

# Biological Applications (IV)

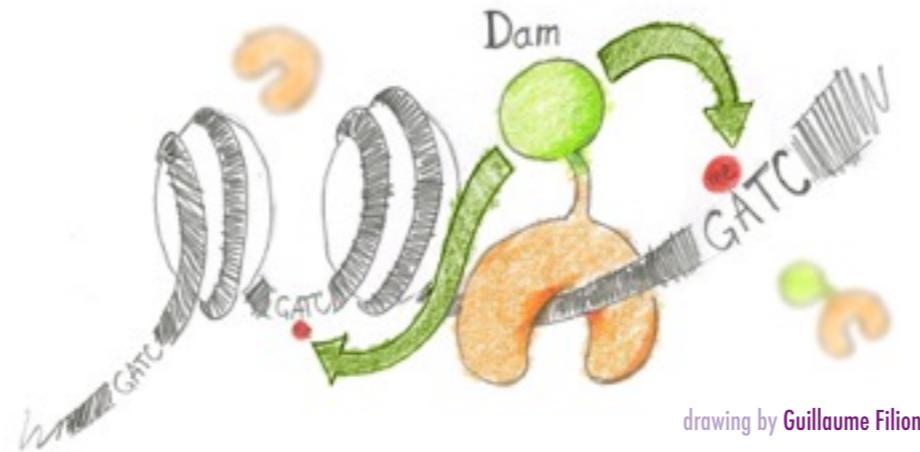
## Does color have structure?

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

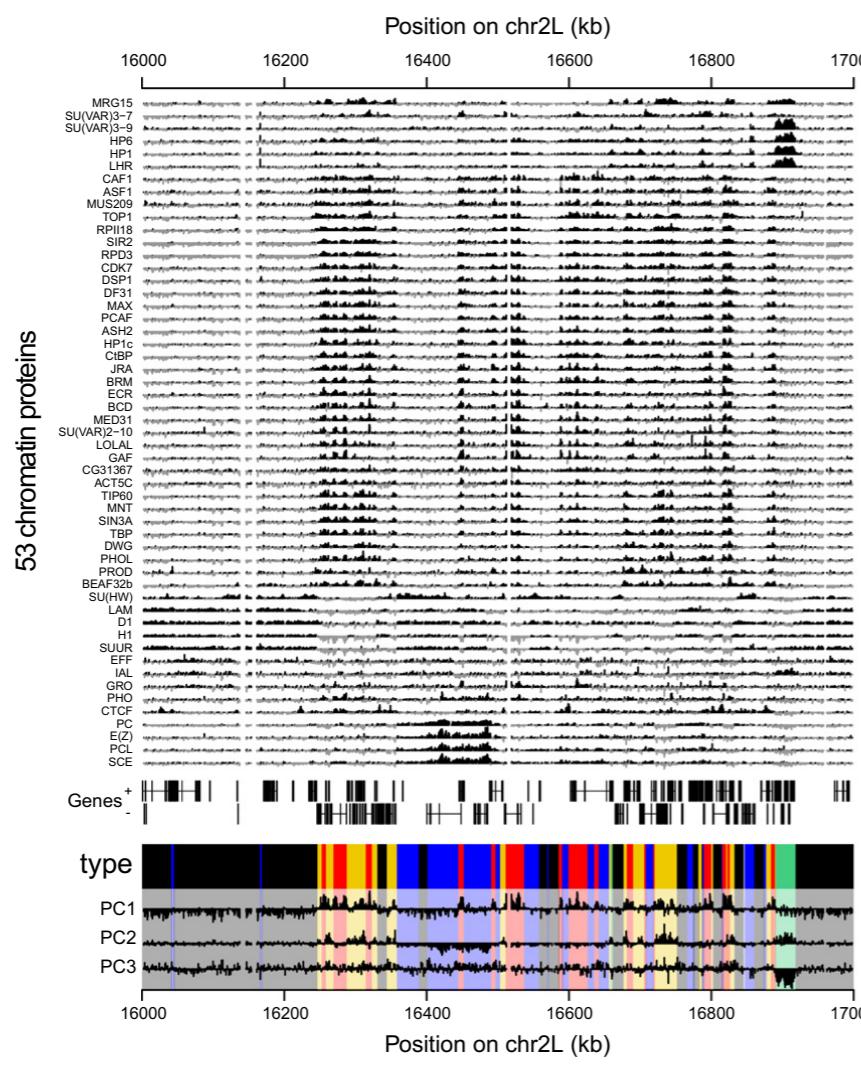


# Fly Chromatin COLORs

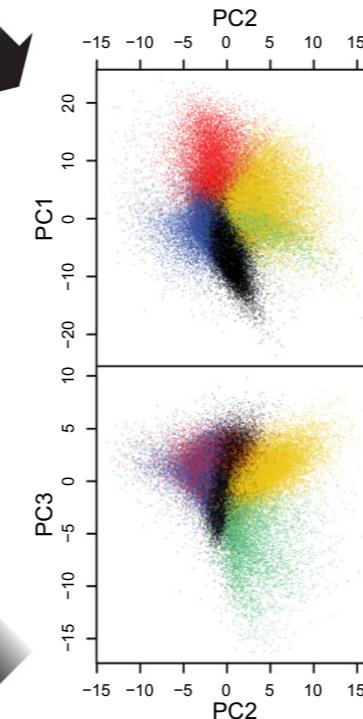
Filion et al. (2010). Cell, 143(2), 212–224.



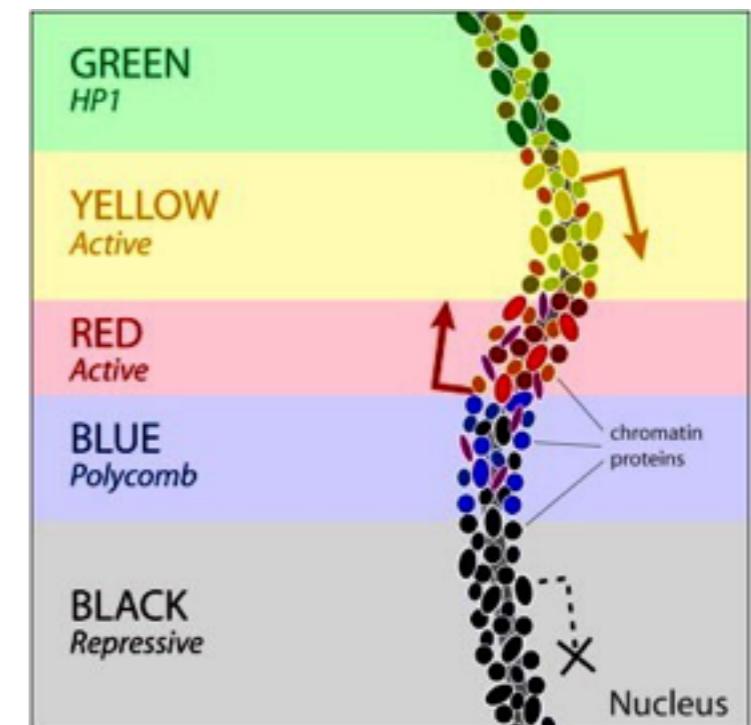
drawing by Guillaume Filion



Principal component analysis

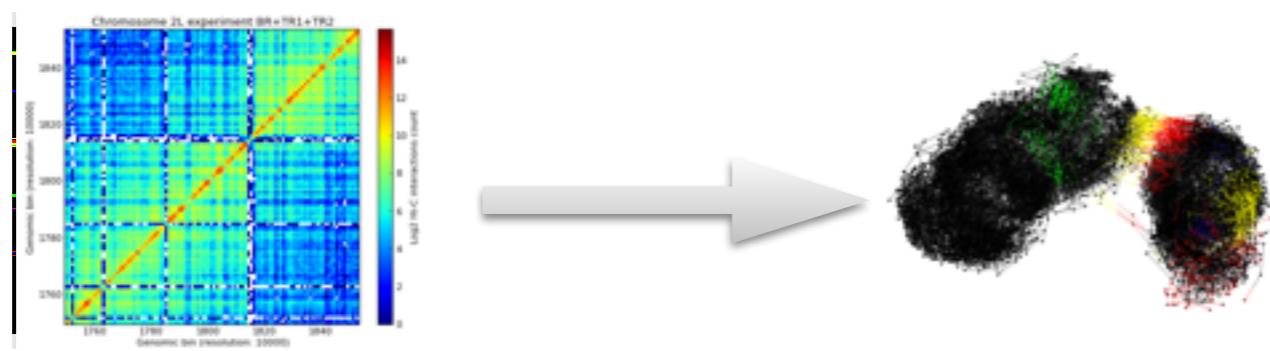
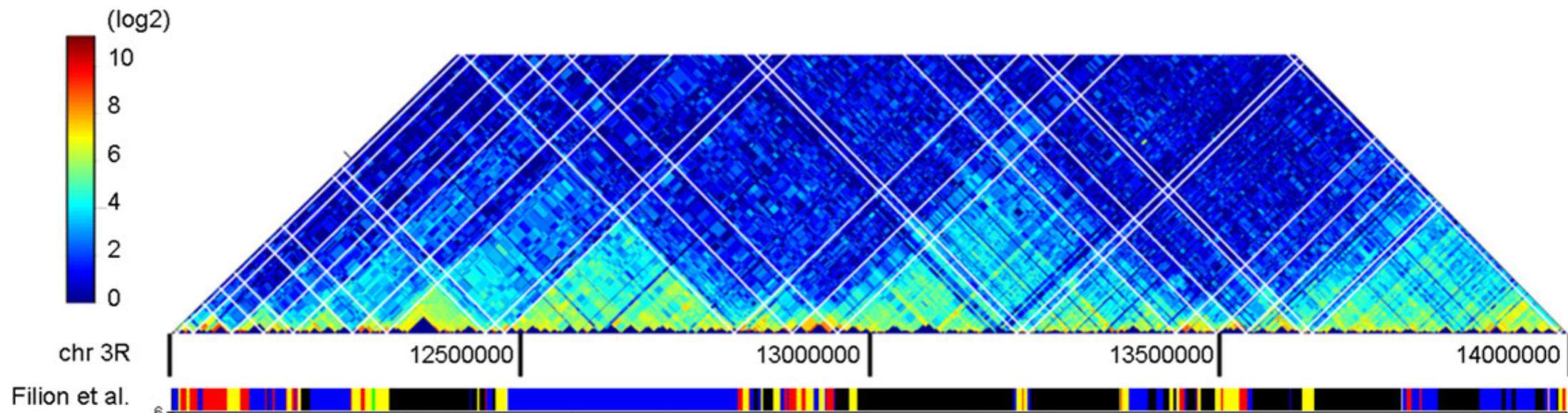


Hidden Markov model



# Fly Chromatin C**O**L**O**R**S**

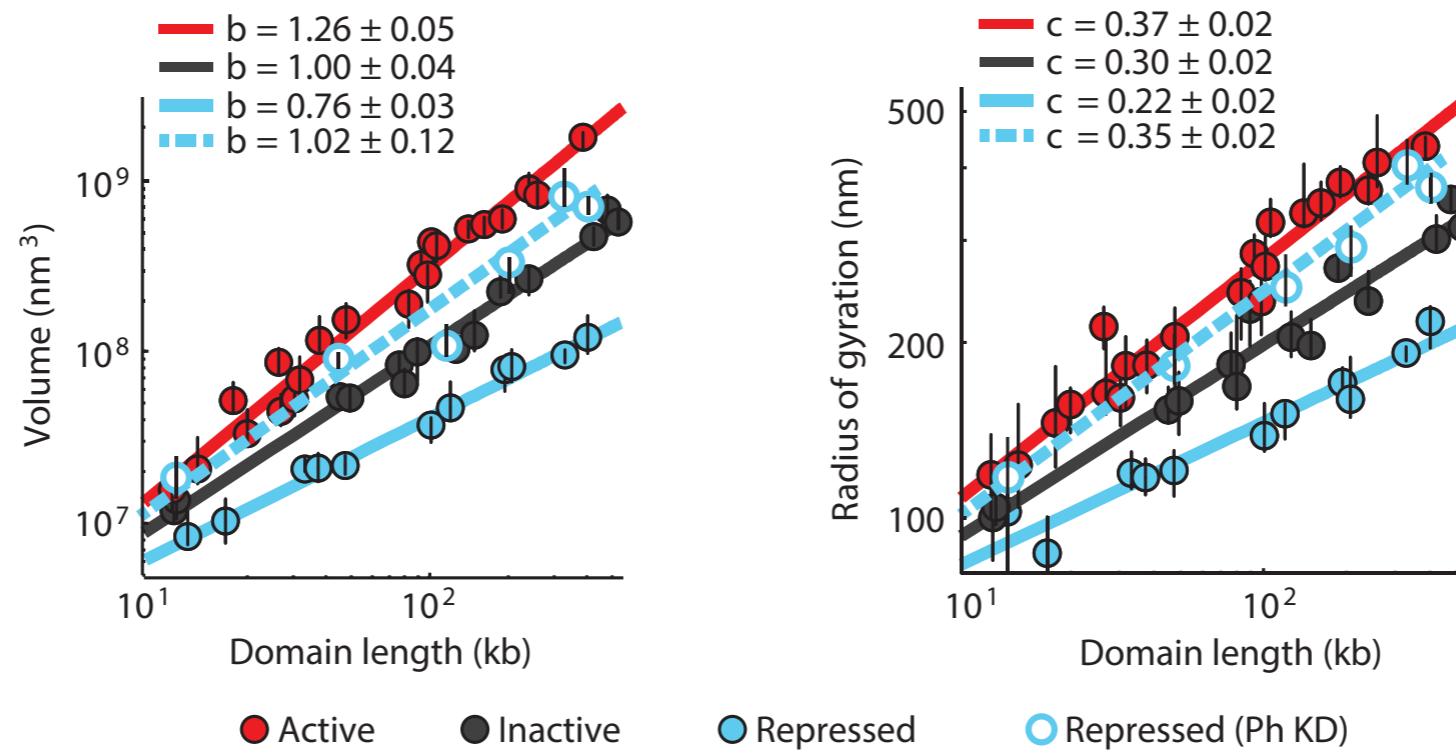
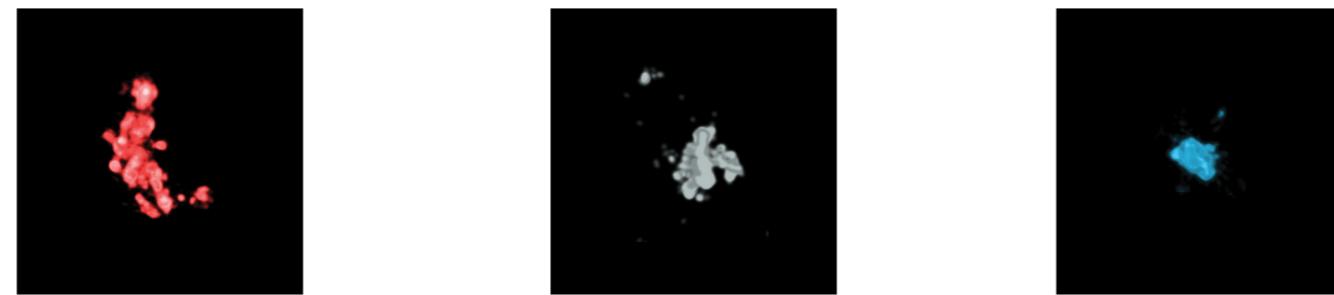
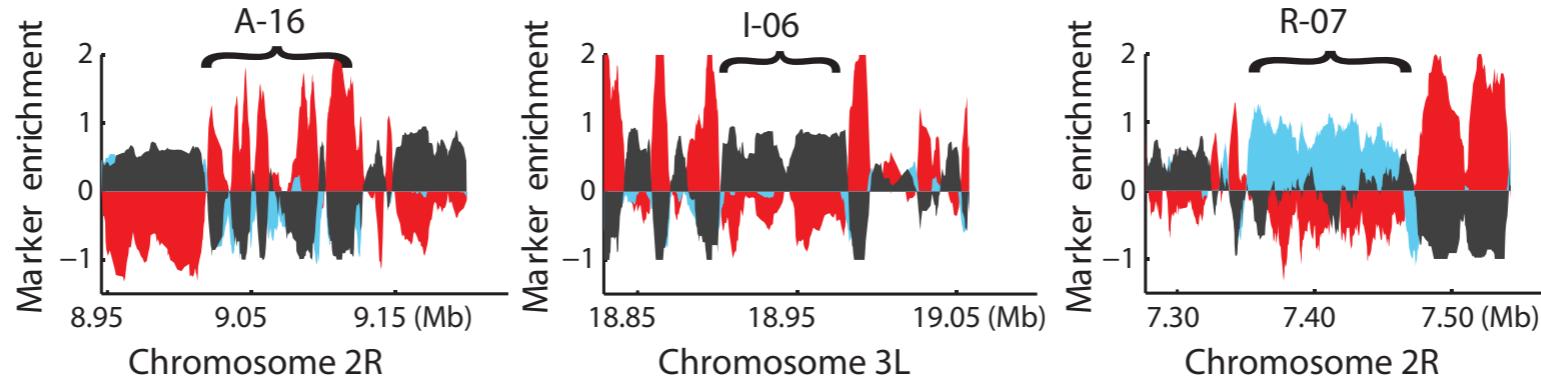
Hou et al. (2012). Molecular Cell, 48(3), 471–484.



50 ~1Mb regions  
10 for each color

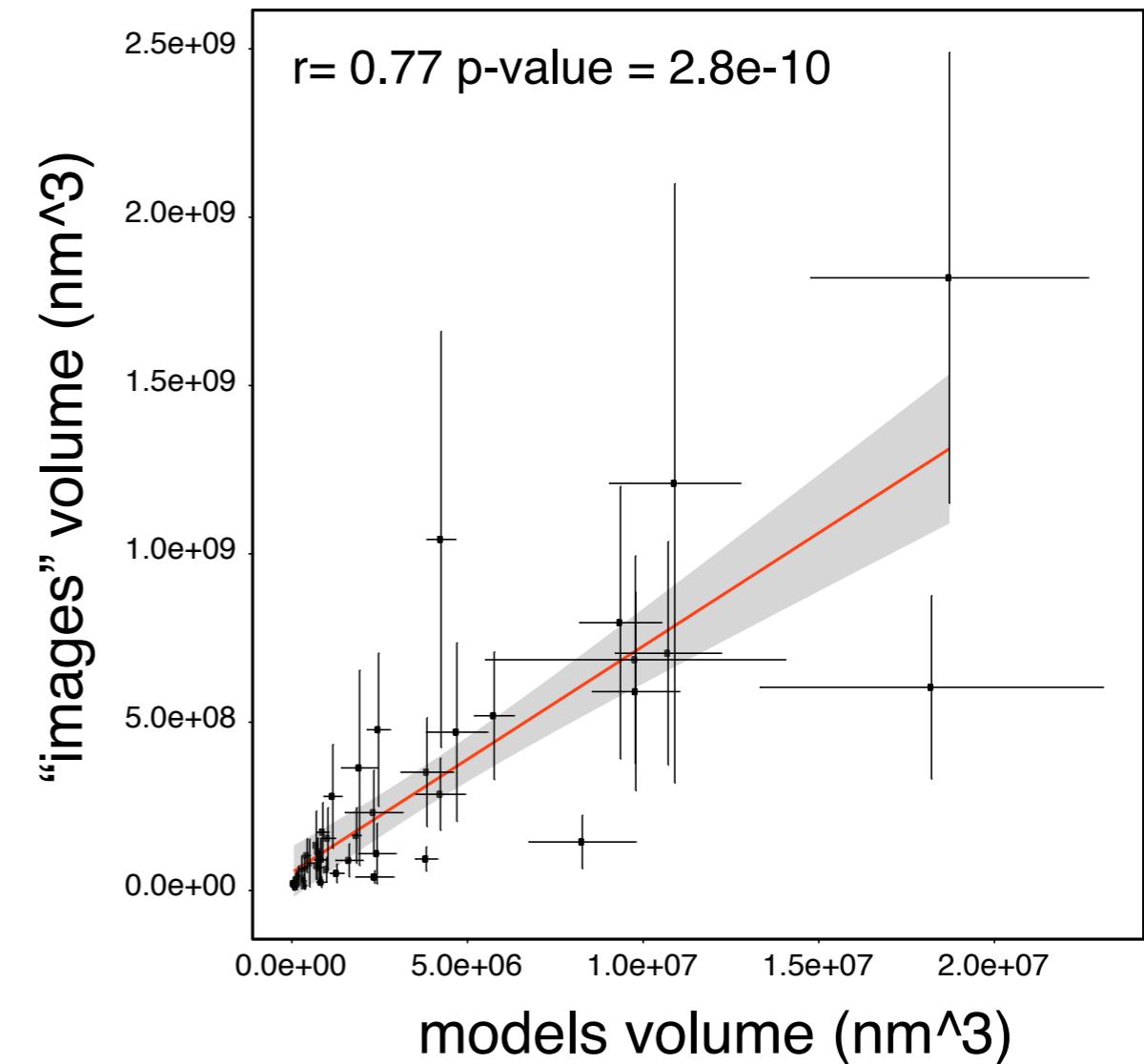
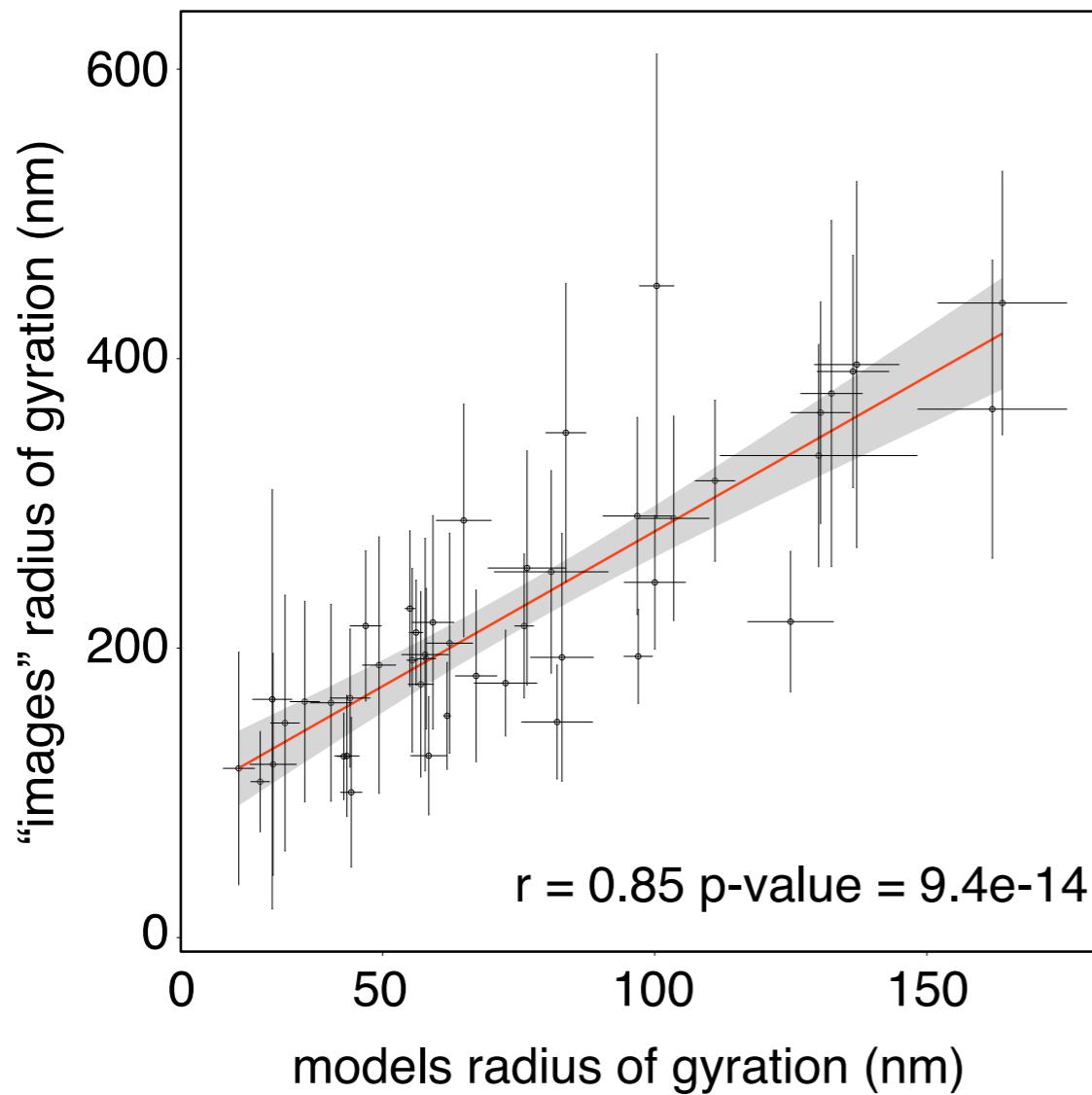
# Model accuracy

Boettiger, A. N., et al. (2016). Nature, 1–15.



# Model accuracy

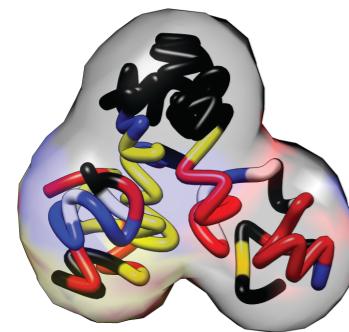
Boettiger, A. N., et al. (2016). Nature, 1–15.



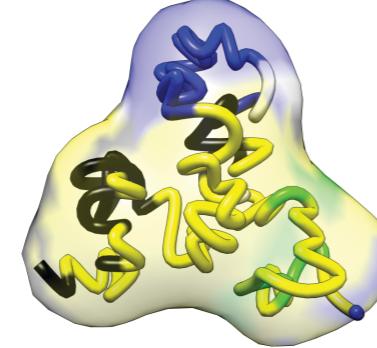
# Structural properties

50 1Mb regions. 10 enriched for each color.

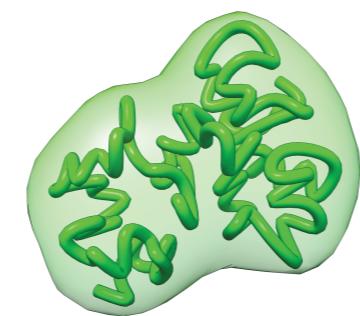
**RED dense region**  
3R:18920000-19920000  
  
22% 17% 0% 11% 45% 6%



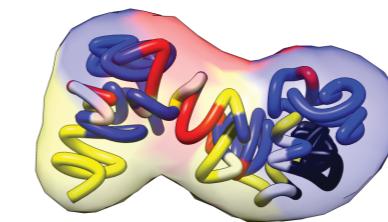
**YELLOW dense region**  
X:15590000-16600000  
  
0% 48% 4% 20% 26% 3%



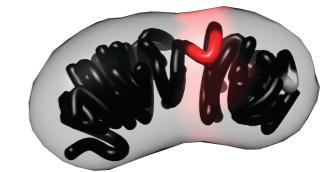
**GREEN dense region**  
2R:510000-1530000  
  
0% 0% 100% 0% 0% 0%



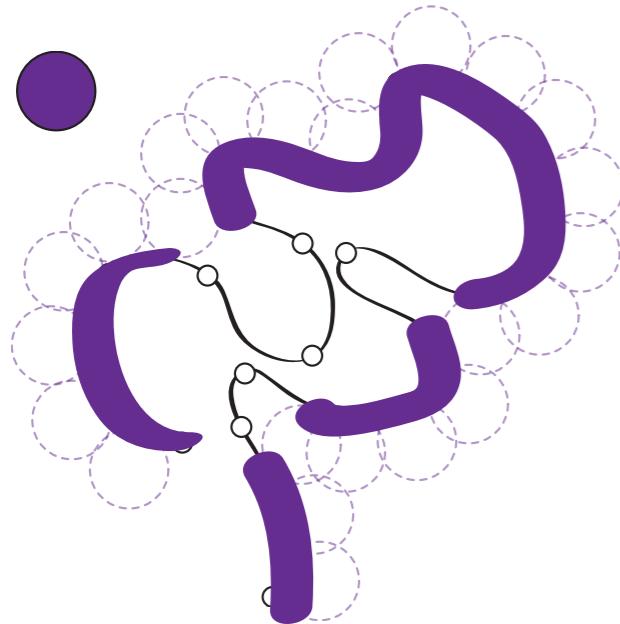
**BLUE dense region**  
3L:210000-1230000  
  
11% 17% 0% 52% 13% 0%



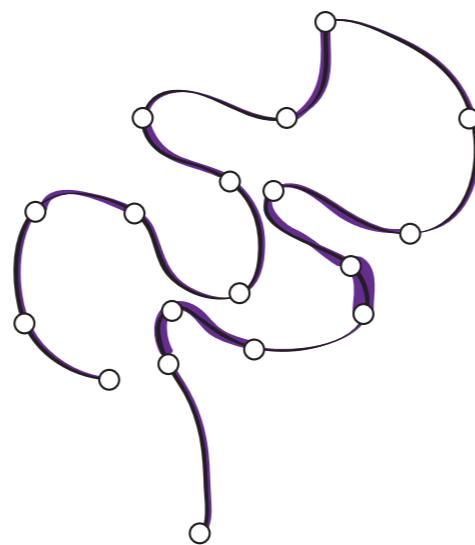
**BLACK dense region**  
2L:17500000-18530000  
  
1% 0% 0% 0% 98% 1%



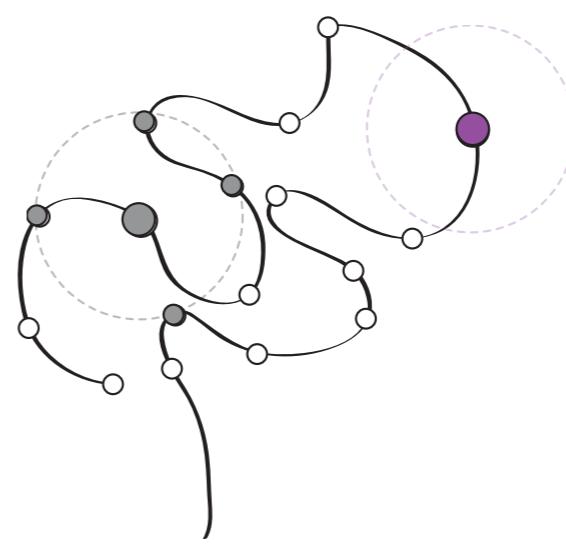
Accessibility (%)



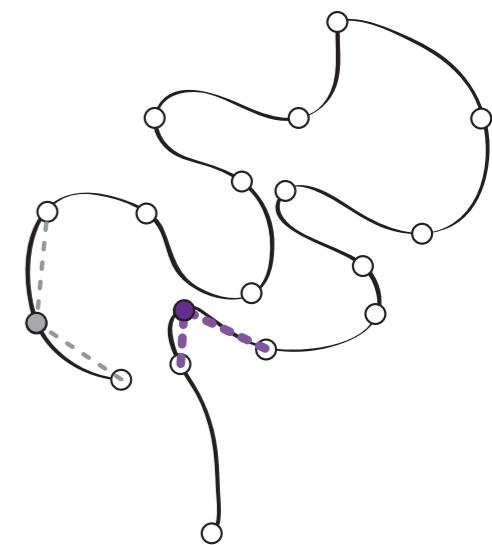
Density (bp/nm)



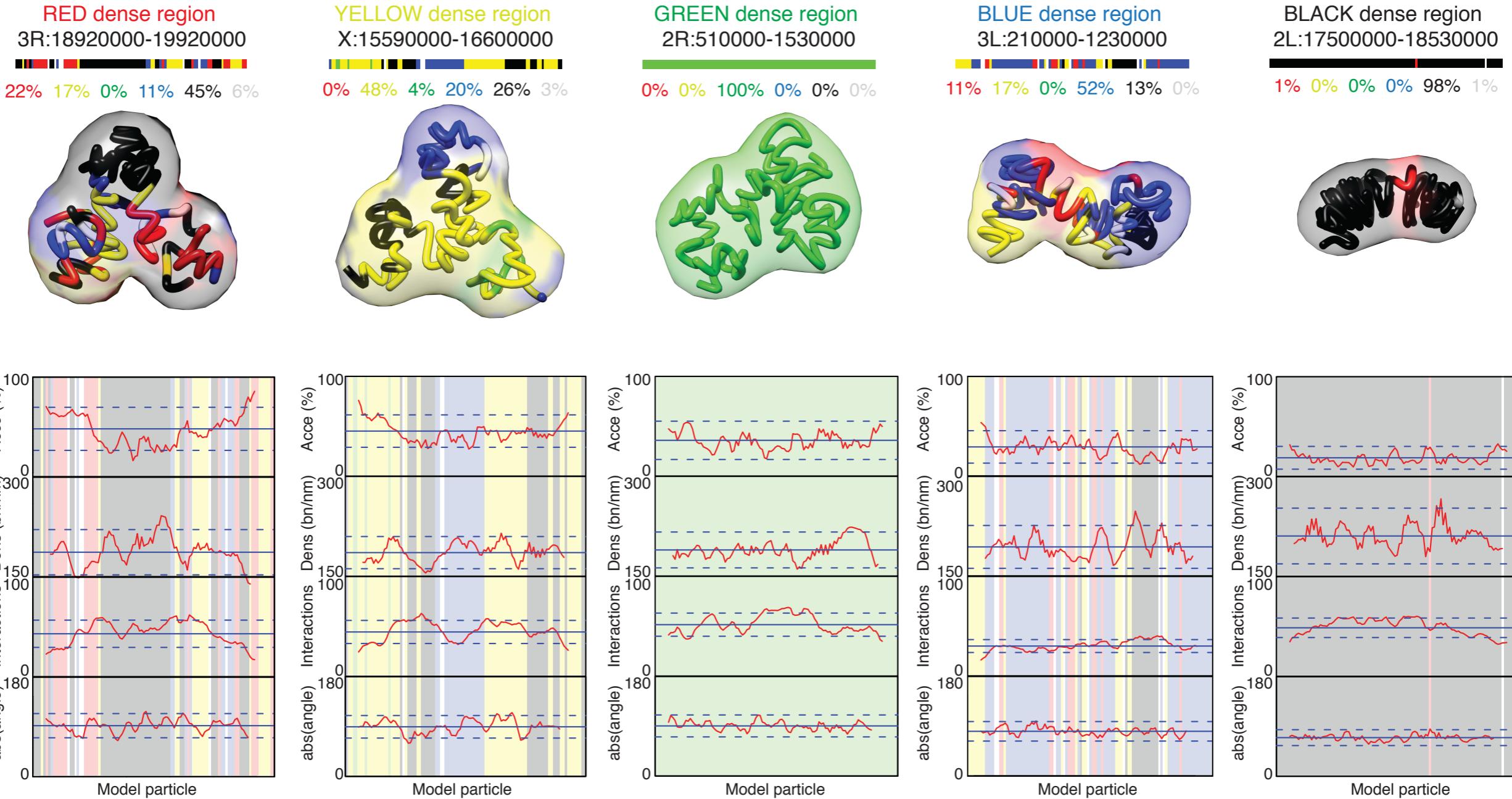
Interactions



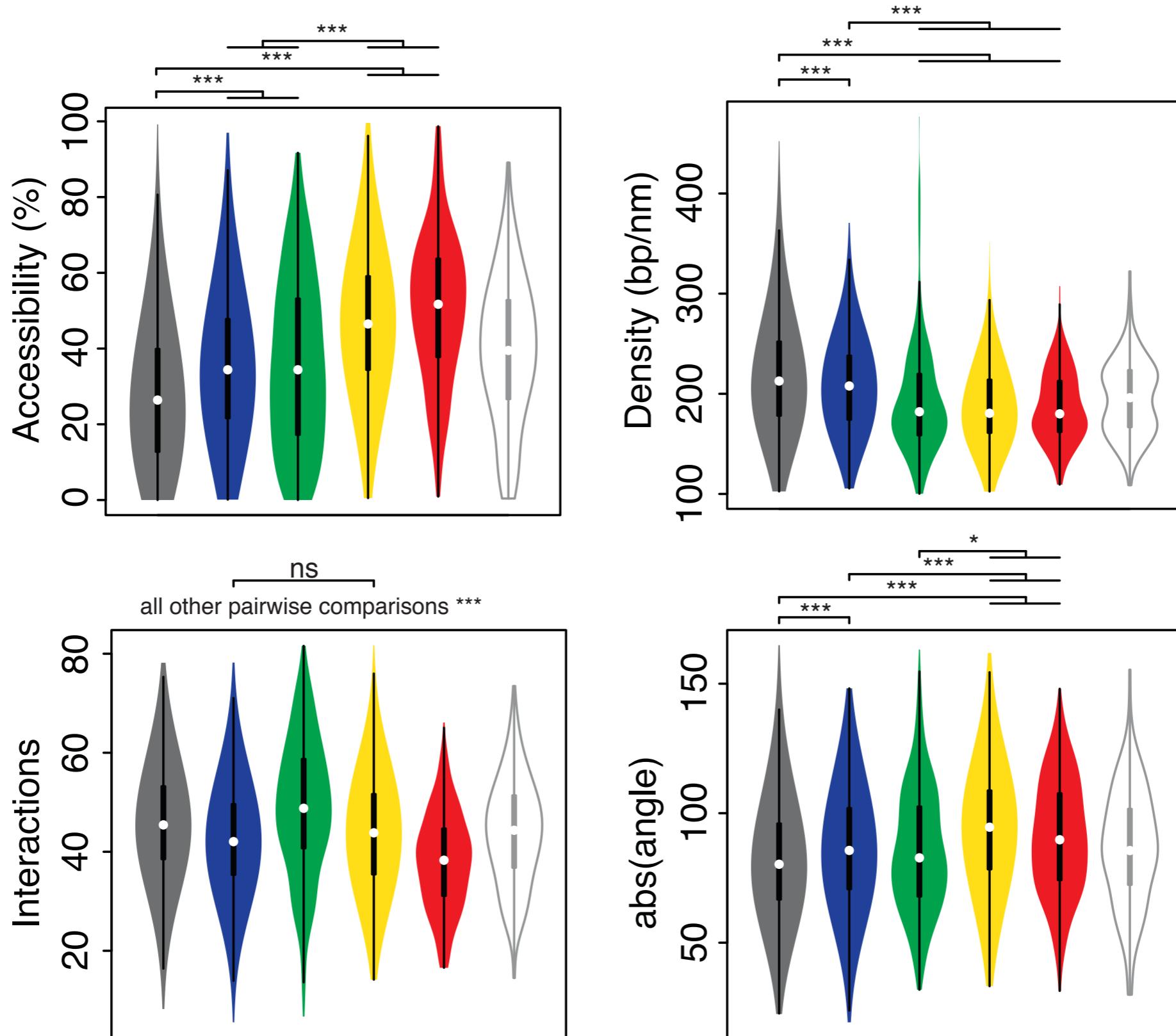
Angle



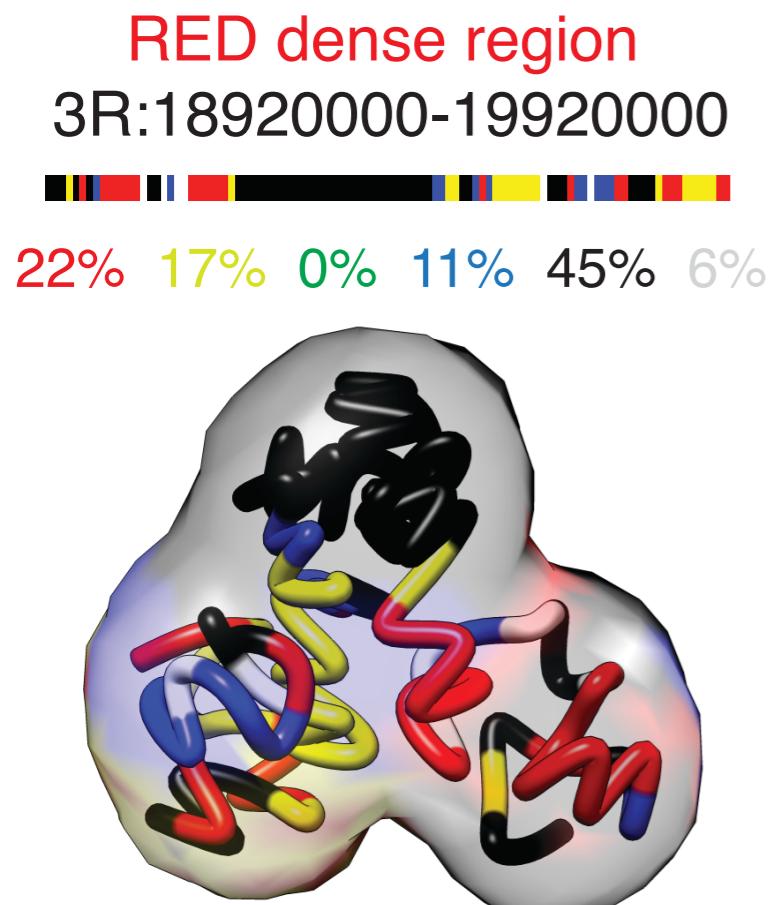
# Structural COLORs



# Structural COLORs



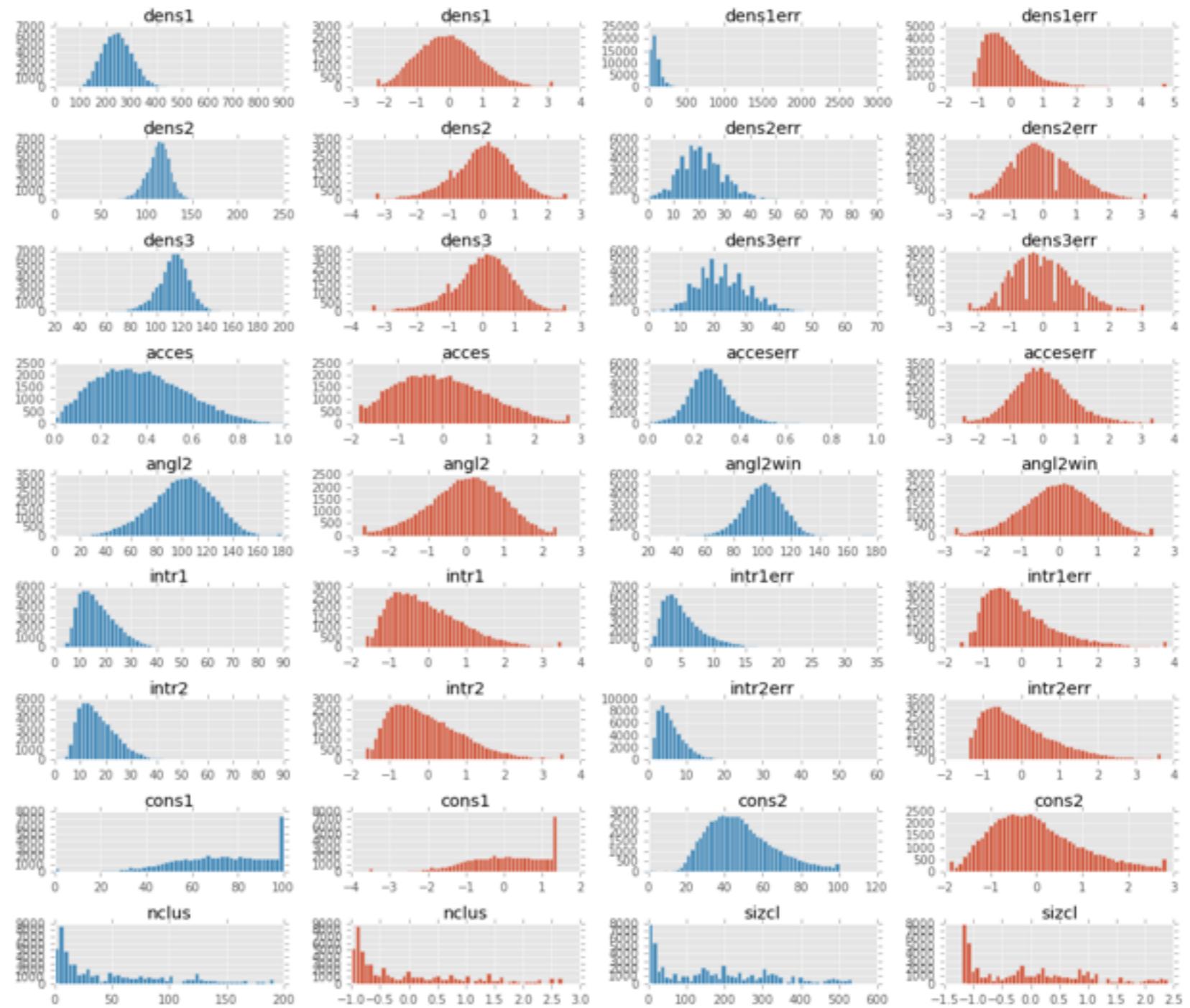
# Color prediction by Self Organizing Maps



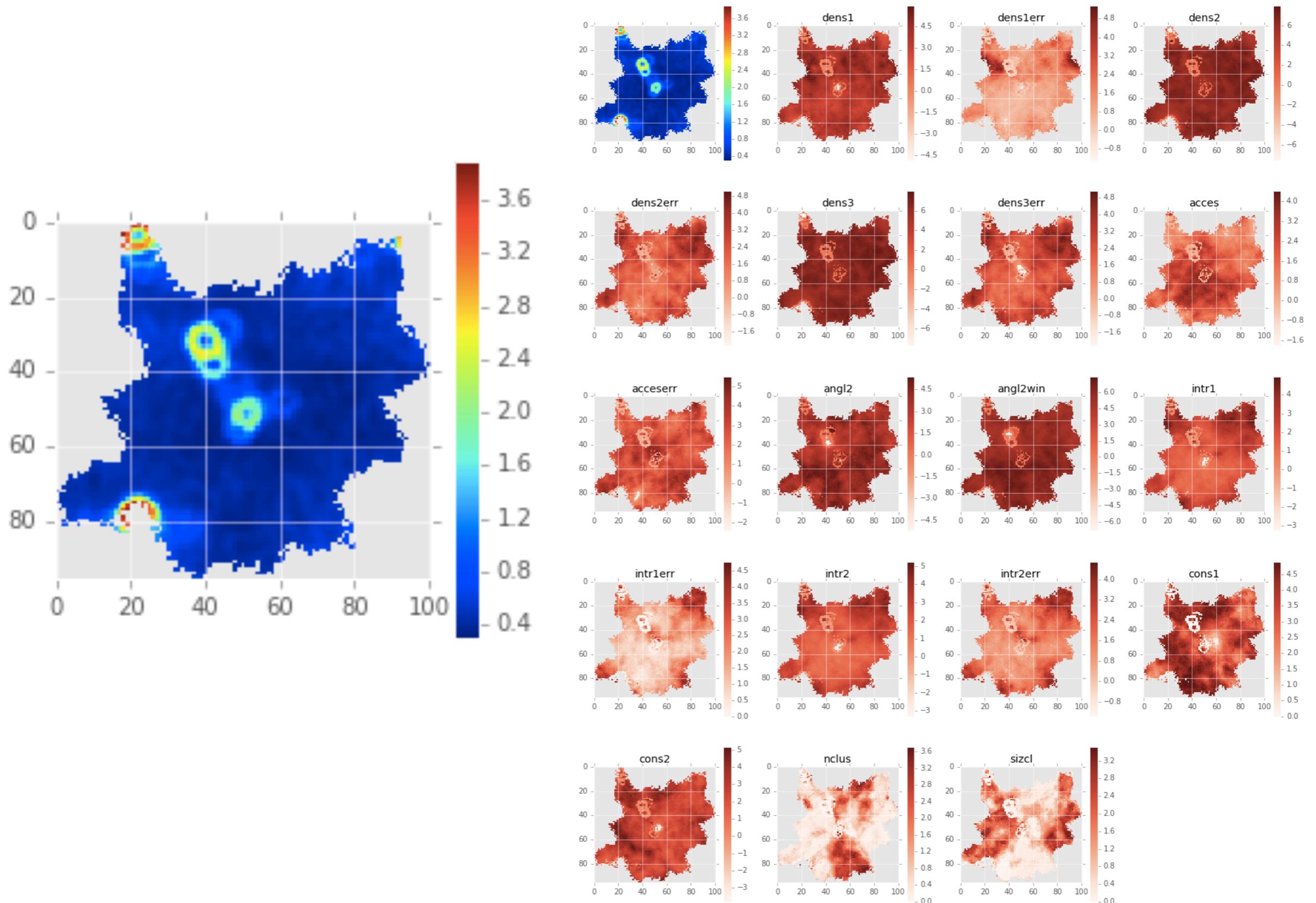
	GainRatio	PCA
interactions all 40 nm	0,25	-0,40
interactions cluster1 40 nm	0,24	-0,40
accessibility radius 20 nm superradius 75 nm	0,18	0,35
stderr of intr2	0,19	-0,34
number of models in cluster 1	0,35	-0,00
stderr of intr1	0,16	-0,34
number of clusters	0,26	-0,02
stderr of dens3	0,13	-0,33
stderr of dens1	0,11	-0,27
unsigned angle with -3 and +3 smoothed over 5 bins	0,10	0,13
density 3 particles (center of mass) cluster 1	0,07	-0,11
stderr of dens2	0,09	-0,31
density 3 particles cluster 1	0,05	0,00
density 3 particles all clusters	0,06	0,00
consistency all 50 nm	0,03	-0,02
unsigned angle with -3 and +3	0,03	0,09
consistency cluster1 50 nm	0,03	0,05
stderr of acces	0,02	0,04

# Selected metrics per particle

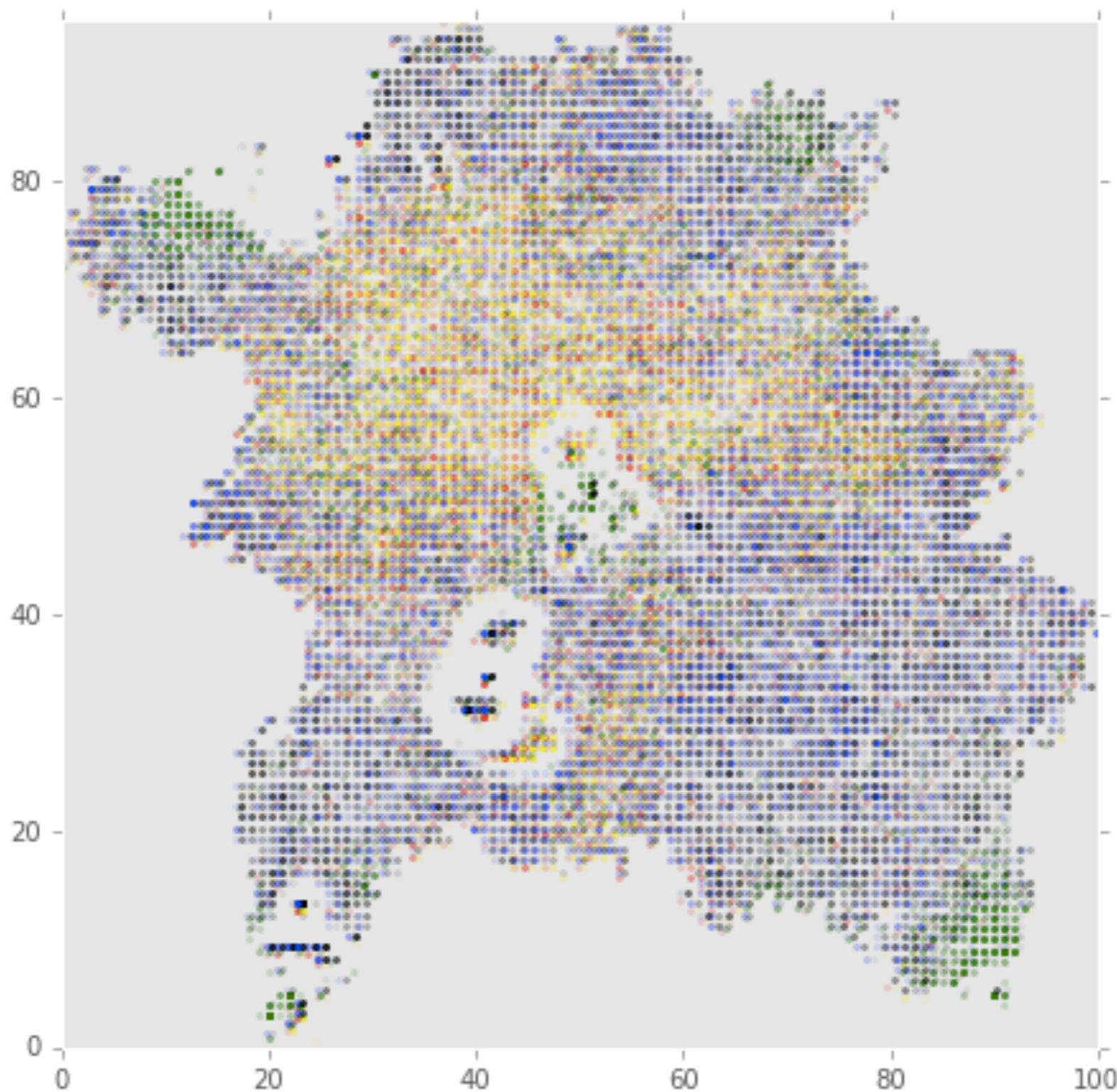
- extract the **18 metrics for each particle** (if particle is present in several models, an average is calculated)
- the **metrics are normalized** (mean=0, std=1), and **outliers removed** (percentile 0.5 and 99.5)
- each of the particles are going to be arranged in the SOM according to their relative **euclidian distance**
- SOM is run with 100.000 iterations



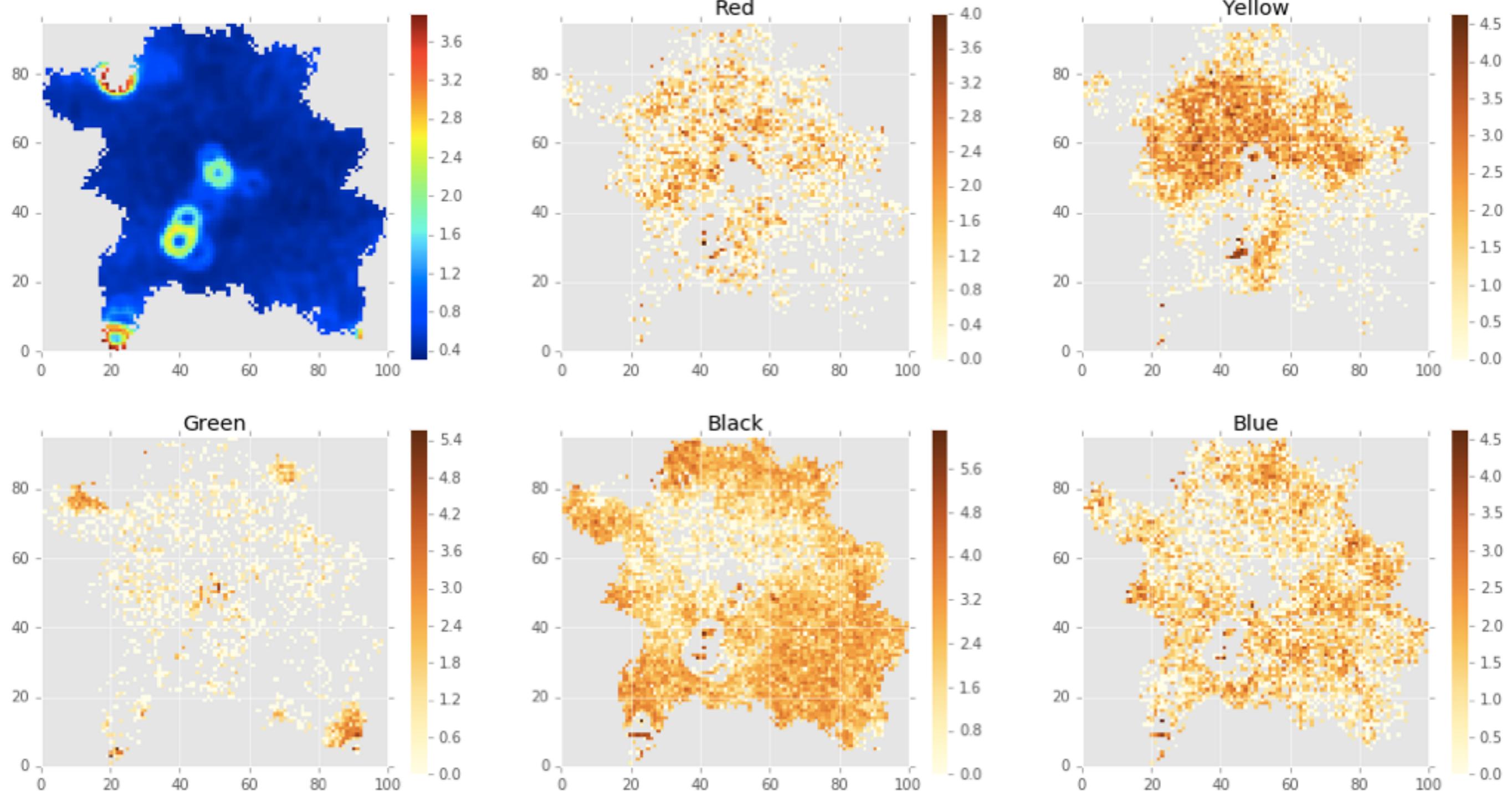
# Self Organizing Maps (SOM)



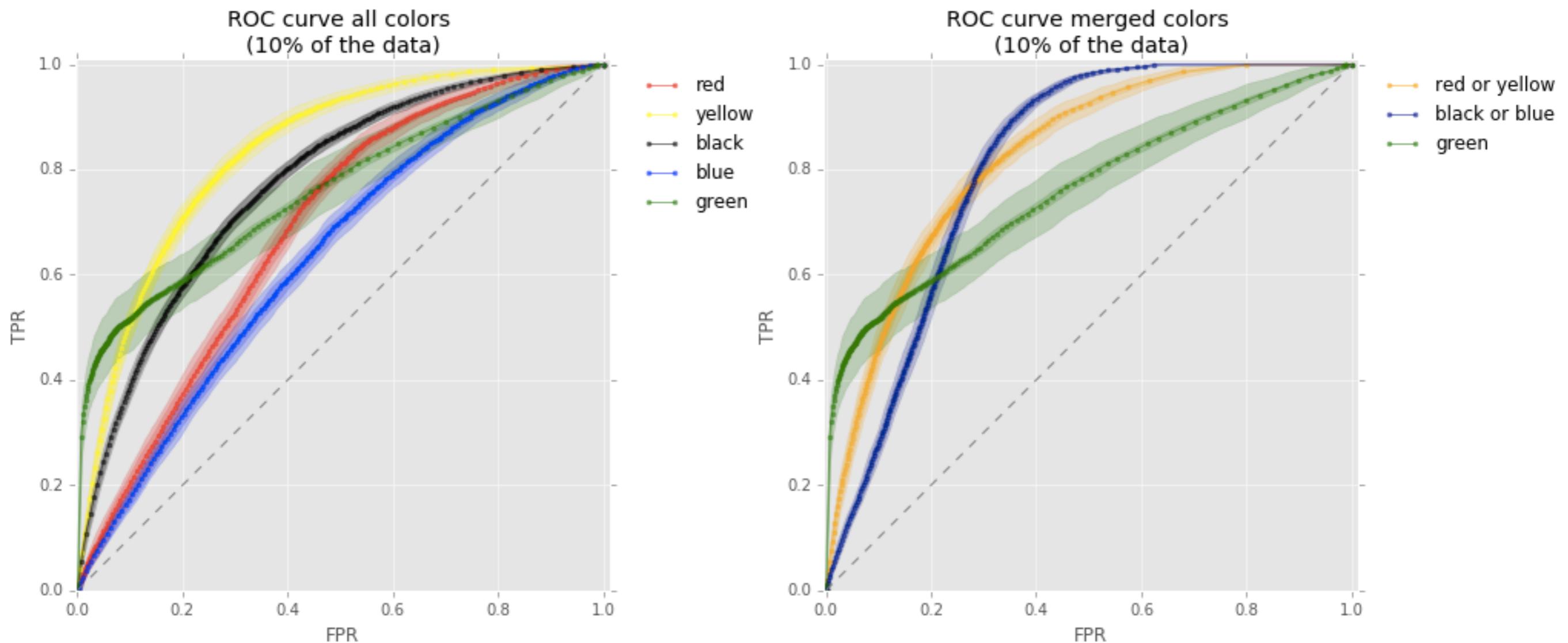
# SOM Models



# SOM Models



# Can we predict the color?



black : 0.77  
blue : 0.64  
green : 0.80  
red : 0.69  
yellow : 0.83

# Structural COLORs

