

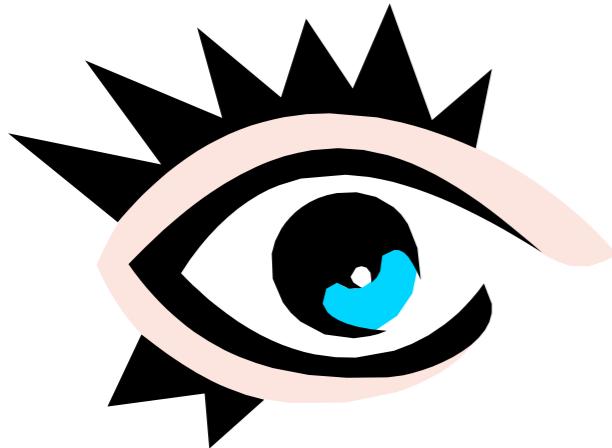
# 3DAROC16

## Summary day #1

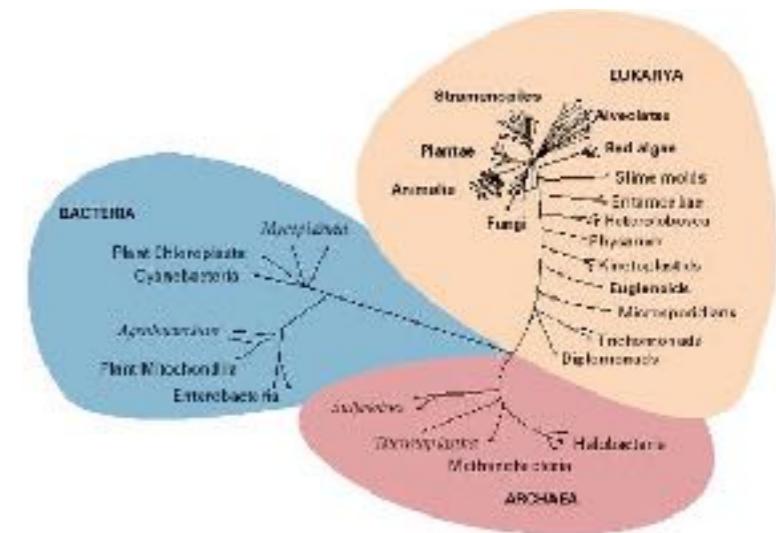
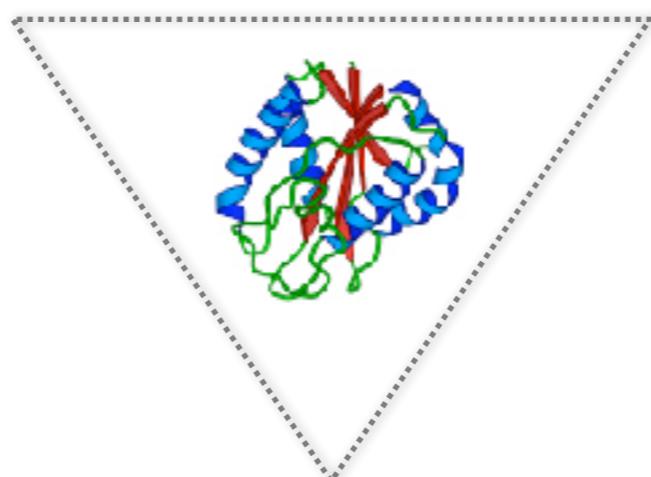
Marco Di Stefano, François Serra &  
Marc A. Marti-Renom  
Structural Genomics Group (CNAG-CRG)



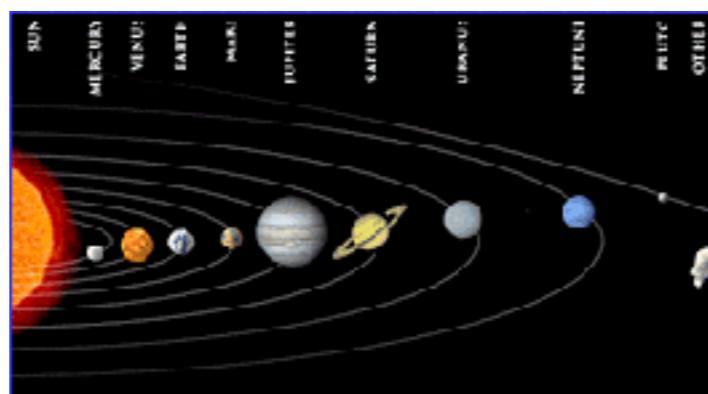
# Data groups



Experimental  
observations

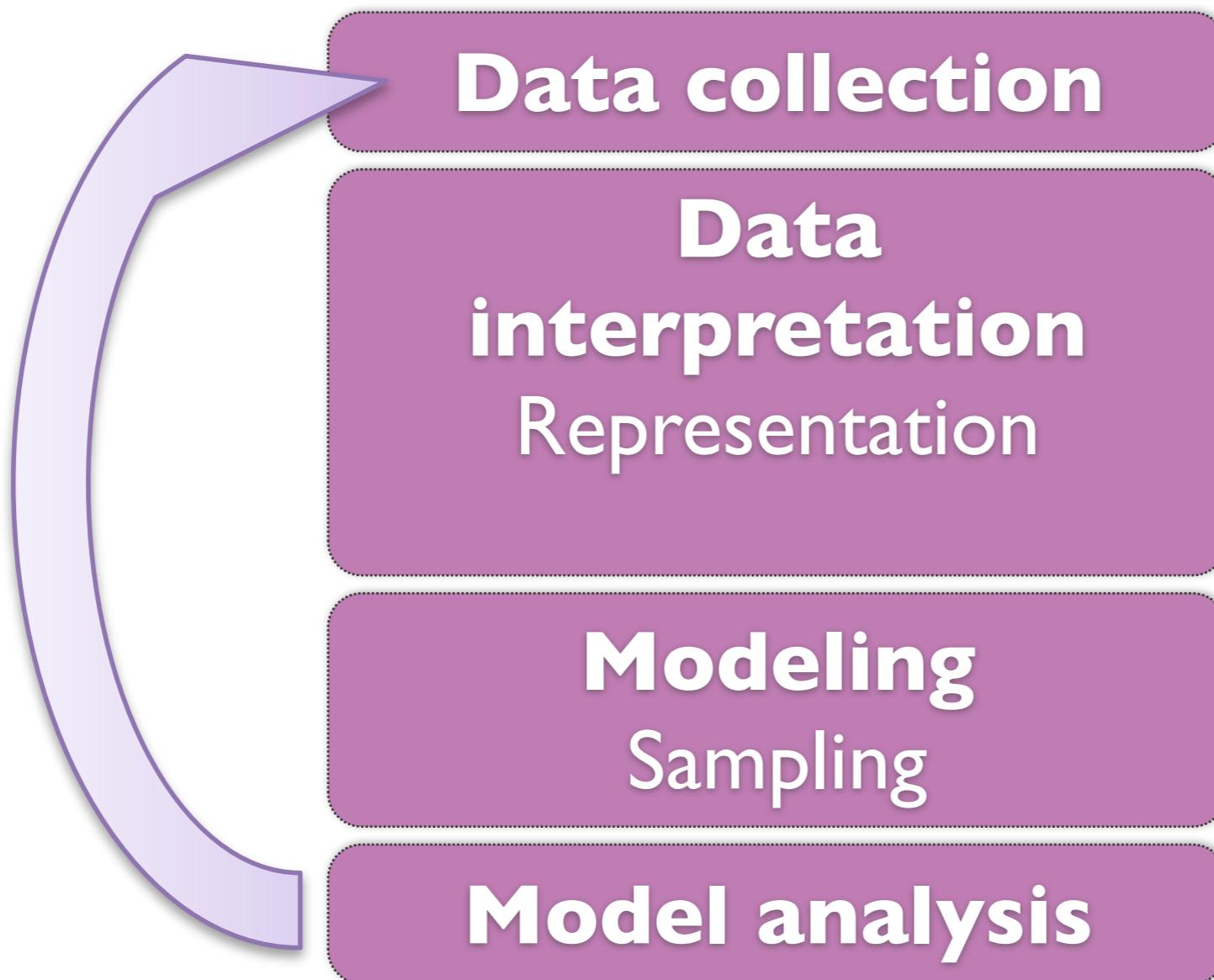


Statistical rules



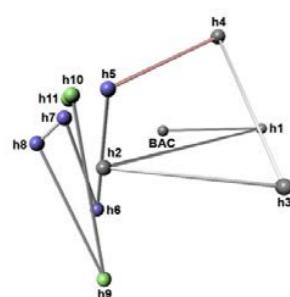
Laws of physics

# Integrative modeling

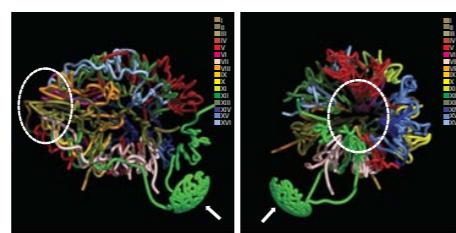


# 3D modeling of genomic domains: other methods

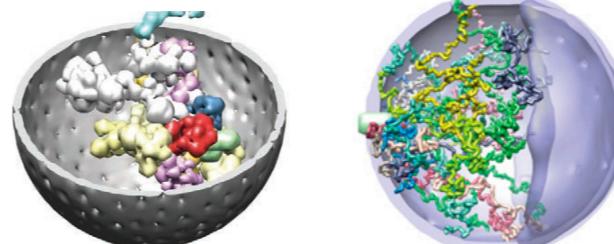
Jhunjhunwala (2008) Cell



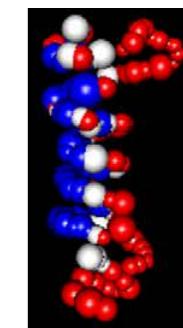
Duan (2010) Nature



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

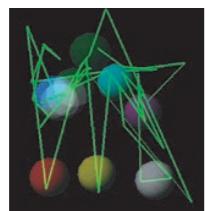


Hu (2013) PLoS Computational Biology

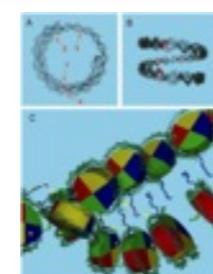
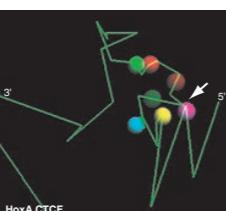


2008

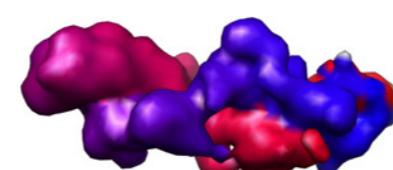
2014



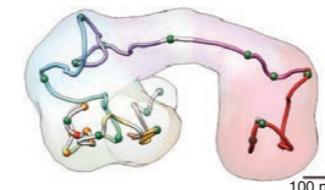
Fraser (2009) Genome Biology  
Ferraiuolo (2010) Nucleic Acids Research



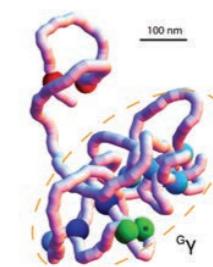
Asbury (2010) BMC Bioinformatics



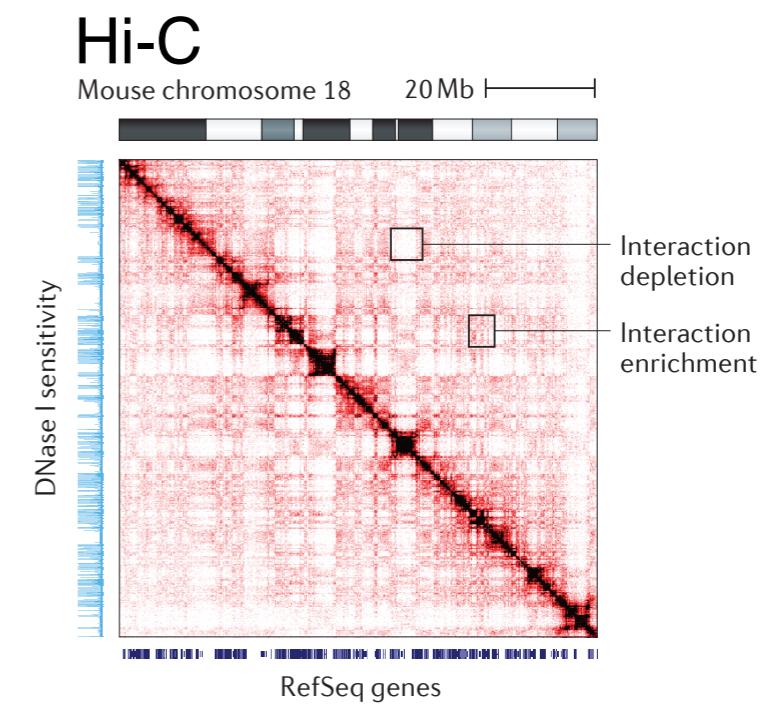
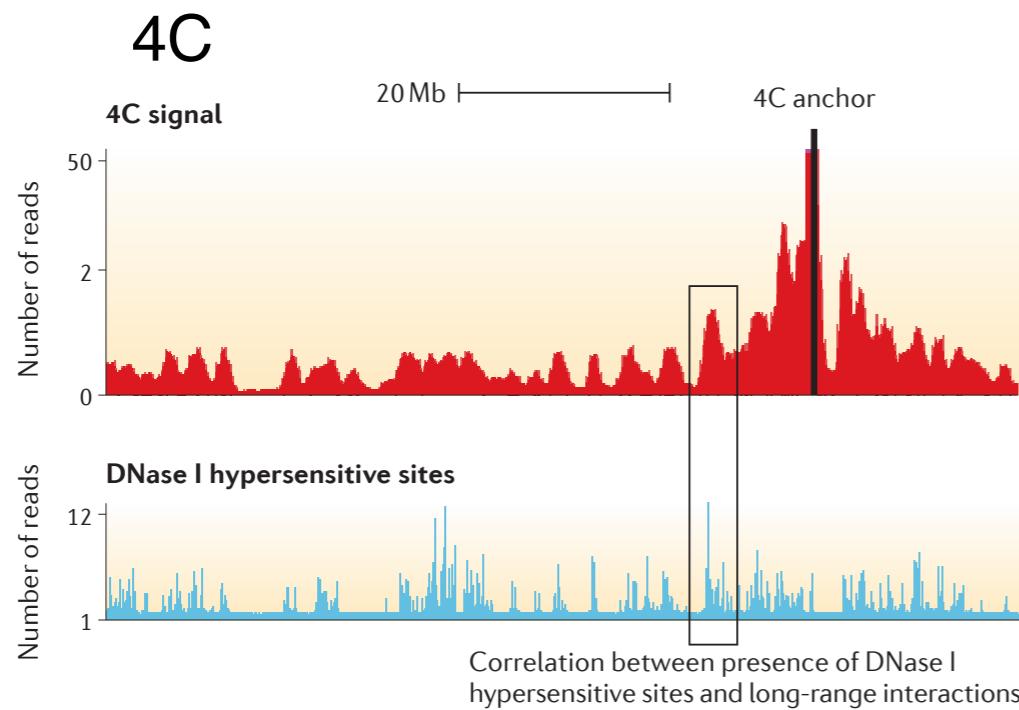
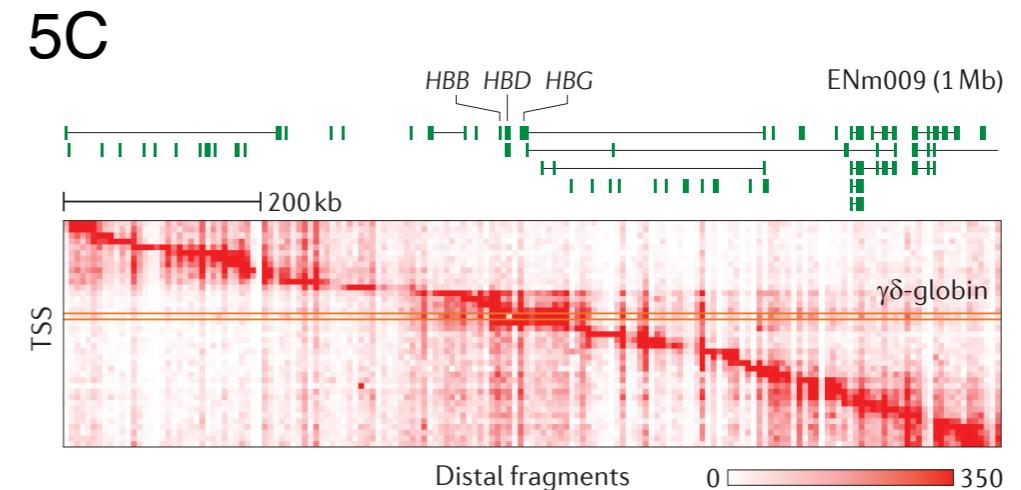
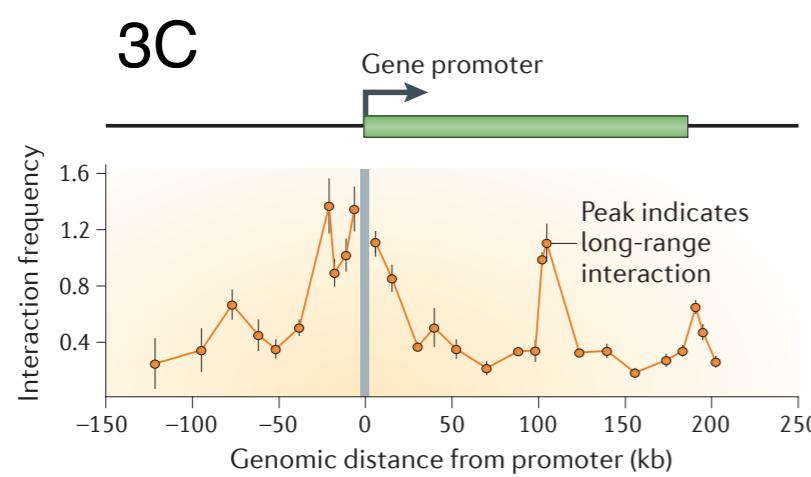
Baù (2011) Nature Structural & Molecular Biology  
Umbarger (2011) Molecular Cell



Junier (2012) Nucleic Acids Research

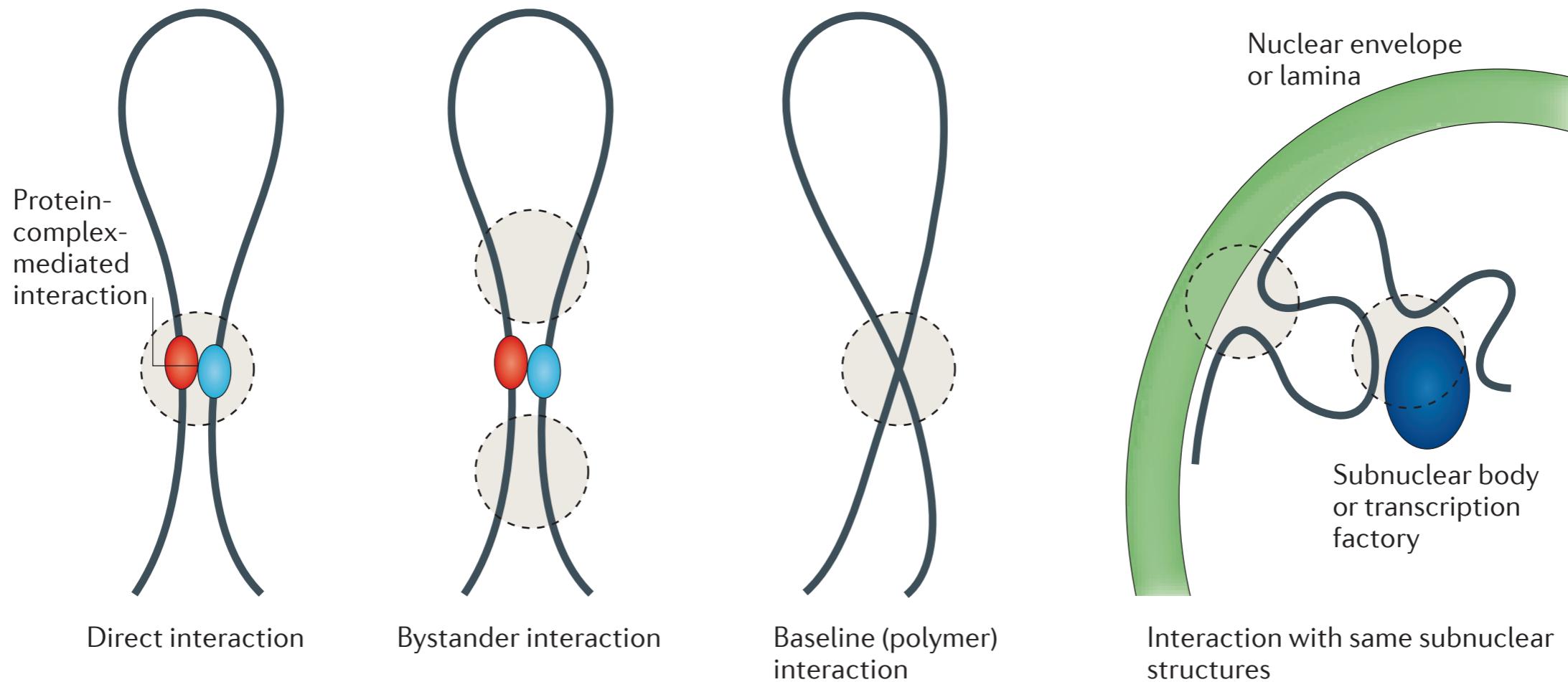


# Insights from 3C-based technologies



Adapted from Dekker et al., (2013) Nat Rev Genetics

# Interpreting chromatin interaction data



Adapted from Dekker et al., (2013) Nat Rev Genetics

# 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
```

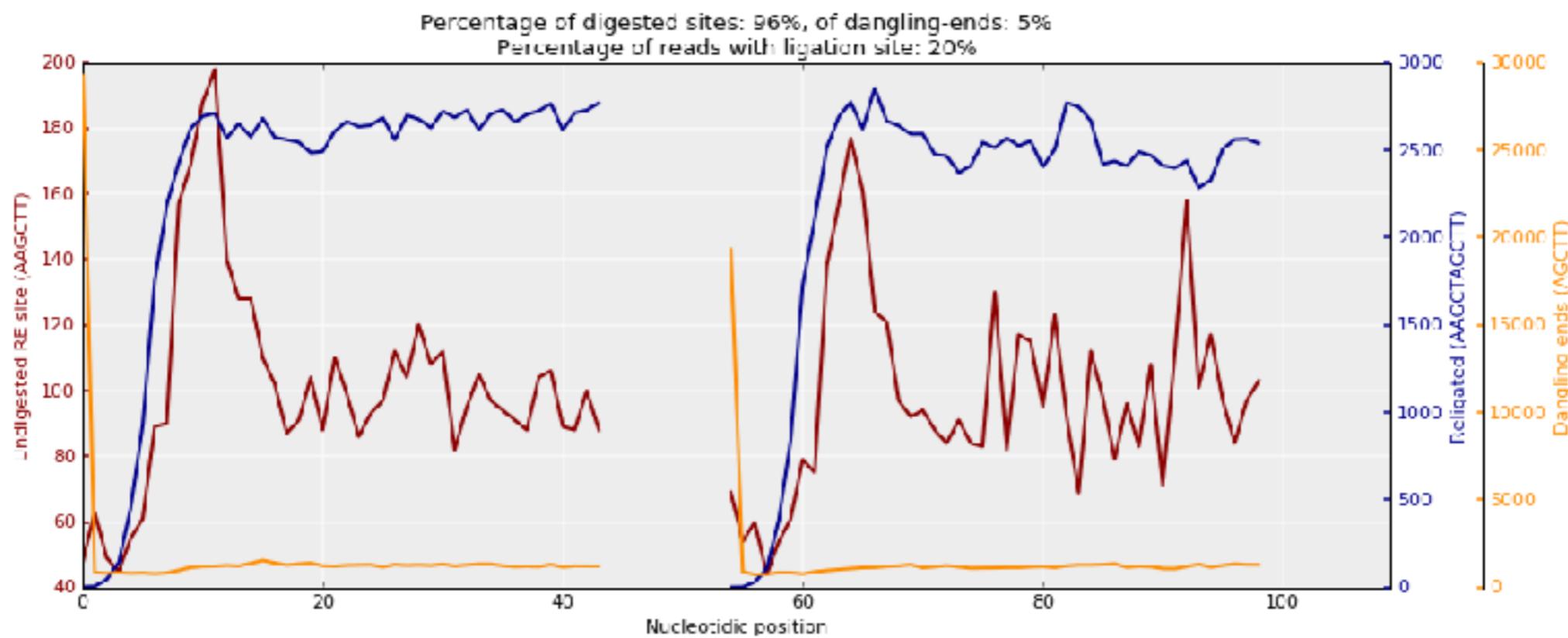
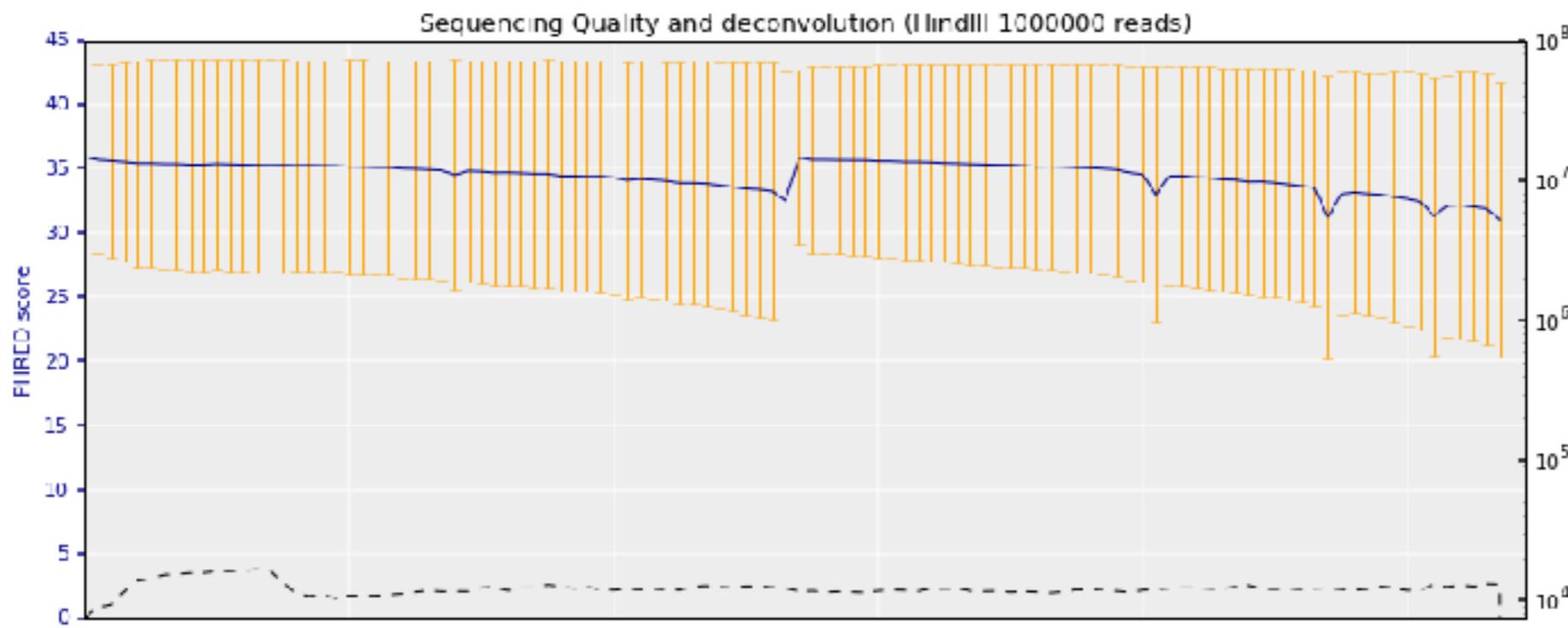
- conditionals

```
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





# Iterative vs. Fragment mapping

## *Human genome*

## Mapping

```
In [45]: from pytadbit.mapping.full_mapper import full_mapping
```

The full mapping function can be used to perform either iterative or fragment-based mapping, or a combination of both.

### Iterative mapping

Here an example of use as iterative mapping:

```
In [1]: r_enz = 'HindIII'  
rep = 'T0'
```

```
In [ ]: ! mkdir -p results/iterativ/${r_enz}_${rep}  
! mkdir -p results/iterativ/${r_enz}_${rep}/01_mapping
```

```
In [51]: # for the first side of the reads  
full_mapping(gem_index_path='genome/Homo_sapiens_contigs.gem',  
             out_map_dir='results/iterativ/{0}_{1}/01_mapping/mapped_{0}_{1}_r1/'.format(r_enz, re  
p),  
             fastq_path='FASTQs/Hi-C_%s_%s_1.fastq.ds' % (r_enz, rep),  
             r_enz='hindIII', frag_map=False, clean=True, nthreads=8,  
             windows=((1,25),(1,30),(1,35),(1,40),(1,45),(1,50)),  
             temp_dir='results/iterativ/{0}_{1}/01_mapping/mapped_{0}_{1}_r1_tmp/'.format(r_enz, r  
ep))
```

# HiC mapping

