

# Public Resources for Bioinformatics

- **Databases**
- **Analysis Tools**

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

## **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**

# Stand-alone tools 1.

## Rules of the thumb:

- ❖ **Make a folder for each program.**
- ❖ **Make a sub-folder for input/output if necessary.**
- ❖ **Read the instructions before installation.**

# Stand-alone tools 3.

Command line applications:

- ❖ Accounts for a large number of high-quality, sophisticated programs.

**Practice – (install and) run standalone blast  
in your own computer**

# Pet Projects:

**Searching for potential ortholog of IL6 in  
the *Drosophila* genome**

## **Practice – Install the blast program (1)**

- 1. Download the BLAST executable file, save the file in a folder, such as c:\GMS6014\blast\**
- 2. Run the installation program by double click. Inspect the folder following installation.**
- 3. Add three more folders to your /blast directory, “/query”, “/dbs”, and “/out”.**

## Practice – Install the blast program (2)

5. **Inspect the contents of the doc, data, and bin folder. *Move the programs from blast\bin to the blast folder.***
6. **Bring a command (cmd) window by typing “cmd” in the Start→Run box.**
7. **Go to the blast folder by typing “cd C:\GMS6014\blast”**
8. **Try to run the program by typing “blastall”, read the output.**

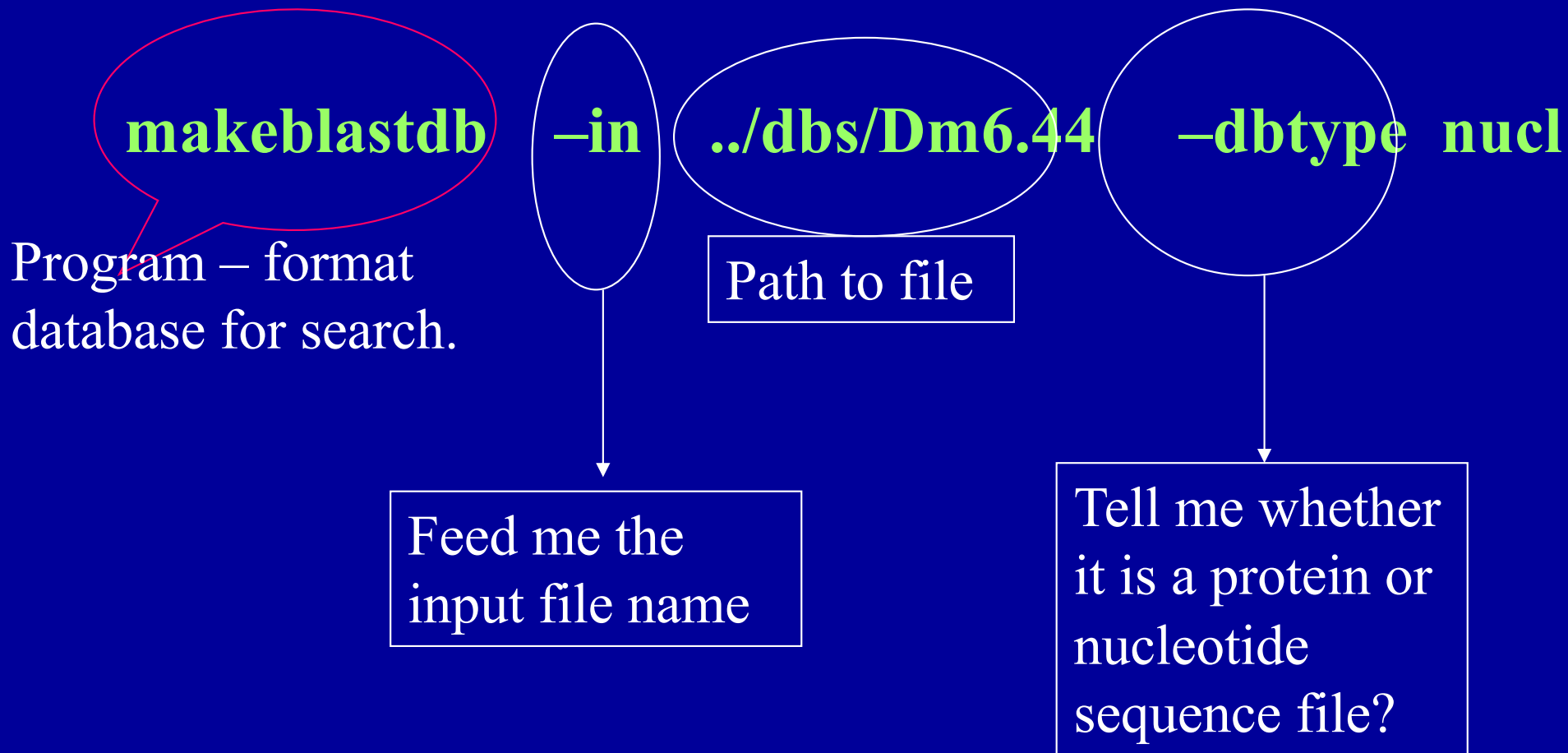
# Practice -- BLAST search in your own computer

1. Download data file from the course web page, or Ensemble. Save in the `blast\dbs` folder.
2. Start a CMD window (or Terminal in Mac), navigate to the `C:\GMS6014\blast` folder.
3. At the prompt `"C:\GMS6014\blast\bin>"` type the command `"makeblastdb -in ../dbs/Dm6.33 -dbtype nucl"*` -- format the dataset for the program.
4. Compose the query sequence save as `"3TNF.txt"` in the `"blast\query\"` folder.
5. Initiated the search by typing `"tblastn -db ../dbs/ Dm6.33 -query ../query/3IL6.txt -out ../out/myblast.html -html"`

\*Command syntax may be different depending on platform and setup



# What's in a command?



For more info, refer to the “user manual” file in the blast\doc folder.

## Advantages of Running BLAST at Your Own Machine

- Do it at any time, no waiting on the line.
- Search for multiple sequences at once.
- Search a defined data set.
- Automate Blast analysis.
- Combine Blast with other analysis.
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