3DAROC18

Summary day #1

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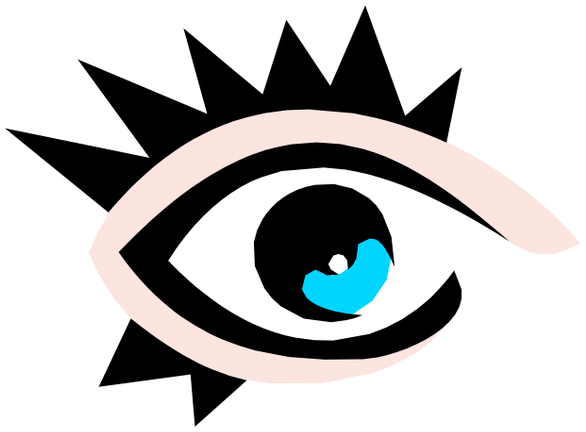
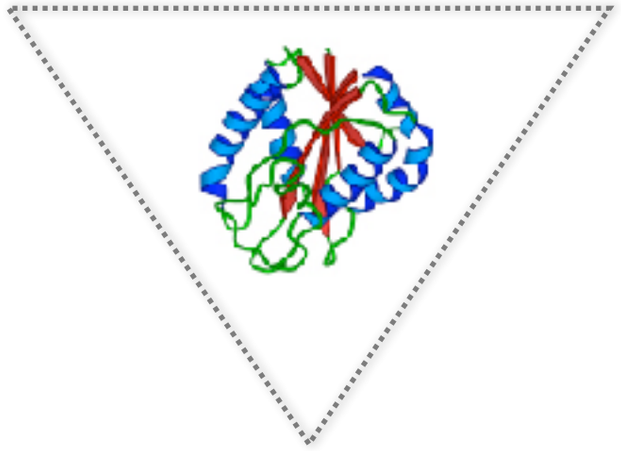
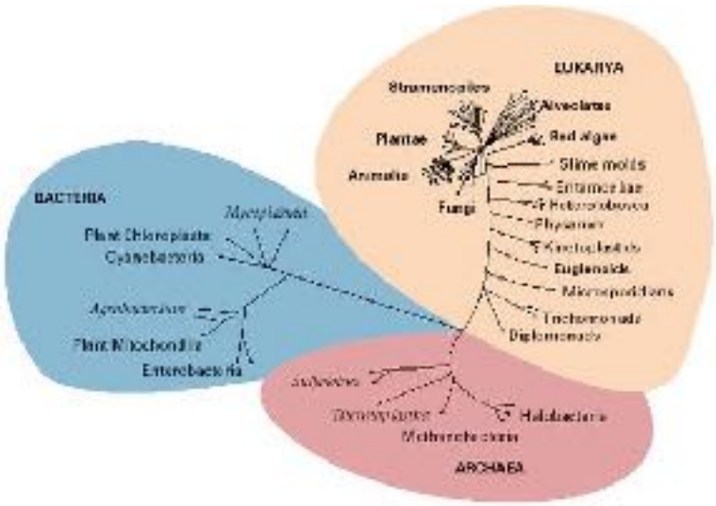
Data groups

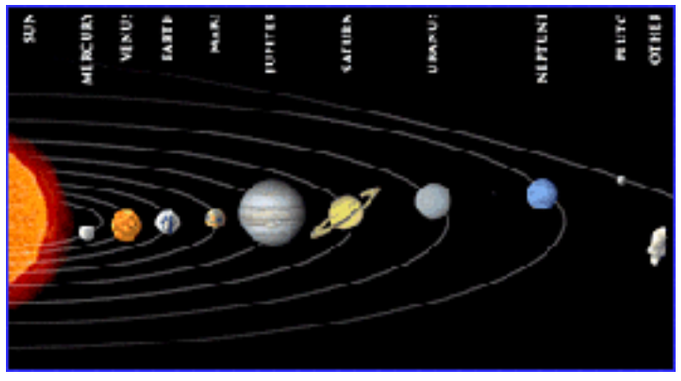


Experimental observations



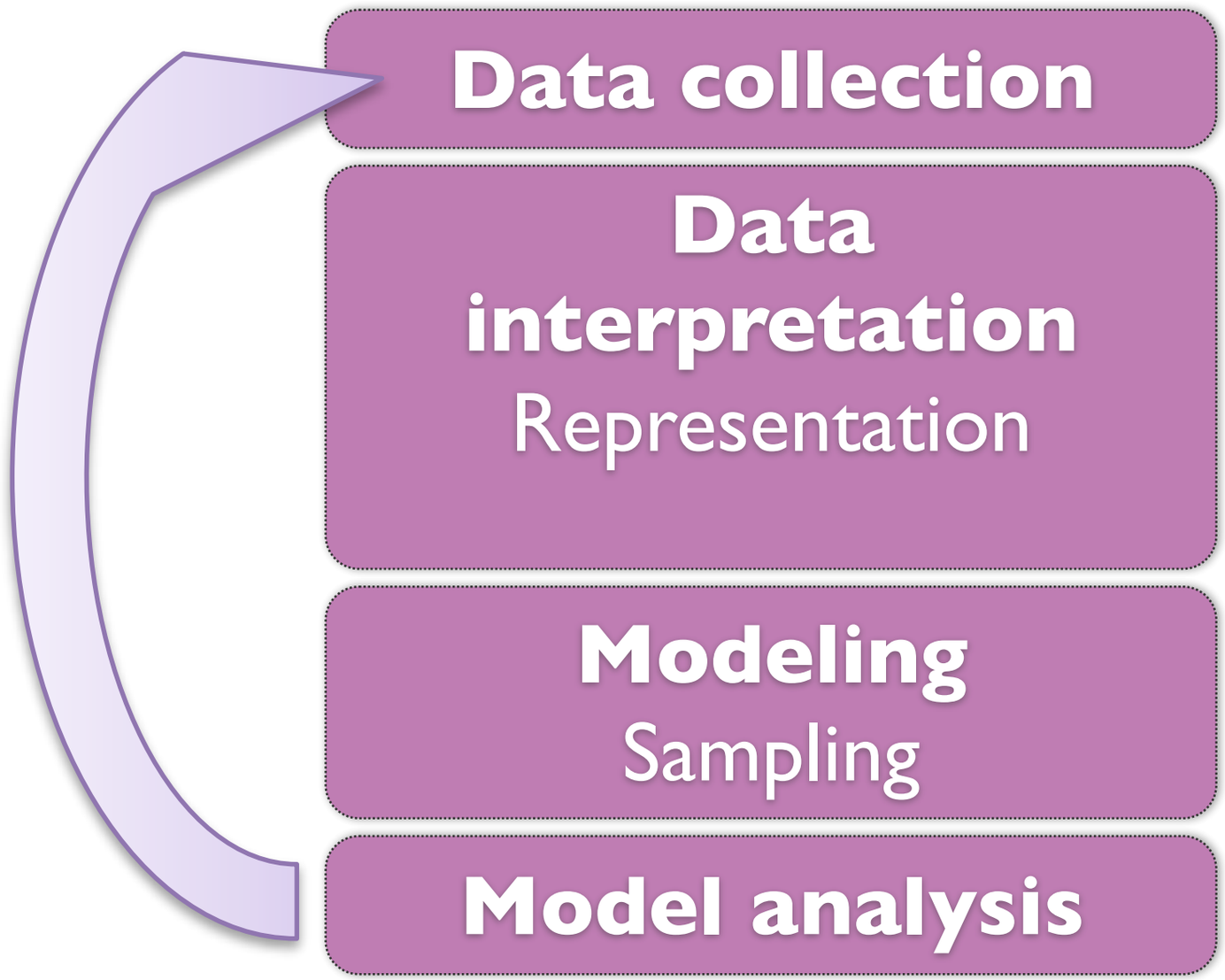


Statistical rules



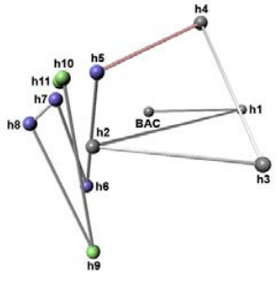
Laws of physics

Integrative modeling

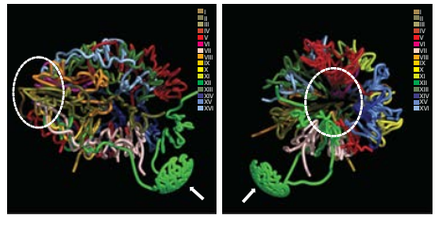


3D modeling of genomic domains: other methods

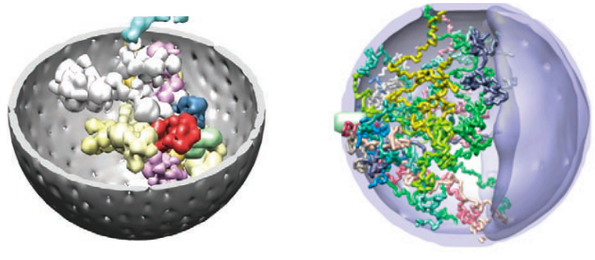
Jhunjhunwala (2008) Cell



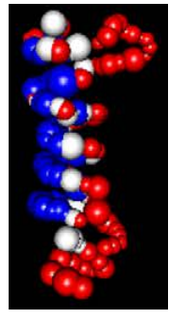
Duan (2010) Nature



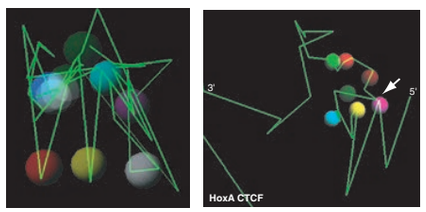
Kalhor (2011) Nature Biotechnology
Tjong (2012) Genome Research



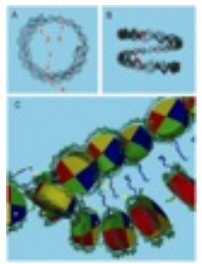
Hu (2013) PLoS Computational Biology



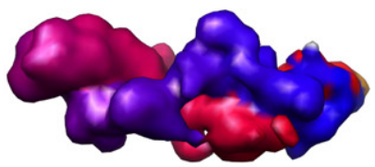
2008 — 2014

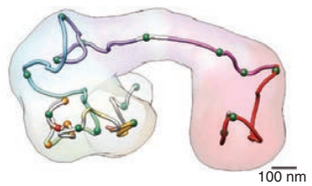


Fraser (2009) Genome Biology
Ferraiuolo (2010) Nucleic Acids Research

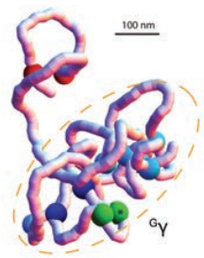


Asbury (2010) BMC Bioinformatics





Baù (2011) Nature Structural & Molecular Biology
Umbarger (2011) Molecular Cell



Junier (2012) Nucleic Acids Research

Linux commands

Command	Description	Example	Action
`pwd`	`print working directory`	pwd	path & name of dir. I am in now
`ls`	`list` contents of directory	ls	list contents of current dir.
		ls test/	list contents of the test dir. that hangs from the current working dir.
		ls -lh	vertical list of dir. contents
`cd`	`change directory`	cd	go to home directory
		cd /home/user/Docs	go to the Docs directory
		cd ..	go to parent directory
`mkdir`	`make directory`	mkdir test	creates directory test/
`rmdir`	`remove directory`	rmdir test	remove test/ if empty
`cp`	`copy`	cp fileA fileB	copy fileA to fileB
`mv`	`move` or rename file or directory	mv a b	change name from a to b
		mv a ..	move a to parent directory
`more`	see file contents	more a.txt	see contents of a.txt
`gedit`	simple text editor!	gedit a.txt	edit a.txt
`firefox`	a web and directory browser	firefox a.html or firefox a.jpg	use web browser to view file
`info` or `man`	`information` on a command	info ls	manual page for the 'ls' command

Python definitions

- variables

```
a = 1
b = 3.14
c = ‘charles’
```

- loops

```
for i in range(0, 10, 1):
    print i
```

```
i = 0
while i < 10:
    # print i
    i = i + 1
```

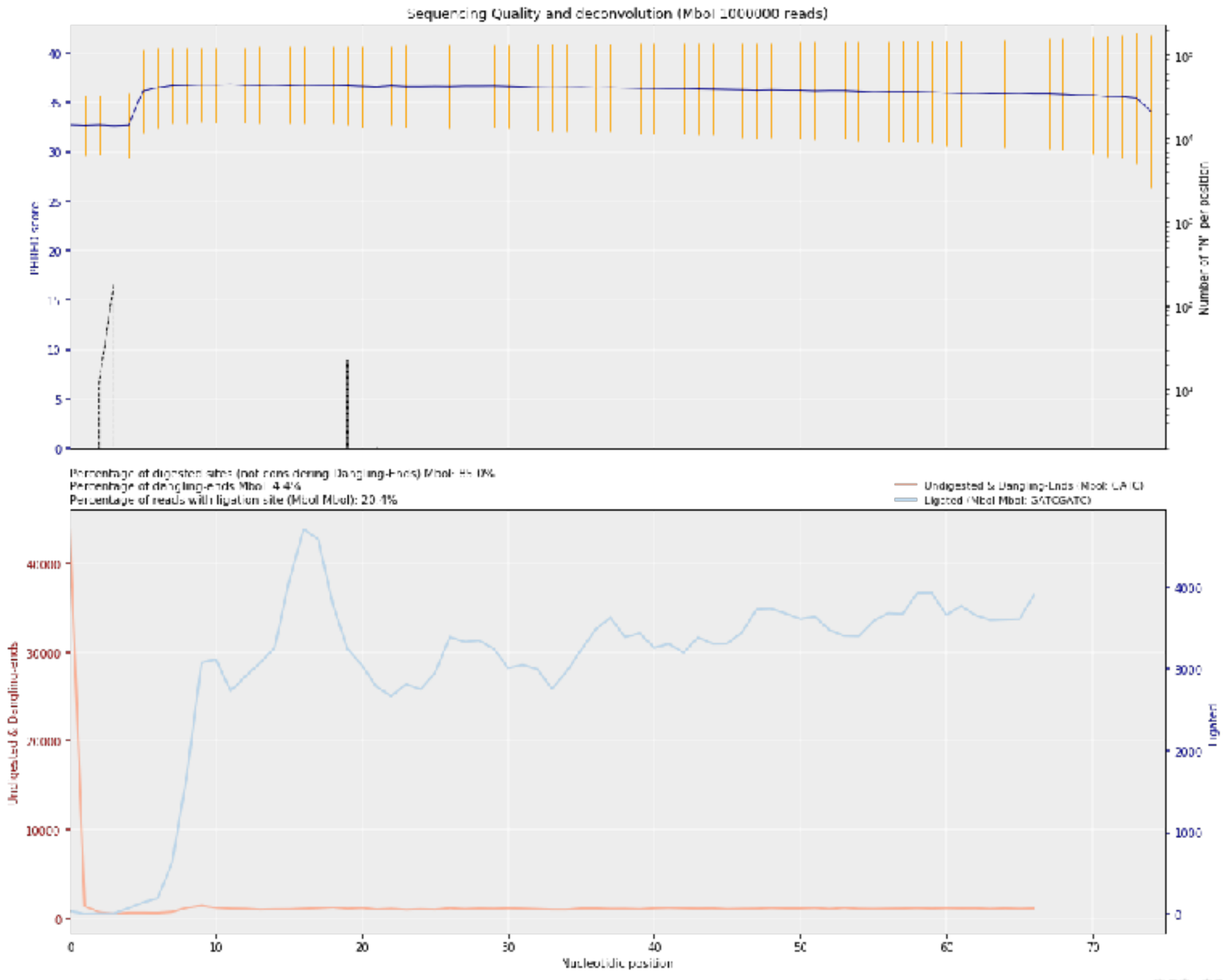
- conditionals

```
for i in range(0, 10, 1):
    if i == 3:
        print ‘we have 3’
    elif i > 3:
        print ‘we have many’
    else:
        print ‘we have few’
```

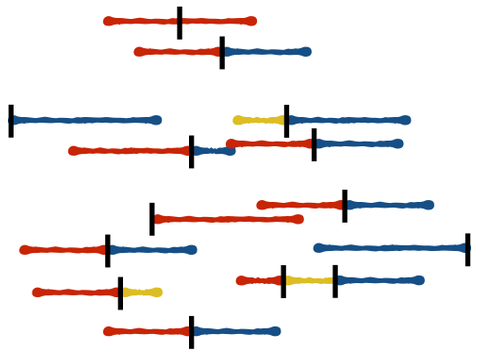
- lists, tuples, dictionaries

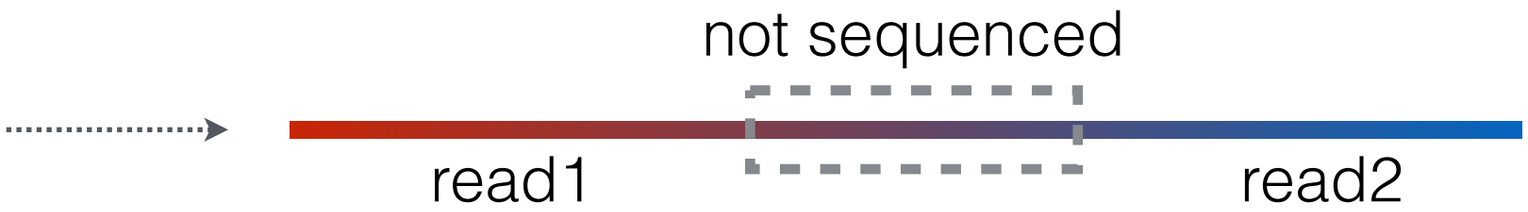
```
a = [0, 1, 2, 3, 4]
b = (0, 1, 2, 3, 4)
c = {‘one’: 11, ‘two’: 22
      ‘three’: 33, ‘four’: 79}
```

Quality plots of the reads



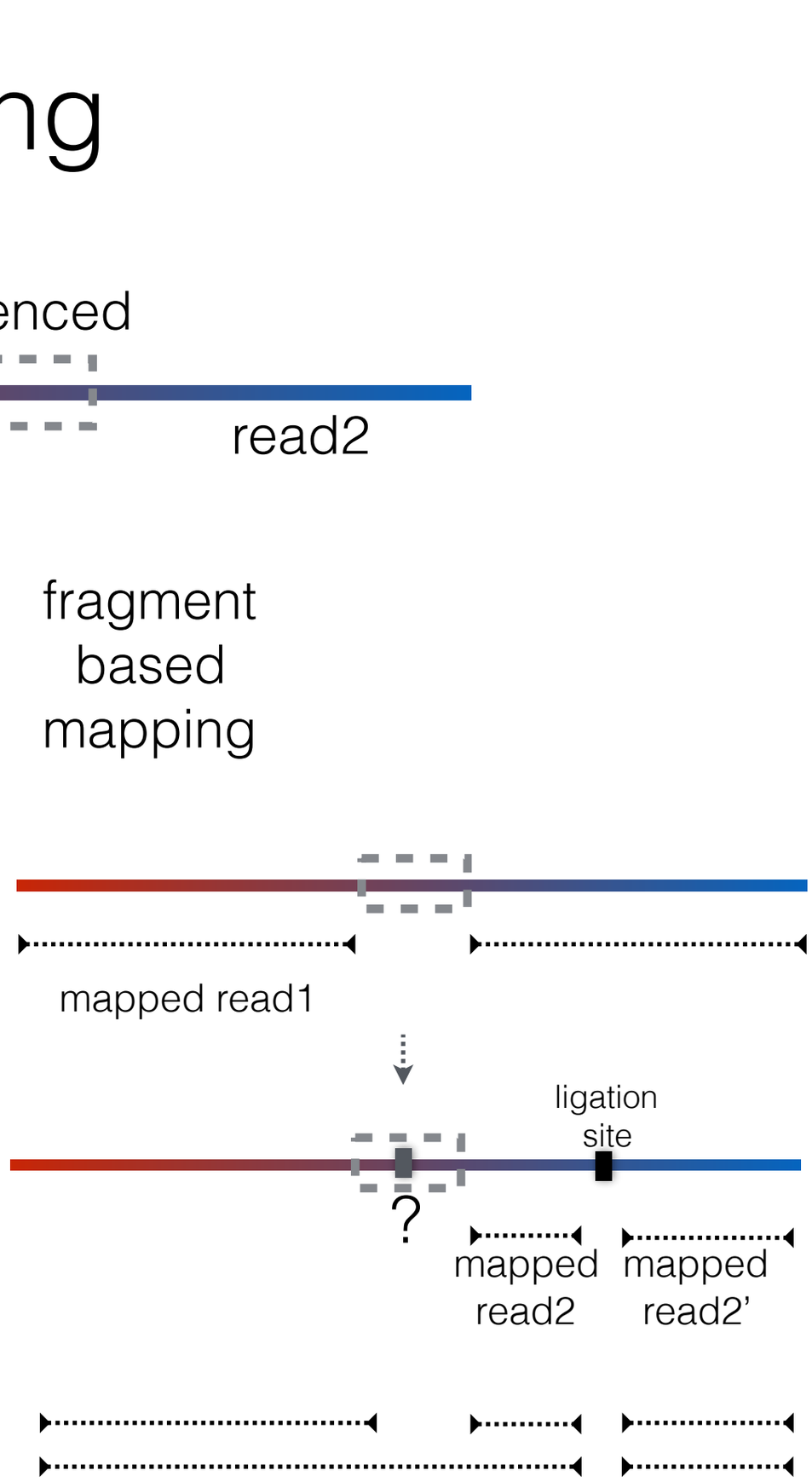
HiC mapping

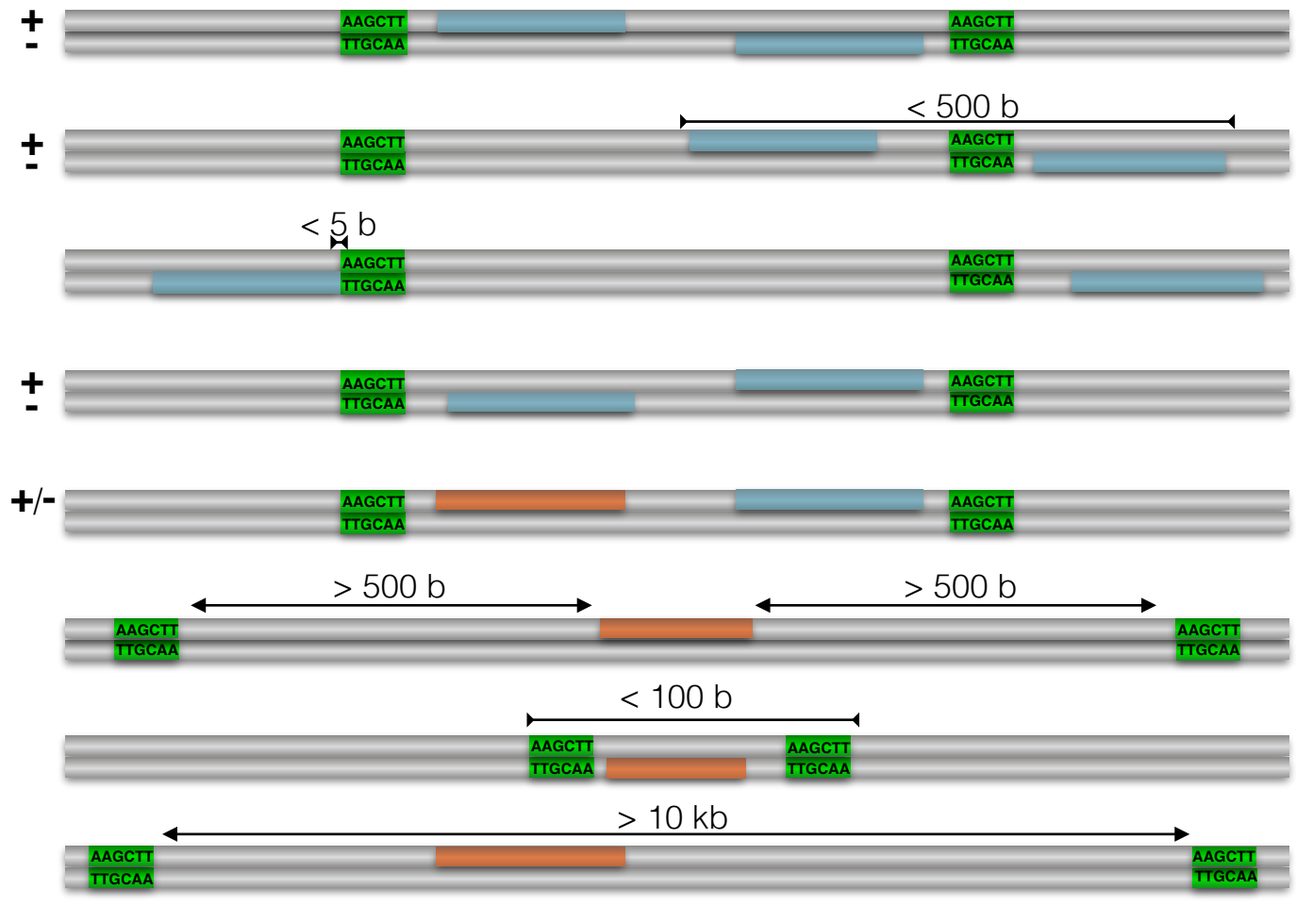


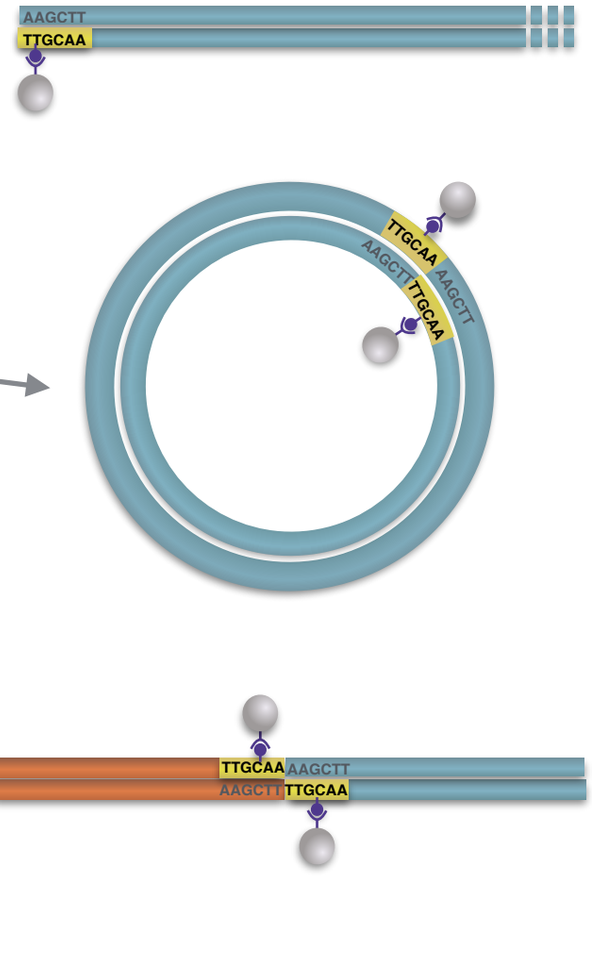


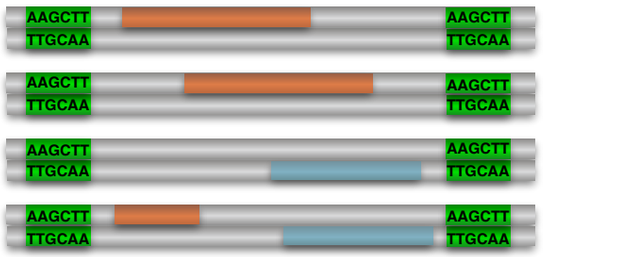
Iterative mapping

fragment based mapping

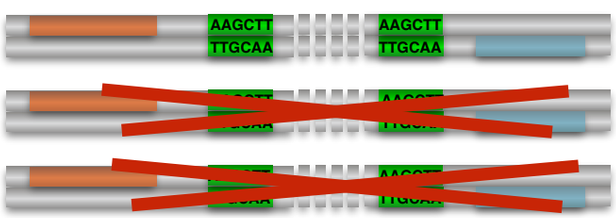




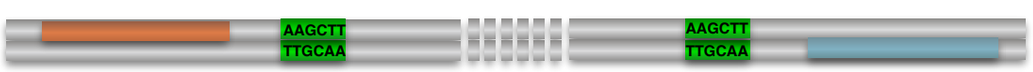




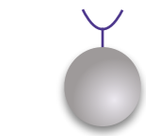
Over-represented (<1%)



Duplicated (20%)



Valid pair
(60% of intersection,
<50% of the total)

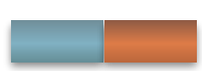


Dynabeads with
streptavidin

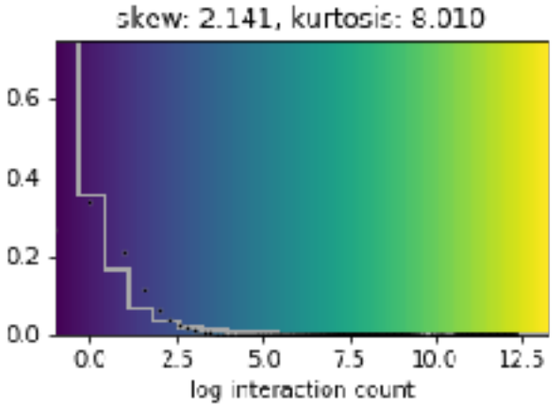
Restriction enzyme (RE) site

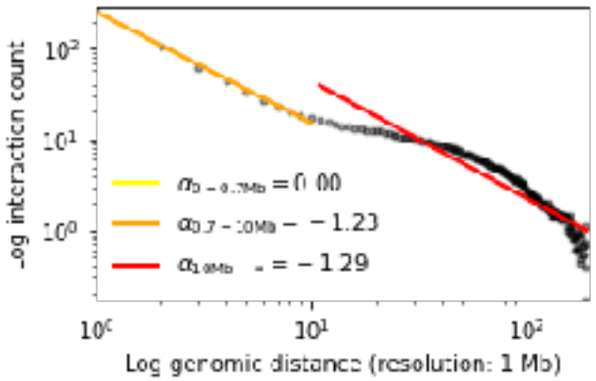
RE ligation site, repaired
nucleotides in yellow (new
cytosins are byotiniliated)

Genomic single strand
regions

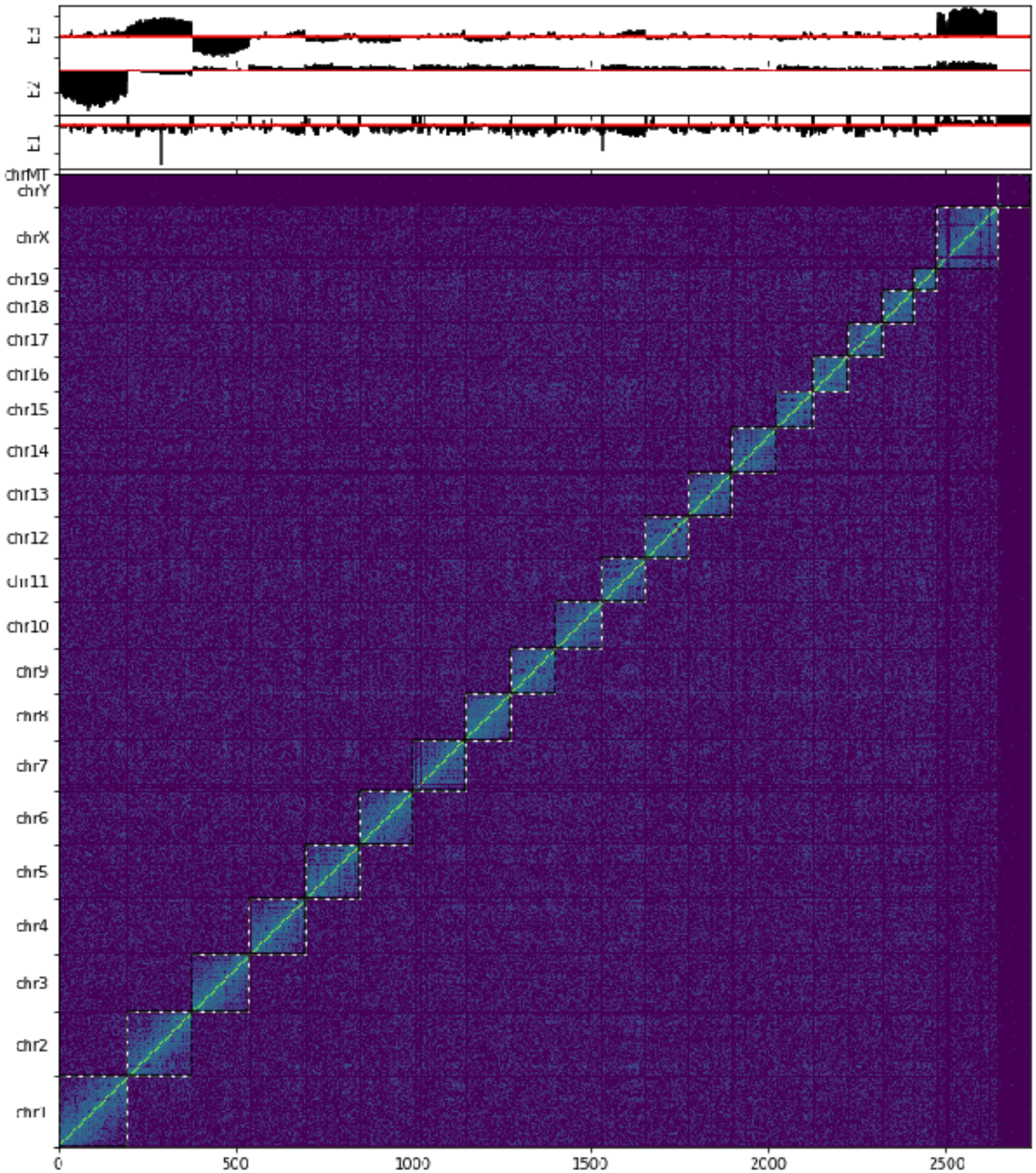


read fragments from Hi-C





Number of interactions: 12809346
Percentage of cis interactions: 71%
Min interactions: 0
Max interactions: 9562



How confortable are you with…

- Linux/Python to follow the tutorials?
- Reading a quality plot of your reads?
- Differences between iterative and fragment-based mapping
- Stats for quality measure of a Hi-C experiment?
- Applied filters to reads?
- Reading out a TADbit Hi-C map?