# Programming in Biology MCDB 170

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#### **Computer Science**



#### **Data Analysis**

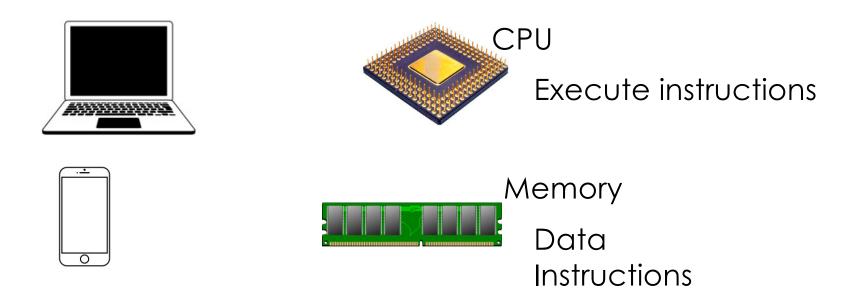
```
generalized linear models
                   octave random forest bayesian statistics oproduct development simulations
    rapidminer normalization teradata
        jupyter pig predictive modeling product design
          deep learning data mining
            goptimization sql d3regression
   hbase &
                                      n matlab
  mongodb communication hive git nosql regularization
decision tree math big data sas java
        natural language processing
         artificial intelligence
             unstructured data
                                 simulation calculus
        neural network mapreduce
           project management
                                      storytelling
                                 relational database
                      structured data
               dimensionality reduction
```

#### Course objectives

- General working knowledge in Python (3 wks)
- DNA sequence analysis using string and Biopython (2 wks)
- Using Numpy and Scipy to simulate biological system (2 wks)
- Using Numpy and Scipy to perform statistical analyses of biological data (2 wks)
- Biological image analysis using scikit-image (will be covered if time allows)

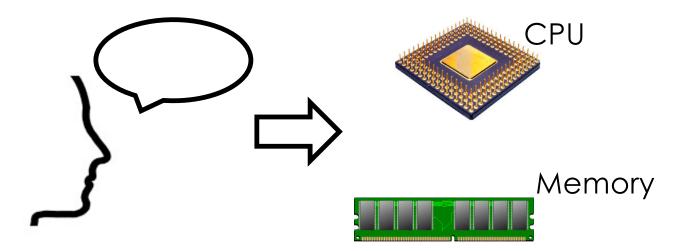
## What is programming?

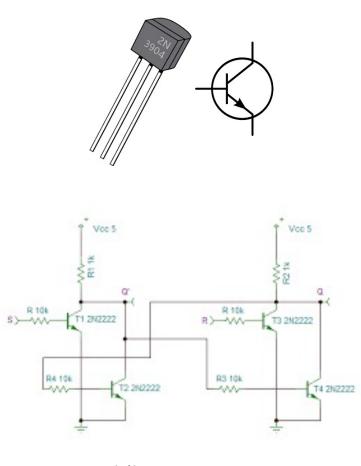
- Writing instructions for computers to perform tasks



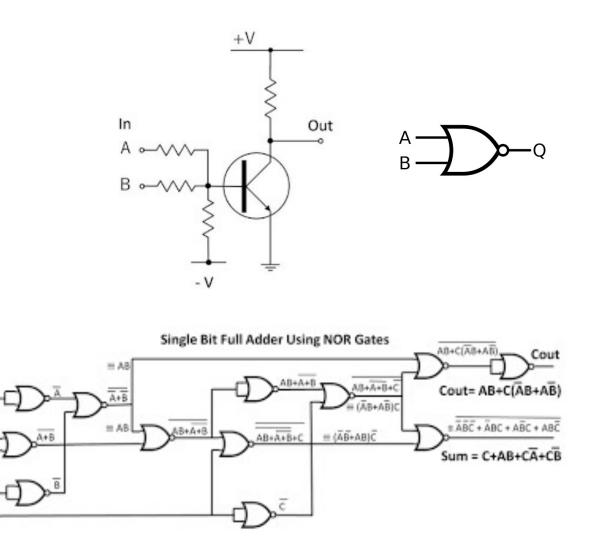
## What is programming Language?

- Writing instructions for computers to perform tasks



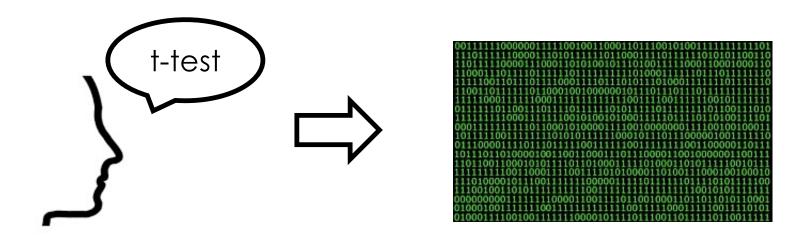


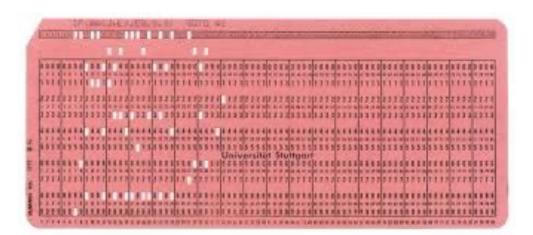
1-bit Memory



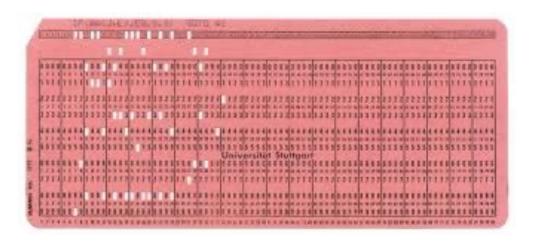
Unit of information: Bit 0, 1

Computer operations are extremely simple (and bits)









push ebp
mov ebp, esp
mov eax, [ebp+0x08]
fld tword [eax]
mov ecx, [ebp+0x0c]
fld tword [ecx]
faddp
mov edx, [ebp+0x10]
fstp tword [edx]
fld tword [eax+0x0A]
fld tword [ecx+0x0A]
fld tword [ecx+0x0A]
for ebp
faddp
fstp tword [edx+0x0A]
pop ebp
ret 0x000c

```
PIN=0.02
IF (DDT.NE.0.0)
                 THEN
DT-DDT
ELSE
DT-PIN
ENDIF
WRITE(*, '(A)') '
                     PLEASE ENTER NAME OF OUTPUT FILE
* B:ZZ.DAT) '
READ (*, '(A)') FNAMEO
OPEN (6, FILE=FNAMEO, STATUS='UNKNOWN')
PV-WFLX/TH
RS=NEQ*ROU*KD/TH
C0=CS
 #include <stdio.h>
 main()
      printf("hello, world\n");
```

```
push ebp
mov ebp, esp
mov eax, [ebp+0x08]
fld tword [eax]
mov ecx, [ebp+0x0c]
fld tword [ecx]
faddp
mov edx, [ebp+0x10]
fstp tword [edx]
fld tword [eax+0x0A]
fld tword [ecx+0x0A]
fld tword [ecx+0x0A]
faddp
fstp tword [edx+0x0A]
pop ebp
ret 0x000c
```

#### **Complied Languages**

C/C++ Fortran Java etc

## Interpretable Languages

Python – in almost all science

Matlab – Most engineering and some biology

R – in almost all statistics

Perl – Extensively used in Human Genome project

Ruby

etc

# Why Python?

- Easy to learn: Syntax is very human friendly
- Extremely popular in every field of science
- Mature scientific libraries (Numpy, Scipy)
- Easy-to-learn programming environment (JupyterLab)

# What you need to do Python programming

- Chrome browser
- UCSB NetID
- Connect to http://mcdb170.lsit.ucsb.edu/

# Required reading (& watching)

- JupyterLab basics
  - https://youtu.be/A5YyoCKxEOU
- Interface, file operations, and notebook basics.
  - https://jupyterlab.readthedocs.io/en/stable/user/interface.html
  - <a href="https://jupyterlab.readthedocs.io/en/stable/user/files.html">https://jupyterlab.readthedocs.io/en/stable/user/files.html</a>
  - <a href="https://jupyterlab.readthedocs.io/en/stable/user/file\_editor.html">https://jupyterlab.readthedocs.io/en/stable/user/file\_editor.html</a>
  - https://jupyterlab.readthedocs.io/en/stable/user/notebook.html