Representation of sequence – sequence file format

1.) FASTA – simple and clean

> gene_name, (other info)
MASASASKJHKLJLKJLDSDFSF
SSDSASFSFD…

Practice / DIY: retrieve sequence in Fasta format and save the file in the local computer.

Public Resources for Bioinformatics

- Databases - how to find relevant information.
- Analysis Tools

Observe: List of databases and service at NCBI, EBI, KEGG, and Ensembl.

Pet Project: Identify an ortholog of..

IL6, or your favorite gene

Make a folder for the project in /GMS6014/

- **Generate subfolders, e.g. “info”, “seqs”.**
  - **/seqs/ for raw sequence files in fasta format.**
  - **/info/ for saving webpages of curated entry.**

Observe/Practice

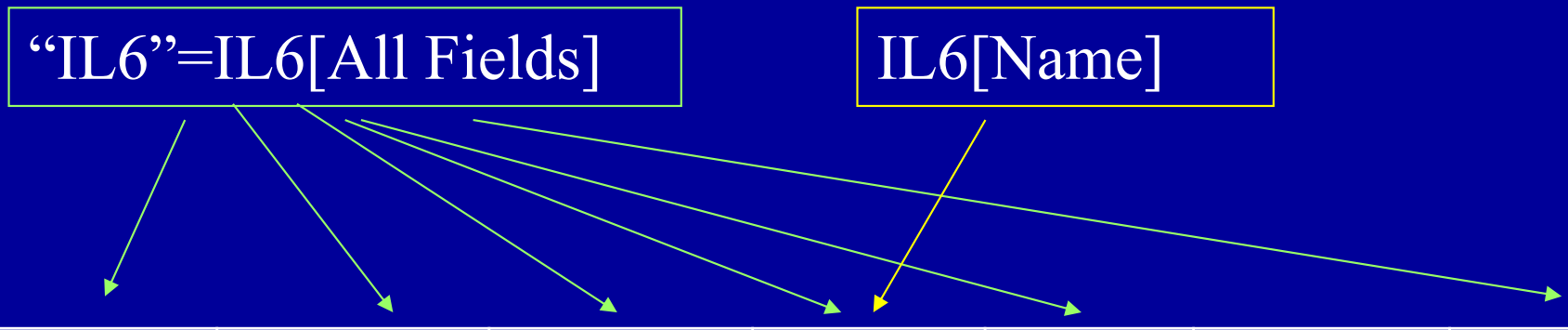
Search for IL6 (or your favorite gene) in the Gene database and the Proteins databases.

- why do we get so many hits?

Search for IL6 in the default “All Text” vs. search in the [Gene Name] field only in the Gene database.

Compare results.

Database concept – tables in relational databases



Accession	Organ.	Ref.	Name	Key words	Features	
….	…..	medline1	TNF	…..	…….	…..
….	….	medline2	P53	….	……..	……

Gene table

Database concept – relationship between tables allows linkage

Accession	Organ.	Ref.	Name	Key words	Features	
….	…..	medline1	P27	…..	…….	…..
….	….	medline2	P53	….	……..	……

Protein table

ID	title	year	author	abstract	
medline1	…..	1970	….	…..	…..
medline2	….	1980	….	….	…

Reference table

Observe/Practice

Observe the links from the IL6 **Gene** page:

- RefSeq
- OMIM
- SNP
- GEO
- Etc.

Gene Entry is the pivotal point for many NCBI resources.

Representation of genes and related information

The need to represent associated info with sequence

- Different aspects of the gene (such as protein, nucleotide, structure (PDB), OMIM etc.)
- Specialized databases (such GEO, SNP)
- Complex / customized data structure
    - Object-oriented data representation

Observe

Observe entries involving IL6 (or your gene) in Reactome.

Pet Project: Identify an ortholog of..

IL6, or your favorite gene

What can we know about this gene?

- **Search for "curated" databases.**
- **To prepare for future analysis, save annotated sequence files as genename.html (in a target folder).**
- **For downstream sequence analysis, save pure sequence as FASTA format file.**

Where and how much information are available for my gene?

Observe: The information contents and presentation format for the same gene in NCBI Genes, NCBI protein, and UniProt, etc..

Public Resources for Bioinformatics

- Databases : how to find relevant information.

- **Analysis Tools**

Public Resources (II) – Analysis tools

- Web-based analysis tools – easy to use, but often with less customization options.
- Stand-alone analysis tools – requires installation and configuration, but provides more customization options.
- Commercial analysis tools.
- Scripting for bioinformatics projects (GMS6232).

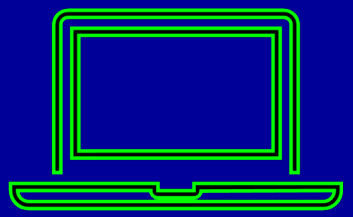
web-based tools

- Identification of web-based bioinformatics resources.
  - Portals, lists,
  - Google search
- Organization
  - Bookmark.
  - html page.

web-based tools

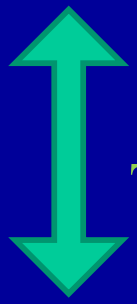
Practice – Identify QPCR primer pairs for your gene of interest.

Your laptop and HiPerGator

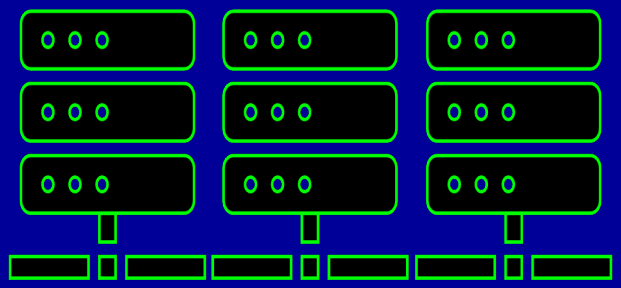


Your own laptop

- How to install program
- How to organize projects



Transfer scripts & results



- **HiPerGator**
  - Log in & navigate
  - Submit a job

Practice: log into UFHPC / Linux server.

Mac user, type in terminal:

$ ssh username@hpg2.rc.ufl.edu

Windows, Open in Putty:

hpg2.rc.ufl.edu

once you are in, move to your working dir:

>cd /blue/gms6014/share/<firstname>