

```
TGC=TGC/length;
```

```
TGG=TGG/length;
```

```
TGT=TGT/length;
```

```
TTA=TTA/length;
```

```
TTC=TTC/length;
```

```
TTG=TTG/length;
```

```
TTT=TTT/length;
```

```
double[]  
e={AAA,AAC,AAG,AAT,ACA,ACC,ACG,ACT,AGA,AGC,AGG,AGT,ATA,ATC,ATG,ATT,CAA,CAC,CAG,CAT,CCA,CCC,CCG,CC  
T,CGA,CGC,CGG,CGT,CTA,CTC,CTG,CTT,GAA,GAC,GAG,GAT,GCA,GCC,GCG,GCT,GGA,GGC,GGG,GGT,GTA,GTC,GTG,GTT,  
TAA,TAC,TAG,TAT,TCA,TCC,TCG,TCT,TGA,TGC,TGG,TGT,TTA,TTT,TTG,TTT};
```

```
return e;
```

```
}
```

```
CategoryDataset GetData1(String s1,String s2) {
```

```
    // row keys...
```

```
    final String series1 = s1+"Dinucleotide Frequency";
```

```
    final String series2 = s2+"Dinucleotide Frequency";
```

```
    // column keys...
```

```
    final String type1 = "AA";
```

```
    final String type2 = "AC";
```

```
    final String type3 = "AG";
```

```
    final String type4 = "AT";
```

```
    final String type5 = "CA";
```

```
    final String type6 = "CC";
```

```
    final String type7 = "CG";
```

```
    final String type8 = "CT";
```

```

final String type9 = "GA";

final String type10 = "GC";

final String type11 = "GG";

final String type12 = "GT";

final String type13 = "TA";

final String type14 = "TC";

final String type15 = "TG";

final String type16 = "TT";

// create the dataset...

final DefaultCategoryDataset dataset = new DefaultCategoryDataset();

double[] d=calcDifreq(s1);

dataset.addValue(d[0], series1,type1);

dataset.addValue(d[1], series1,type2);

dataset.addValue(d[2], series1,type3);

dataset.addValue(d[3], series1,type4);

dataset.addValue(d[4], series1,type5);

dataset.addValue(d[5], series1,type6);

dataset.addValue(d[6], series1,type7);

dataset.addValue(d[7], series1,type8);

dataset.addValue(d[8], series1,type9);

dataset.addValue(d[9], series1,type10);

dataset.addValue(d[10], series1,type11);

dataset.addValue(d[11], series1,type12);

dataset.addValue(d[12], series1,type13);

dataset.addValue(d[13], series1,type14);

dataset.addValue(d[14], series1,type15);

dataset.addValue(d[15], series1,type16);

d=calcDifreq(s2);

dataset.addValue(d[0], series2,type1);

dataset.addValue(d[1], series2,type2);

```

```

dataset.addValue(d[2], series2,type3);

dataset.addValue(d[3], series2,type4);

dataset.addValue(d[4], series2,type5);

dataset.addValue(d[5], series2,type6);

dataset.addValue(d[6], series2,type7);

dataset.addValue(d[7], series2,type8);

dataset.addValue(d[8], series2,type9);

dataset.addValue(d[9], series2,type10);

dataset.addValue(d[10], series2,type11);

dataset.addValue(d[11], series2,type12);

dataset.addValue(d[12], series2,type13);

dataset.addValue(d[13], series2,type14);

dataset.addValue(d[14], series2,type15);

dataset.addValue(d[15], series2,type16);

return dataset;

}

CategoryDataset GetData2(String s1,String s2) {

// row keys...

final String series1 = s1+"Trinucleotide Frequency";

final String series2 = s2+"Trinucleotide Frequency";

// column keys...

final String type1a = "AAA";

final String type1b = "AAC";

final String type1c = "AAG";

final String type1d = "AAT";

```

```
final String type2a = "ACA";
final String type2b = "ACC";
final String type2c = "ACG";
final String type2d = "ACT";

final String type3a = "AGA";
final String type3b = "AGC";
final String type3c = "AGG";
final String type3d = "AGT";

final String type4a = "ATA";
final String type4b = "ATC";
final String type4c = "ATG";
final String type4d = "ATT";

final String type5a = "CAA";
final String type5b = "CAC";
final String type5c = "CAG";
final String type5d = "CAT";

final String type6a = "CCA";
final String type6b = "CCC";
final String type6c = "CCG";
final String type6d = "CCT";

final String type7a = "CGA";
final String type7b = "CGC";
final String type7c = "CGG";
final String type7d = "CGT";

final String type8a = "CTA";
final String type8b = "CTC";
final String type8c = "CTG";
final String type8d = "CTT";
```

```
final String type9a = "GAA";
```

```
final String type9b = "GAC";
```

```
final String type9c = "GAG";
```

```
final String type9d = "GAT";
```

```
final String type10a = "GCA";
```

```
final String type10b = "GCC";
```

```
final String type10c = "GCG";
```

```
final String type10d = "GCT";
```

```
final String type11a = "GGA";
```

```
final String type11b = "GGC";
```

```
final String type11c = "GGG";
```

```
final String type11d = "GGT";
```

```
final String type12a = "GTA";
```

```
final String type12b = "GTC";
```

```
final String type12c = "GTG";
```

```
final String type12d = "GTT";
```

```
final String type13a = "TAA";
```

```
final String type13b = "TAC";
```

```
final String type13c = "TAG";
```

```
final String type13d = "TAT";
```

```
final String type14a = "TCA";
```

```
final String type14b = "TCC";
```

```
final String type14c = "TCG";
```

```
final String type14d = "TCT";
```

```
final String type15a = "TGA";
```

```
final String type15b = "TGC";
```

```
final String type15c = "TGG";
```

```
final String type15d = "TGT";
```

```

final String type16a = "TTA";
final String type16b = "TTC";
final String type16c = "TTG";
final String type16d = "TTT";

// create the dataset...
final DefaultCategoryDataset dataset = new DefaultCategoryDataset();

double[] d=calcTrifreq(s2);

dataset.addValue(d[0], series2,type1a);
dataset.addValue(d[1], series2,type1b);
dataset.addValue(d[2], series2,type1c);
dataset.addValue(d[3], series2,type1d);

dataset.addValue(d[4], series2,type2a);
dataset.addValue(d[5], series2,type2b);
dataset.addValue(d[6], series2,type2c);
dataset.addValue(d[7], series2,type2d);

dataset.addValue(d[8], series2,type3a);
dataset.addValue(d[9], series2,type3b);
dataset.addValue(d[10], series2,type3c);
dataset.addValue(d[11], series2,type3d);

dataset.addValue(d[12], series2,type4a);
dataset.addValue(d[13], series2,type4b);
dataset.addValue(d[14], series2,type4c);
dataset.addValue(d[15], series2,type4d);

dataset.addValue(d[16], series2,type5a);
dataset.addValue(d[17], series2,type5b);
dataset.addValue(d[18], series2,type5c);
dataset.addValue(d[19], series2,type5d);

```

```
dataset.addValue(d[20], series2,type6a);
dataset.addValue(d[21], series2,type6b);
dataset.addValue(d[22], series2,type6c);
dataset.addValue(d[23], series2,type6d);

dataset.addValue(d[24], series2,type7a);
dataset.addValue(d[25], series2,type7b);
dataset.addValue(d[26], series2,type7c);
dataset.addValue(d[27], series2,type7d);

dataset.addValue(d[28], series2,type8a);
dataset.addValue(d[29], series2,type8b);
dataset.addValue(d[30], series2,type8c);
dataset.addValue(d[31], series2,type8d);

dataset.addValue(d[32], series2,type9a);
dataset.addValue(d[33], series2,type9b);
dataset.addValue(d[34], series2,type9c);
dataset.addValue(d[35], series2,type9d);

dataset.addValue(d[36], series2,type10a);
dataset.addValue(d[37], series2,type10b);
dataset.addValue(d[38], series2,type10c);
dataset.addValue(d[39], series2,type10d);

dataset.addValue(d[40], series2,type11a);
dataset.addValue(d[41], series2,type11b);
dataset.addValue(d[42], series2,type11c);
dataset.addValue(d[43], series2,type11d);

dataset.addValue(d[44], series2,type12a);
dataset.addValue(d[45], series2,type12b);
dataset.addValue(d[46], series2,type12c);
dataset.addValue(d[47], series2,type12d);
```

```
dataset.addValue(d[48], series2,type13a);
dataset.addValue(d[49], series2,type13b);
dataset.addValue(d[50], series2,type13c);
dataset.addValue(d[51], series2,type13d);

dataset.addValue(d[52], series2,type14a);
dataset.addValue(d[53], series2,type14b);
dataset.addValue(d[54], series2,type14c);
dataset.addValue(d[55], series2,type14d);

dataset.addValue(d[56], series2,type15a);
dataset.addValue(d[57], series2,type15b);
dataset.addValue(d[58], series2,type15c);
dataset.addValue(d[59], series2,type15d);

dataset.addValue(d[60], series2,type16a);
dataset.addValue(d[61], series2,type16b);
dataset.addValue(d[62], series2,type16c);
dataset.addValue(d[63], series2,type16d);

d=calcTrifreq(s1);
dataset.addValue(d[0], series1,type1a);
dataset.addValue(d[1], series1,type1b);
dataset.addValue(d[2], series1,type1c);
dataset.addValue(d[3], series1,type1d);

dataset.addValue(d[4], series1,type2a);
dataset.addValue(d[5], series1,type2b);
dataset.addValue(d[6], series1,type2c);
dataset.addValue(d[7], series1,type2d);

dataset.addValue(d[8], series1,type3a);
dataset.addValue(d[9], series1,type3b);
dataset.addValue(d[10], series1,type3c);
dataset.addValue(d[11], series1,type3d);
```



```
dataset.addValue(d[12], series1,type4a);
dataset.addValue(d[13], series1,type4b);
dataset.addValue(d[14], series1,type4c);
dataset.addValue(d[15], series1,type4d);

dataset.addValue(d[16], series1,type5a);
dataset.addValue(d[17], series1,type5b);
dataset.addValue(d[18], series1,type5c);
dataset.addValue(d[19], series1,type5d);

dataset.addValue(d[20], series1,type6a);
dataset.addValue(d[21], series1,type6b);
dataset.addValue(d[22], series1,type6c);
dataset.addValue(d[23], series1,type6d);

dataset.addValue(d[24], series1,type7a);
dataset.addValue(d[25], series1,type7b);
dataset.addValue(d[26], series1,type7c);
dataset.addValue(d[27], series1,type7d);

dataset.addValue(d[28], series1,type8a);
dataset.addValue(d[29], series1,type8b);
dataset.addValue(d[30], series1,type8c);
dataset.addValue(d[31], series1,type8d);

dataset.addValue(d[32], series1,type9a);
dataset.addValue(d[33], series1,type9b);
dataset.addValue(d[34], series1,type9c);
dataset.addValue(d[35], series1,type9d);

dataset.addValue(d[36], series1,type10a);
dataset.addValue(d[37], series1,type10b);
dataset.addValue(d[38], series1,type10c);
dataset.addValue(d[39], series1,type10d);
```

```
dataset.addValue(d[40], series1,type11a);
```

```
dataset.addValue(d[41], series1,type11b);
```

```
dataset.addValue(d[42], series1,type11c);
```

```
dataset.addValue(d[43], series1,type11d);
```

```
dataset.addValue(d[44], series1,type12a);
```

```
dataset.addValue(d[45], series1,type12b);
```

```
dataset.addValue(d[46], series1,type12c);
```

```
dataset.addValue(d[47], series1,type12d);
```

```
dataset.addValue(d[48], series1,type13a);
```

```
dataset.addValue(d[49], series1,type13b);
```

```
dataset.addValue(d[50], series1,type13c);
```

```
dataset.addValue(d[51], series1,type13d);
```

```
dataset.addValue(d[52], series1,type14a);
```

```
dataset.addValue(d[53], series1,type14b);
```

```
dataset.addValue(d[54], series1,type14c);
```

```
dataset.addValue(d[55], series1,type14d);
```

```
dataset.addValue(d[56], series1,type15a);
```

```
dataset.addValue(d[57], series1,type15b);
```

```
dataset.addValue(d[58], series1,type15c);
```

```
dataset.addValue(d[59], series1,type15d);
```

```
dataset.addValue(d[60], series1,type16a);
```

```
dataset.addValue(d[61], series1,type16b);
```

```
dataset.addValue(d[62], series1,type16c);
```

```
dataset.addValue(d[63], series1,type16d);
```

```
return dataset;
```

```

}

void drawchart1(CategoryDataset dataset)

{
    JFrame frame1 = new JFrame();

JFreeChart chart;

    chart = ChartFactory.createLineChart(

        "Line Chart For "+a+" and "+b,    // chart title

        "Frequency",                    // domain axis label

        "Type",                          // range axis label

        dataset,                          // data

        PlotOrientation.VERTICAL, // orientation

        true,                             // include legend

        true,                             // tooltips

        false                             // urls

    );

    ChartPanel chartPanel = new ChartPanel(chart);

    chartPanel.setPreferredSize(new Dimension(700, 350));

    frame1.setContentPane(chartPanel);

    frame1.setSize(1300,500);

    frame1.setVisible(true);

    final CategoryPlot plot = (CategoryPlot) chart.getPlot();

    plot.setBackgroundPaint(Color.lightGray);

    plot.setRangeGridlinePaint(Color.white);

    plot.setDomainGridlinePaint(Color.white);

    plot.setDomainGridlinesVisible(true);

    plot.setRangeGridlinesVisible(true);

    chart.setBackgroundPaint(Color.white);

    final NumberAxis rangeAxis = (NumberAxis) plot.getRangeAxis();

    rangeAxis.setStandardTickUnits(NumberAxis.createStandardTickUnits());

    rangeAxis.setAutoRangeIncludesZero(true);

    final LineAndShapeRenderer renderer = (LineAndShapeRenderer) plot.getRenderer();

//    renderer.setDrawShapes(true);

```

```
renderer.setSeriesStroke(  
    0, new BasicStroke(  
        2.0f, BasicStroke.CAP_ROUND, BasicStroke.JOIN_ROUND,  
        1.0f, new float[] {10.0f, 6.0f}, 0.0f  
    )  
);  
  
renderer.setSeriesStroke(  
    1, new BasicStroke(  
        2.0f, BasicStroke.CAP_ROUND, BasicStroke.JOIN_ROUND,  
        1.0f, new float[] {6.0f, 6.0f}, 0.0f  
    )  
);  
  
renderer.setSeriesStroke(  
    2, new BasicStroke(  
        2.0f, BasicStroke.CAP_ROUND, BasicStroke.JOIN_ROUND,  
        1.0f, new float[] {2.0f, 6.0f}, 0.0f  
    )  
);  
}  
}
```