

APPENDIXES

Appendix 1A

Preparation of a 1% Agarose Gel for Gel Electrophoresis

2. For a **1% agarose gel**, weigh out **1 gram** of agarose (powder) on a weighing scale.
Note: percentage of the gel reflects the amount of agarose in gram in 100 mL of 1X TAE buffer, depending on the final percentage of agarose in the gel.
Example: If you want to make a 0.7% agarose gel (0.7 g/100 mL, w/v), weigh out 0.7 g of agarose for 100 mL of agarose solution
3. Carefully, put the agarose in a 250-mL Erlenmeyer flask.
4. Measure out 100 mL of 1X TAE buffer using a plastic or glass graduated cylinder.
5. Add 100 mL of 1X TAE buffer into the flask in step 2.
6. Cover the flask with a piece of plastic wrap. Poke 3-4 holes on the plastic wrap using a pointed end of a pencil or pen (*Note: the holes allow the steam to escape during microwaving in step 6 below*). Swirl the solution to break up any lumps of agarose granules.
7. Microwave the solution for about 2 minutes or until the agarose granules have completely melted.
 - *Be careful with the flask. The solution gets very hot.*
 - *Constantly watch over the solution because when it starts boiling, it might overflow.*
 - *Swirl gently the solution several times while microwaving to help melt agarose evenly.*
 - *Once the agarose has melted completely, the solution is clear.*
8. Cool down the agarose solution for at least 30 min in a 55°C water bath.
9. While the agarose solution is cooling, prepare the gel cast with the appropriate comb.
 - *The comb depends on the number of samples to be loaded on the gel. For example, if there are less than 18 samples, then use a 20-tooth comb; but, if there are 21 samples, then use a 30-tooth comb.*

- *Remember to add two more wells to the number of wells needed for the samples. These two wells will be for loading 1kb DNA ladder in the first and the last wells (or left and right sides of loaded samples).*

10. After the agarose solution has been cooled down, add 5 μ L of Ethidium Bromide (EtBr) into the solution and swirl the flask GENTLY to mix. Note: Do NOT swirl vigorously to generate many bubbles.

11. Pour the agarose/EtBr solution into the gel cast. Wait for 30 min for the agarose solution to solidify.

Note: IMMEDIATELY after pouring the agarose solution, inspect the agarose solution's surface for the present of bubbles. If there are many bubbles floating on the surface of the gel solution, use a pipette tip to pop them before the gel is completely solidified.

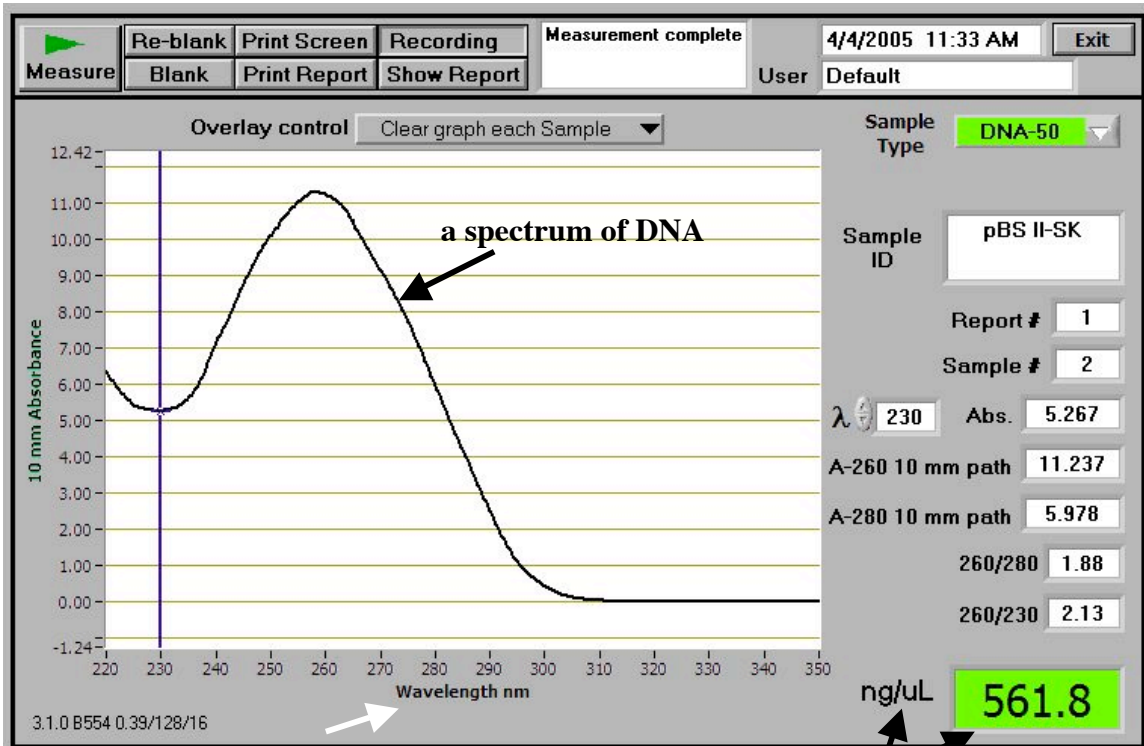
12. Pour ~600 mL of 1X TAE buffer into the gel box.

After the agarose has solidified into a gel, take out the comb gently by pulling it straight up out of the gel and put the gel in the gel box containing the 1XTAE running buffer.

Appendix 1B

What is a **spectrophotometer**?

It is an **instrument** that **measures** the **amount** of **molecules** **absorbing** at a **given wavelength of energy**. In this exercise, we measure the amount of DNA molecules in a given volume in the **ultraviolet wavelengths** of **200 – 280 nm** (nm stands for **nanometer**, which is **1 billionth** of a **meter**). The bases of DNA have the absorbance at the wavelength of 254 nm. The absorbance of DNA molecules over the wavelength range of 220 - 350 nm is represented as a **spectrum** with a **peak** at **near 260 nm** as illustrated by the **Nanodrop spectrophotometer readout** below:

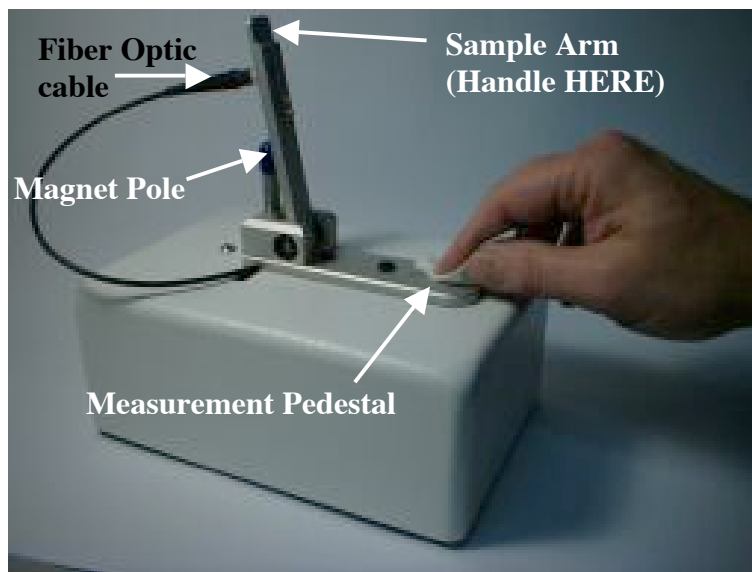


DNA concentration

OPERATION OF NANODROP SPECTROPHOTOMETER ND-1000

Note: The Nanodrop is powered by the computer via the USB port.

1. **Turn ON** the **Computer (laptop)** that connects to the Nanodrop.
2. **Turn ON** the **Nanodrop** by clicking an "ND-1000 v3.1.0" icon on the computer desktop. Wait for a few seconds for the Nanodrop to be up. You see the Nanodrop 3.1.0 Diagnose panel with **User field** as **Default**.
3. **Click** on "**Nucleic Acid**" button on the top left column for reading concentration of DNA and RNA solutions.
 - ❖ You see a following message:
"Ensure Sample Pedestals are clean and then load a water sample. After loading water sample, click OK to initialize instrument"
4. a. **Clean the sample pedestals as followings:**
 - i. **Raise the Sample Arm up** by holding at its end as shown on the picture below.
Caution: NEVER hold the Optical Cord when lifting and lowering the Sample Arm because the cord is fragile; and it is very expensive to replace it.
 - ii. **Wipe both the Measurement Pedestal** and the **Sample Arm** with a piece of Kimwipes slightly wetted with distilled water.



b. Pipet **1.5 - 2 μL** of water on the **Measurement pedestal**.

Note: Even though the Nanodrop Inc. claims that the Nanodrop can read as low as **1 μL** , the concentration reading is NOT consistent at this volume. Therefore, the **minimal** volume for the concentration reading is **1.5 μL**

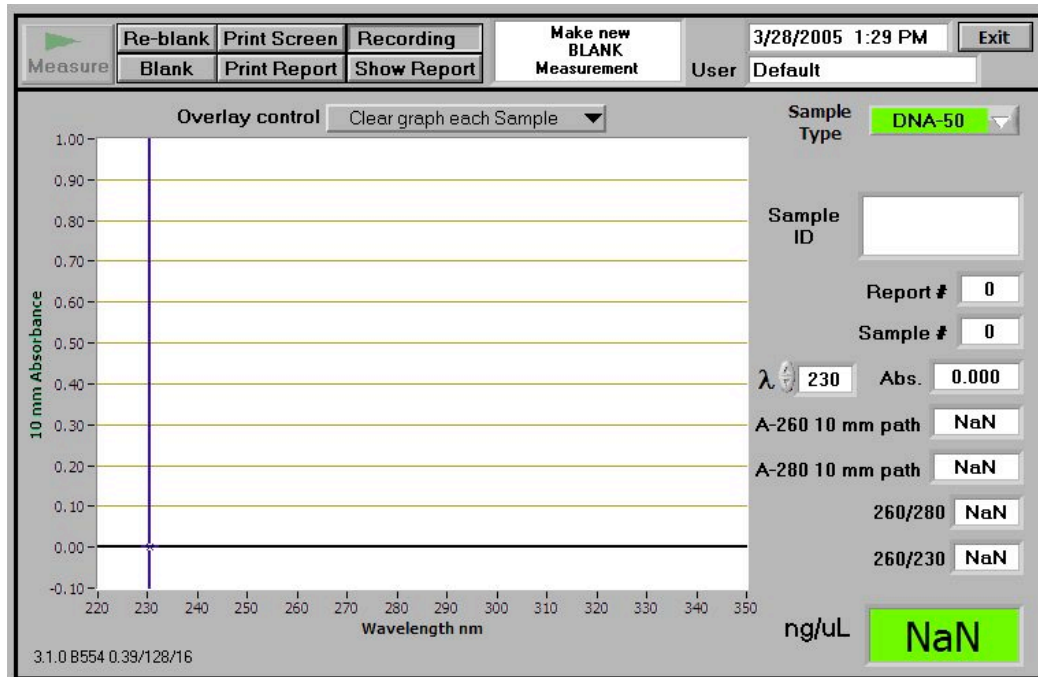


c. **Slowly Lower** the SAMPLE Arm to its horizontal position.

Caution: NEVER let the arm fall freely.

d. Click the **OK** button. The Nanodrop is **INITIALIZED**.

You see a **Dialog panel** as shown below



What do you need to do, NEXT?

- a. **Change SAMPLE TYPE** (if necessary) from **DNA-50** (by Default) to **RNA-40** or **Other** (for Oligonucleotides), depending on your sample.
 - b. **Type in** the **SAMPLE ID** field the Information of your sample.
 - c. **Make** a **NEW BLANK measurement**
 - d. (Option) **Change** the **OVERLAY CONTROL** field from the Default setting of “CLEAR GRAPH EACH SAMPLE” to “CLEAR GRAPH ON NEW REPORT” or “ACCUMULATE UNTIL CLEAR” or “CLEAR GRAPH NOW”
-
5. **Wipe off** the **liquid** on **BOTH** the **ARM** and **Measurement pedestals** with a piece of Kimwipes.
 6. **Make** a **Blank measurement** by pipetting 1.5 - 2.0 mL of either double-distilled water or TE (depending on whether your sample solution is in double-distilled water or TE) on the Measurement Pedestal. Then lower the Sample Arm to its horizontal position.
 7. **Click** the **BLANK** button. The blank was made.
 8. After the reading is done, **bring** the Sample Arm **up** to the vertical position and **Wipe off** the **liquid** on **BOTH** the **ARM** and **Measurement pedestals** with a piece of Kimwipes.
 9. **Pipet** 1.5 - 2.0 mL of **SAMPLE** on the Measurement Pedestal and lower the Sample Arm.
 10. **Type in** the **SAMPLE ID** field **Information** of a sample solution.
 11. **Click** the **MEASURE** button to determine concentration of your sample.
 12. After the reading is done, a sample concentration (in **ng/mL**) and a spectrum of the sample along other information are shown. You can either
 - a. **Save** the **window** of measured sample by clicking on **FILE** → choose **SAVE WINDOW** → Select an existing folder or Create a **NEW** folder (give a name for the **NEW** folder) → Type in a Name file in the **FILE NAME** field → Click the **SAVE** button to save the file **or**
 - b. **Print** the **window** by **clicking** the **PRINT SCREEN** button.

Note: To print the current spectrum of the sample, you **MUST** print it before reading the next sample. Otherwise, you need to repeat reading the sample.

13. **Repeat** steps 8-12 for other samples.
14. After reading the **last sample**, **click** the **PRINT BATCH** button to print concentrations of all read samples.
15. If done with the Nanodrop, **click** the **EXIT** buttons.
16. **Clean** the **Measurement Pedestal** and the **Sample Arm** with a piece of Kimwipes slightly wetted with distilled water.

Appendix 1C

1-kb DNA Ladder (Taken from Invitrogen website)



1 Kb DNA Ladder

Cat. No. 15615-016

Size: 250 µg

Conc.: 1.0 µg/µl

Store at -20°C.

Description:

The 1 Kb DNA Ladder (U.S. Patent No. 4,403,036) is suitable for sizing linear double-stranded DNA fragments from 500 bp to 12 kb. The bands of the ladder each contain from 1 to 12 repeats of a 1018-bp DNA fragment. In addition to these 12 bands, the ladder contains vector DNA fragments that range from 75 to 1636 bp. The 1636-bp band contains 10% of the mass applied to the gel. The ladder may be radioactively labeled by one of the following methods: (i) Partial exonucleolytic degradation and resynthesis with T4 DNA polymerase. This method is preferred because higher specific activity is achieved with less ³²P input; (ii) Labeling the 5' ends with T4 polynucleotide kinase; (iii) Filling in the 3' recessed ends with *E. coli* DNA polymerase I or the large fragment of DNA polymerase I.

Storage Buffer:

10 mM Tris-HCl (pH 7.5)

50 mM NaCl

0.1 mM EDTA

Recommended Procedure:

Invitrogen recommends the use of 10X BlueJuice[®] Gel Loading Buffer (10816-015) at a concentration of 2X [for electrophoresis of this ladder on agarose gels]. Alternatively, the DNA ladder can be diluted in a buffer such that the final concentration of NaCl is 20 mM. Apply approximately 0.1 µg of standard per mm lane width. **DO NOT HEAT!**

Quality Control:

Agarose gel analysis shows that all bands larger than 500 bp are distinguishable.

Doc. Rev.: 011602

This product is distributed for laboratory research only. CAUTION: Not for diagnostic use. The safety and efficacy of this product in diagnostic or other clinical uses has not been established.

For technical questions about this product, call the Invitrogen Tech-LineSM U.S.A. 800 955 6288

APPENDIX 2 - BIOINFORMATICS (PARTS I AND II)

HC70AL Spring 2004

An Introduction to Bioinformatics -- Part I

By

Brandon Le

April 6, 2004

What is a Gene?

An ordered sequence of nucleotides

What are the 4 Nucleotides in DNA?

**A - Adenine
T - Thymine
C - Cytosine
G - Guanine**

What are the Characteristics of a Gene?

- An ordered sequence of nucleotides
- A unique position/location in the genome
- Polarity (5' to 3')
- Exons and Introns

What are the Anatomical Features of Genes?

- Discrete beginning and discrete end
- Two strands of DNA
- Double helical
- Strand one (5' to 3')
- Strand two (3' to 5')
- Sense strand (5' to 3')
 - specifies the trait
- Nonsense strand (3' to 5')
 - template for transcription

Sense Strand

5' - ACGTCAGTCGATGCATGCTAGCTAGC - 3'
3' - TGCAGTCAGCTACGTACGATCGATCG - 5'

Nonsense Strand

Genes Have a Unique Position in the Genome!

Task: Where is your gene located in the genome?

Tools: The Arabidopsis Information Resources (TAIR)
(<http://www.arabidopsis.org>)

Procedure:

1. Select Seqviewer
2. Enter gene number (ex. AT1G18260)
3. Submit

Results/Question:

1. What chromosome is your gene in?
2. What other genes/markers are next to your gene?
3. What is the exact position of your gene in the genome?

01 AT2G22800
02 AT2G23290
03 AT2G37120
04 AT3G09735
05 AT3G12840
06 AT3G50060
07 AT3G53370
08 AT4G37260
09 AT4G37790
10 AT5G03220
11 AT5G03500
12 AT5G19490
13 AT5G67300

Genes Have a Unique Order of Nucleotides!

Task: What is the order of nucleotides for your gene?

Tools: The Arabidopsis Information Resources (TAIR)
(<http://www.arabidopsis.org>)

Procedure: (Continue from previous slide)

1. Click on Location

Results/Question:

1. What are your neighbor genes?
2. What is the orientation of your gene?
3. How big is your gene?

Genes Have Exons and Introns!

Task: How many exons and introns does your gene have?

Tools: The Arabidopsis Information Resources (TAIR)
(<http://www.arabidopsis.org>)

Procedure: (Continue from previous slide)

1. Click on gene information on the right

Results/Question:

1. How many exons/introns in your gene?
2. What are exons?
3. What are introns?

Gene Encodes a Protein

Task: Determine the protein encoded by gene?

Tools: The Arabidopsis Information Resources (TAIR)
(<http://www.arabidopsis.org>)

Results/Question:

1. How large is your protein?
2. What are the anatomy of a protein?

N-terminal



C-terminal

What is the identity of your gene?

Task: What does your gene code for?

Tools: NCBI BLAST Tools
(<http://www.ncbi.nlm.nih.gov/BLAST>)

What is BLAST?

Basic Local Alignment Search Tool (BLAST)

What does BLAST do?

A family of programs that allows you to input a query sequence and compare it to DNA or protein sequences in db.

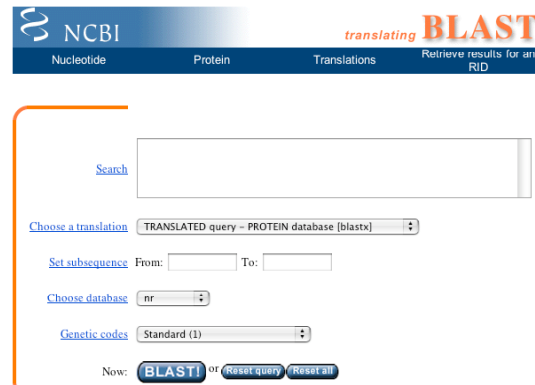
What are the steps to performing BLAST search?

Paste sequence of interest into BLAST input box

Select BLAST program

Select db

Select Optional Parameters



The screenshot shows the NCBI BLAST search interface. At the top, there is a navigation bar with the NCBI logo and the text "translating BLAST". Below the navigation bar, there are several input fields and buttons. A large text input box is labeled "Search". Below it, there is a dropdown menu for "Choose a translation" with the selected option "TRANSLATED query - PROTEIN database [blastx]". There are also fields for "Set subsequence" (From: and To:), "Choose database" (nr), and "Genetic codes" (Standard (1)). At the bottom, there are buttons for "BLAST!", "Reset query", and "Reset all".

What are the different BLAST Programs?

Fastest

blastp - protein query vs protein db

blastn - DNA query vs DNA db

blastx - translated DNA query vs protein db

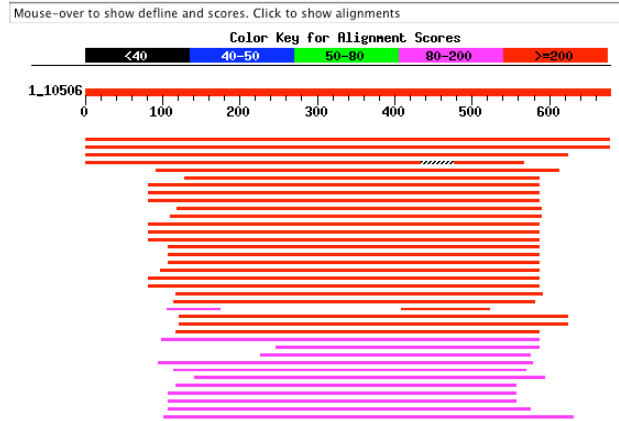
tblastx - protein query vs translated DNA db

Slowest

tblastn - translated DNA query vs translated DNA db

Anatomy of a BLAST Result -- Part I

Distribution of 339 Blast Hits on the Query Sequence



Anatomy of a BLAST Result -- Part II

Sequences producing significant alignments:	Score	E
	(bits)	Value
gi 14532716 gb AAK64159.1 unknown protein [Arabidopsis tha...	1206	0.0
gi 18394588 ref NP_564049.1 suppressor of lin-12-like prot...	1209	0.0
gi 15219499 ref NP_177498.1 suppressor of lin-12-like prot...	877	0.0
gi 11120786 gb AAG30966.1 hypothetical protein, 3' partial...	426	e-118
gi 41151276 ref XP_046437.5 chromosome 20 open reading fra...	291	3e-77
gi 13559241 emb CAB65792.2 dJ842G6.2 (novel protein imilar...	282	2e-74
gi 19923669 ref NP_005056.3 sel-1 suppressor of lin-12-lik...	268	4e-70
gi 6851089 gb AAF29413.1 SEL1L [Homo sapiens] >gi 17646138...	268	4e-70
gi 9967440 dbj BAB12403.1 SEL1L [Mesocricetus auratus]	264	4e-69
gi 31203035 ref XP_310466.1 ENSANGP00000019196 [Anopheles ...	263	1e-68
gi 21355295 ref NP_651179.1 CG10221-PA [Drosophila melanog...	263	1e-68
gi 20857527 ref XP_127076.1 Sell (suppressor of lin-12) 1 ...	261	4e-68
gi 4159995 gb AAD05210.1 SEL1L [Mus musculus] >gi 20073079...	259	1e-67
gi 29336095 ref NP_808794.1 Sell (suppressor of lin-12) 1 ...	259	2e-67
gi 29612522 gb AAH49959.1 Sellh protein [Mus musculus]	258	4e-67
gi 17563256 ref NP_506144.1 Suppressor/Enhancer of Lin-12 ...	247	9e-64
gi 1255199 gb AAC47112.1 sel-1 gene product	247	9e-64

Anatomy of a BLAST Result -- Part III

```
>gi|14532716|gb|AAK64159.1| unknown protein [Arabidopsis thaliana]
Length = 678

Score = 1206 bits (3120), Expect = 0.0
Identities = 614/678 (90%), Positives = 614/678 (90%)

Query: 1 MRILSYGIVILSLLVFSFIEFGVHARPVVLVXXXXXXXXXXXXXXXXXXXXXXXXXXXX 60
MRILSYGIVILSLLVFSFIEFGVHARPVVLV V
Sbjct: 1 MRILSYGIVILSLLVFSFIEFGVHARPVVLVLSNDDLNSGGDDNGVGESSDFDFGESEP 60

Query: 61 XXXXXLDPGSWRSIFEPDDSTVQAASPQYYSGLKKILSAASEGNFRLMEEAVDEIEAASS 120
LDPGSWRSIFEPDDSTVQAASPQYYSGLKKILSAASEGNFRLMEEAVDEIEAASS
Sbjct: 61 KSEEEIDPGSWRSIFEPDDSTVQAASPQYYSGLKKILSAASEGNFRLMEEAVDEIEAASS 120

Query: 121 AGDPHAQSIMGFVYIGIMMREKSKSKSFLHHNFAAAGNMQSKMALAFTYLRQDMHDKAV 180
AGDPHAQSIMGFVYIGIMMREKSKSKSFLHHNFAAAGNMQSKMALAFTYLRQDMHDKAV
Sbjct: 121 AGDPHAQSIMGFVYIGIMMREKSKSKSFLHHNFAAAGNMQSKMALAFTYLRQDMHDKAV 180

Query: 181 QLYAELAETAVNSFLISKDSPVVEPTRIHSGTEENKGLRKSARGEEDDFQILEYQAQKG 240
QLYAELAETAVNSFLISKDSPVVEPTRIHSGTEENKGLRKSARGEEDDFQILEYQAQKG
Sbjct: 181 QLYAELAETAVNSFLISKDSPVVEPTRIHSGTEENKGLRKSARGEEDDFQILEYQAQKG 240

Query: 241 NANAMYKIGLFYFGLRGLRRDHTKALHWFLKAVDKGEPRSMELLGEIYARGAGVERNYT 300
NANAMYK GLFYFGLRGLRRDHTKALHWFLKAVDKGEPRSMELLGEIYARGAGVERNYT
Sbjct: 241 NANAMYKNGLFYFGLRGLRRDHTKALHWFLKAVDKGEPRSMELLGEIYARGAGVERNYT 300
```

PubMed - Endless Resources

The screenshot shows the PubMed website interface. At the top, there are logos for NCBI, PubMed, and the National Library of Medicine (NLM). Below the logos is a search bar with the text "Search PubMed" and a "Go" button. To the right of the search bar are tabs for "Limits", "Preview/Index", "History", "Clipboard", and "Details". On the left side, there is a sidebar with links for "About Entrez", "Text Version", "Entrez PubMed Overview", "Help | FAQ", "Tutorial", "New/Noteworthy", "E-Utilities", "PubMed Services", "Journals Database", "MeSH Database", and "Single Citation". In the center, there is a list of search tips:

- Enter one or more search terms, or click [Preview/Index](#) for advanced searching.
- Enter [author names](#) as smith jc. Initials are optional.
- Enter [journal titles](#) in full or as MEDLINE abbreviations. Use the [Journals Database](#) to find journal titles.

Below the list, there is a yellow highlighted box with the following text:

PubMed, a service of the National Library of Medicine, includes over 14 million citations for biomedical articles back to the 1950's. These citations are from MEDLINE and additional life science journals. PubMed includes links to many sites providing full text articles and other related resources.

HC70AL Spring 2004

An Introduction to Bioinformatics -- Part II

By

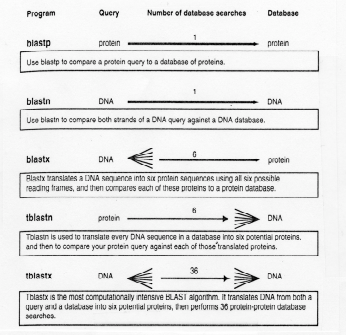
Brandon Le

April 8, 2004

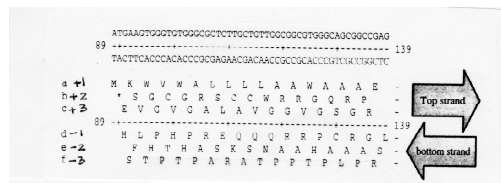
Review of BLAST Search

1. **What is the purpose of running BLAST Search?**
2. **What are the steps to performing BLAST search?**
3. **What does the e-value from a blast result tell you?**
4. **How many BLAST programs can you perform?**
5. **What BLAST program(s) takes the least computational time?**
6. **What BLAST program(s) takes the most computational time? Why?**

What are the Five BLAST Search Programs?



•How many proteins can a short DNA sequence potentially encode?



Question:

You have DNA Sequence. You want to know which protein in the main protein database is most similar to some protein encoded by your DNA.

Which BLAST program should you use?

Suppose you have a protein sequence.
Which BLAST program should you use?

HOW to interpret BLAST results?

Expect = 8×10^{-74}
 probability of finding this alignment in a database by chance and chance alone.

Identifier of protein in database
 d384206.2 (novel protein similar to SELL (sw1-112), C101999n1-118); (Homo sapiens) origin of protein sequence

Score = 207 bits (760), Expect = 8×10^{-74}
 Identical = 177/468 (37%), Positives = 269/468 (57%), Gaps = 9/468 (1%)
 Frame = +1

What does frame mean?

Query: 388 MGFV--YGIHMKSEKSEKSLHNFPAAGNMQSKHALAFTYLRQ---DHDKAVQLY 549
 +GF+ YGIH+ E +*+* +*+ *+ AGNM +*R L+ ID + + A+ 3
 Sbjct: 2 MGLFQVYQSM--EYDQASALIVTVTSGAGSHMGHGLGVVLDGIIVLQNEVALQVY 59

Query: 540 ARLAFTAVNEPLTKDSEVVEPRTRISGTEENKGLRKSERGEDEDFOILEYQAGKGNAN 729
 +*A+ +*F S+ IV E + TE + E + + *G +* +*+*+
 Sbjct: 60 KKVADYIADTFESESSEVY-EVRL---TEPENLSESEILMDIYQVYFLAERGQVQ 115

Query: 730 AMYKIGLFYFGLRGLRDHTKALNFKAVDKGPRMELGELIYAG-AVERNYTA 708
 +G+ +G +*G +*+ KALNFKKA G +*+ +*+*+ G A V +*+ A
 Sbjct: 116 IQVSLGQLLISMGLEQDVTKAVYFLRAAKAGAHANFISHTYLGAAVFGHNA 175
 exact match at amino acid

Query: 907 LENLZLAKEGLYAFNGIGYLVKGVVDKKNYKAREFEKAVDNEPDSCHYHLGVLY 1086
 +*+AA +G +*+G LV G GV NY +A +*F+KA + + + LG +3
 Sbjct: 176 FKTFMARSCHSGLRGLGILLFPGKGYL--NIAALITFQFAEKGNPDAQGLGFNY 234

Query: 1087 LKGIQVNRDVRQATYFFVAANAGQPFAYGLAKMFTGVLKELNEMATFVKLVAEKG 1240
 G G +*D + A RIF+*A +*QD A Y LAKM+ TQ G+ +* A YK V E G
 Sbjct: 235 YSRSHMDEVFLAPFYVLAAGQSGALVYLAHVATQGVVNSCHTAVELVREGVSLG 294

Query: 1247 PWEELEWALRAVLRDVEKALIVSRHAEKGYEVAQSNAMLDKYGERSMCHGVSGFC 1446
 W+ A AV GD+ +L+ YK +AENGYEVAQSN+A+IL+ + +-----+546
 Sbjct: 295 HWAKEFLTATFAYKGGDSEELVQALLRNCYVAQSNAILSEKKNIL 546
 what is this?

Query: 1447 TDKER-HERASLWRAEQGNEHAALLIGDAYTGGTERDFVRAAEAY-NHAKSQSNA 1620
 +*K+ + A LW RA+ QUN A + IGL +YIG G*+*D+ AA Y + A HA
 Sbjct: 347 +EERDHYFALSLWRAEQGNAFAVHLSGQIYVQVYERDYGTAATDQYAAKRVHNA 405

Query: 1471 QAMFELGVNHFHGGLEFQDLHLKAVYDESLOSDAARLPTVLALSL 1764
 QAMFELVYVHFG G+ D+HL+*+ YD + O+ A +PV A+ L
 Sbjct: 406 QAMFLAVYHFGGTTTILKFLYDQVTPDRIYVAVHIL 453
 what does these number corresponds to?

what is query?
 what is sbjct?
 positively charged amino acids
 what does the "+" mean?
 K = Lysine
 R = Arginine
 4

Review of gene transcription

1. What product is made after transcription?
2. How is the product similar/different from the gene?
3. What is cDNA?
4. What important information does a cDNA tell you about a gene?
5. What are ESTs?
6. What important information does ESTs tell you about a gene?

Annotation of your gene

1. What chromosome is your gene in?
2. How “big” is your gene?
3. How many exons and introns in your gene?
4. What orientation is your gene in the genome?
5. What is the specific position of your gene in the genome?
6. What gene is “upstream” of your gene?
7. What gene is “downstream” of your gene?
8. How far are the other genes (6 & 7) from your gene?
9. What is the “structure” of your gene?
10. What is the size of the protein in your gene encodes?
11. What protein does your gene encode
12. Is your gene structure predicted by a program?

Webbook - A Virtual Lab Notebook

Webbook is a web lab notebook

Purpose/goal: To have access to experiments carried out by
Lab members, etc... from anywhere
Also serves as a repository for protocols, stocks/reagents

Created by: Harry Hahn
Brandon Le
Bob Goldberg

<http://estdb.biology.ucla.edu/webbook>

Using the Webbook

- 1. Username: email username**
Password: 9 digit student id
- 2. Check message board for important news/updates**
- 3. An overview of the different sections**
 - Projects** - list of experiments
 - Stocks** - catalog of stocks/reagent in the lab
 - Protocols** - procedures carried out in the lab (pdf format)
 - Calendar** - calendar to plant your experiments
 - Browse** - search and look at other members experiments
 - Contact** - email for help
 - Logout** - will logout if idle for 30 min

Webbook Login Page

Help Login

webBOOK Login

Username: ble Password: Login

Last modified August 03 2003 21:16:09.
Copyrighted by the University of California (2003)
Created by Harry Hahn and Brandon Le, Laboratory of Bob Goldberg, UCLA

Creating Projects / Experiments

1. Title of project
2. Questions/Purpose of project
3. Summary of project (ideas)

Entering Gene Information

Genes

Create gene

Fields marked with a red asterisk (*) are **REQUIRED**

Gene Name:*	<input type="text"/>
Species:	<input type="text"/>
Sequence:	<input type="text"/>
Sequence Type:*	-- Select --
Amino Acid Sequence:	<input type="text"/>
Chromosome:	<input type="text"/>
EST Data:	<input type="text"/>
Functional Category:	<input type="text"/>
Promoter:	<input type="text"/>
Domains:	<input type="text"/>
Hits:	<input type="text"/>
Attach a file:	Title: <input type="text"/>
	File: <input type="button" value="Choose File"/> no file selected
	Description: <input type="text"/>

Entering Experiments Information Part 1

Experiments	
Fields marked with a red asterisk (*) are REQUIRED	
Title:*	<input type="text"/>
Goal:*	<input type="text"/>
Background Info:*	<input type="text"/>
Approach:*	<input type="text"/>
Controls:*	<input type="text"/>
Discussion:	<input type="text"/>
Next:	<input type="text"/>

Entering Experiment Information Part II

Materials	Primer * <input type="text" value="AT2G22800-FW
AT2G22800-RV
AT2G23290-FW
AT2G23290-RV
AT2G37120-FW
AT2G37120-RV
AT3G09735-FW
AT3G09735-RV"/>
Protocols:	Protocols * <input type="text" value="*Sequencing Using SPPCR
Alkali Lysis Plasmid Isolation
Arabidopsis Tissue Harvest for GeneChip Experiment
Bacteria Chromosome Mini-Prep
Bacteriophage
Chromatin Immunoprecipitation with Leaves from Arabidopsis"/>
Attach a file:	Title: <input type="text"/> File: <input type="button" value="Choose File"/> no file selected Description: <input type="text"/> <small>All files must have a file name extension. Images must end in .jpg, .png, or .gif. Additional files can be attached by later editing this record.</small>

Entering References Relating to your Gene

References

Create reference record

Fields marked with a red asterisk (*) are **REQUIRED**

Author(s):*	<input type="text"/>
Title:*	<input type="text"/>
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Year*	<input type="text"/>
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