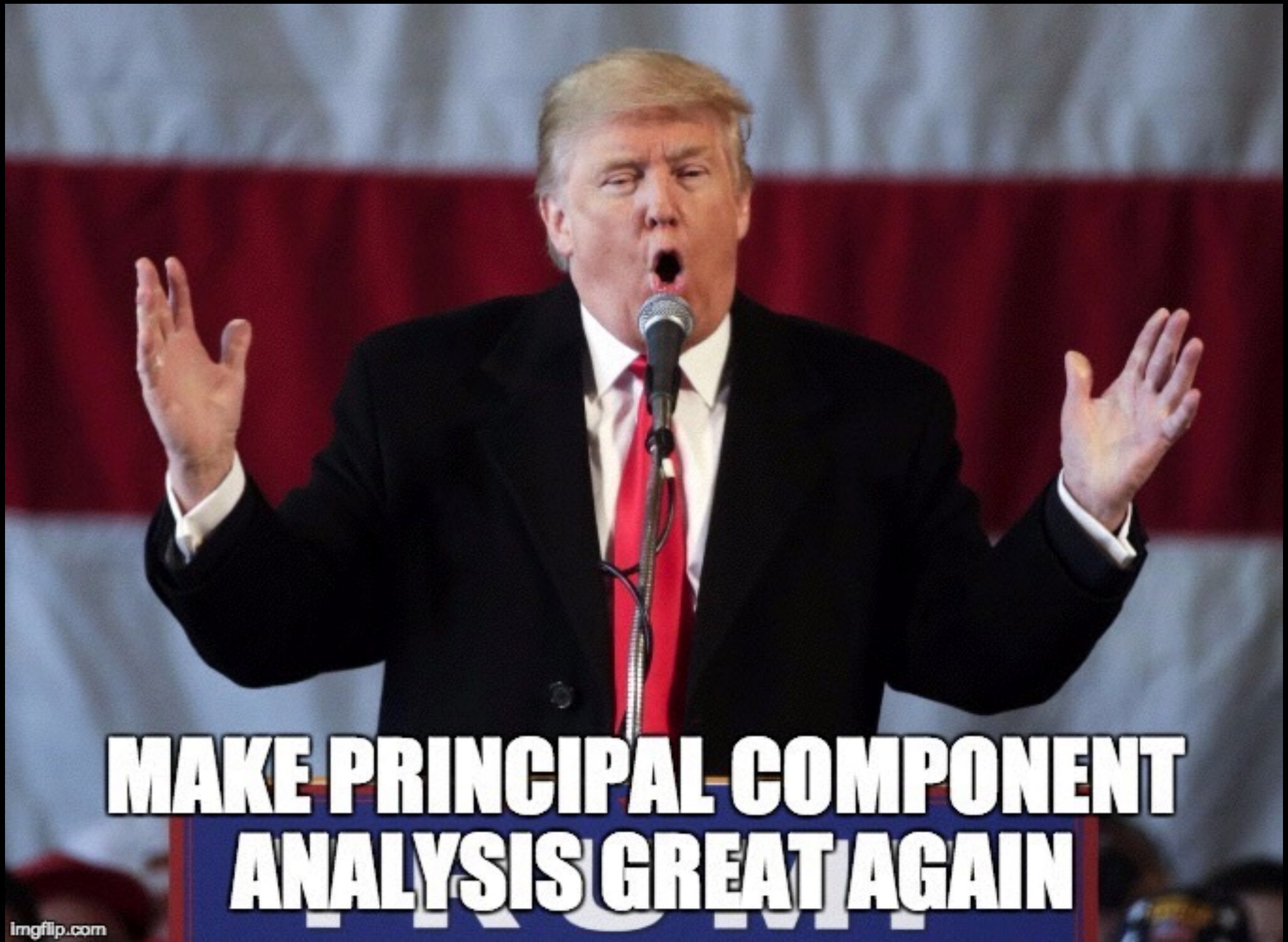


Exploring chemical space using random matrix theory

Alpha Lee

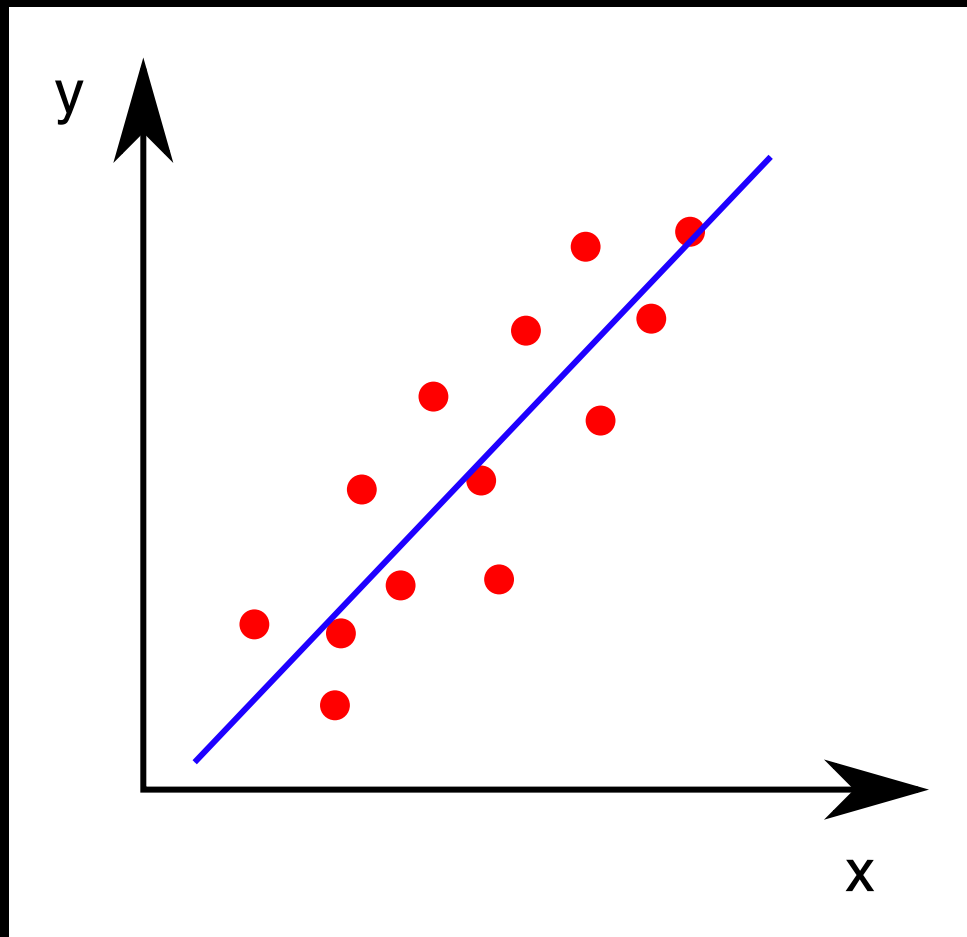
Department of Physics, University of Cambridge
aal44@cam.ac.uk
www.alpha-lee.com



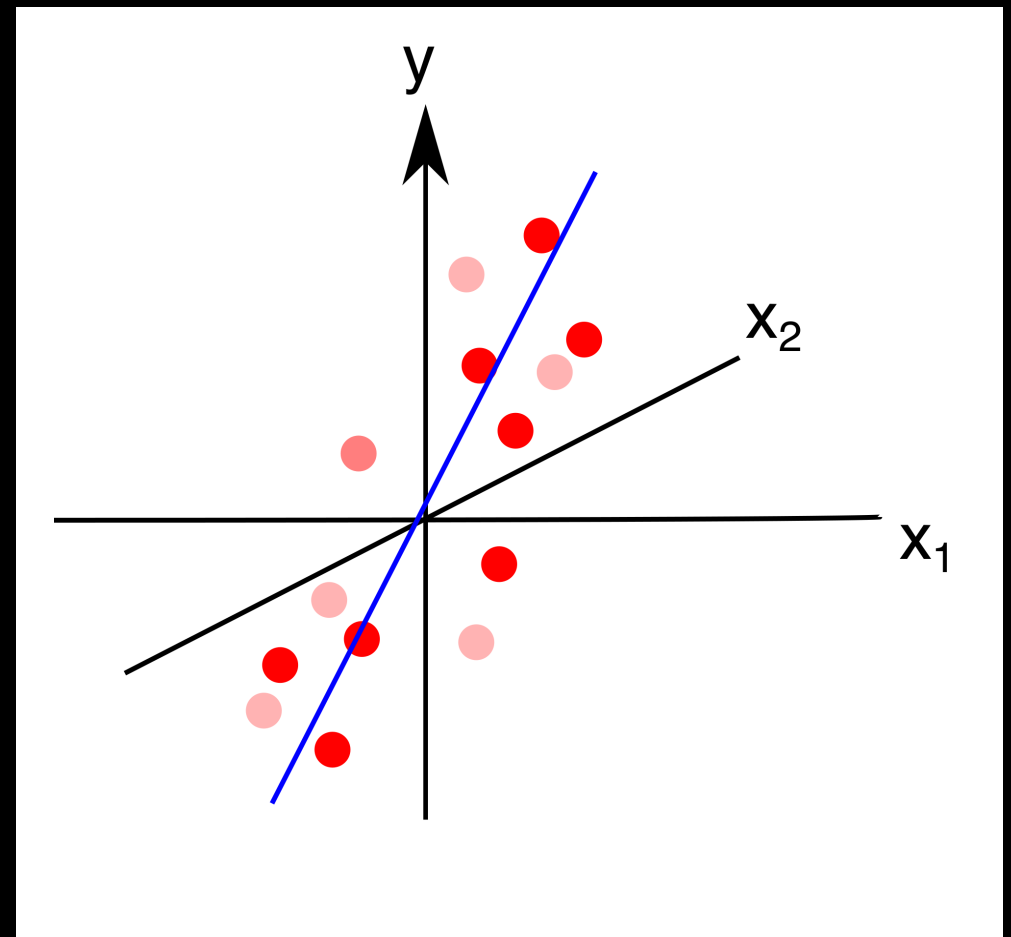
Chemical space is high dimensional

p = number of variables

n = number of samples

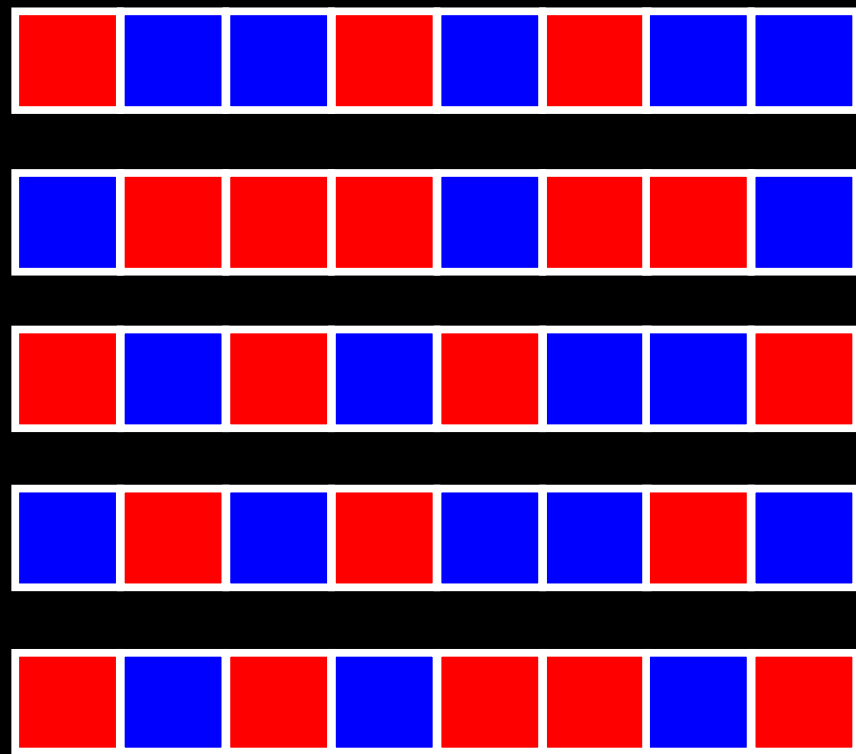


$$p = O(1)$$
$$p/n \rightarrow 0$$



$$n \rightarrow \infty$$
$$p/n = O(1)$$

Random matrix theory

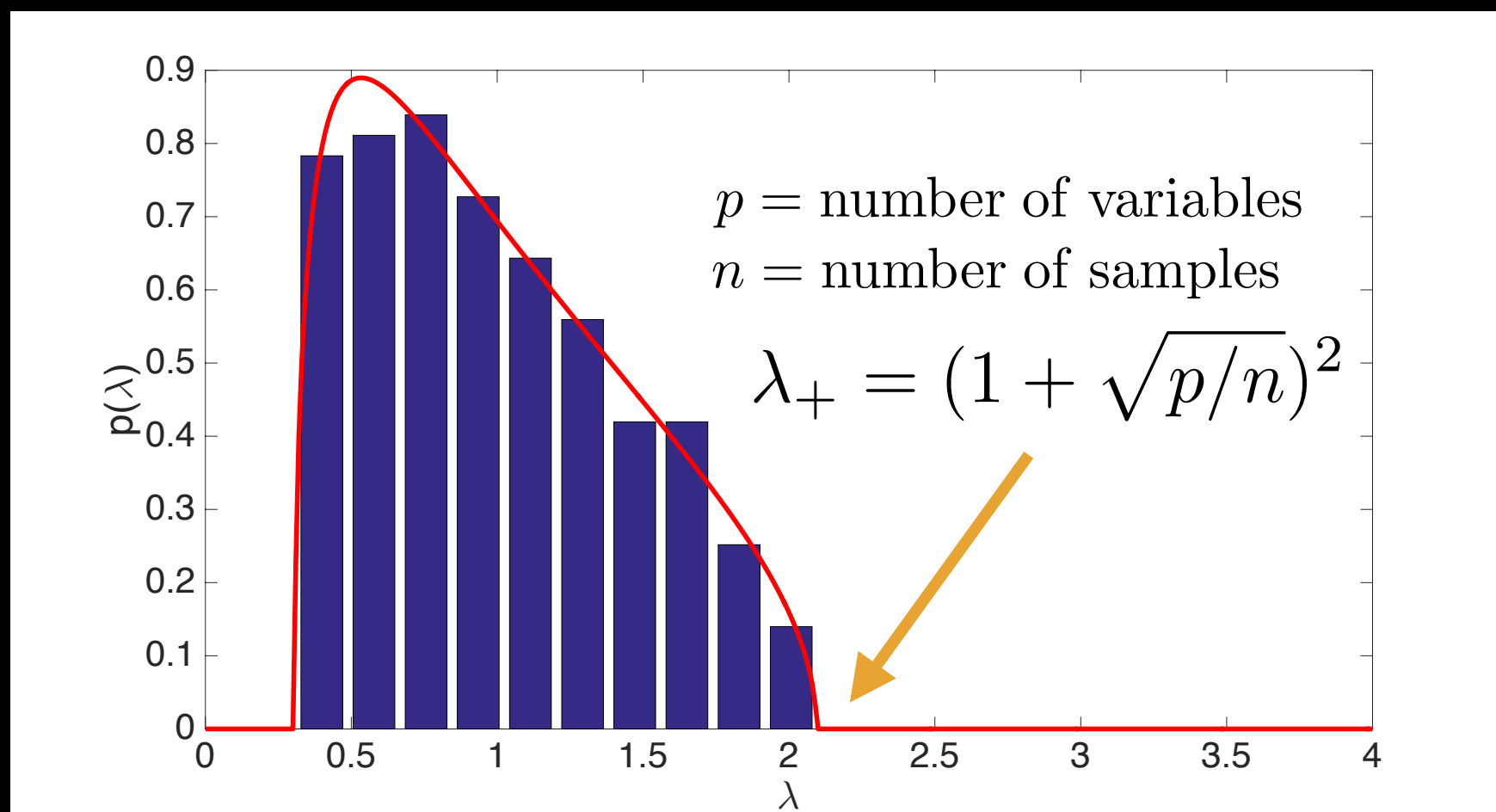


$$C_{ij} = \frac{\langle f_i f_j \rangle - \langle f_i \rangle \langle f_j \rangle}{\sigma_i \sigma_j}$$

E. T. Jaynes, *Physical Review*, 106, 620 (1957)
V. A. Mitchenko, L. A. Pastur, *Math. USSR Sb.*, 1, 457 (1967)

The null model

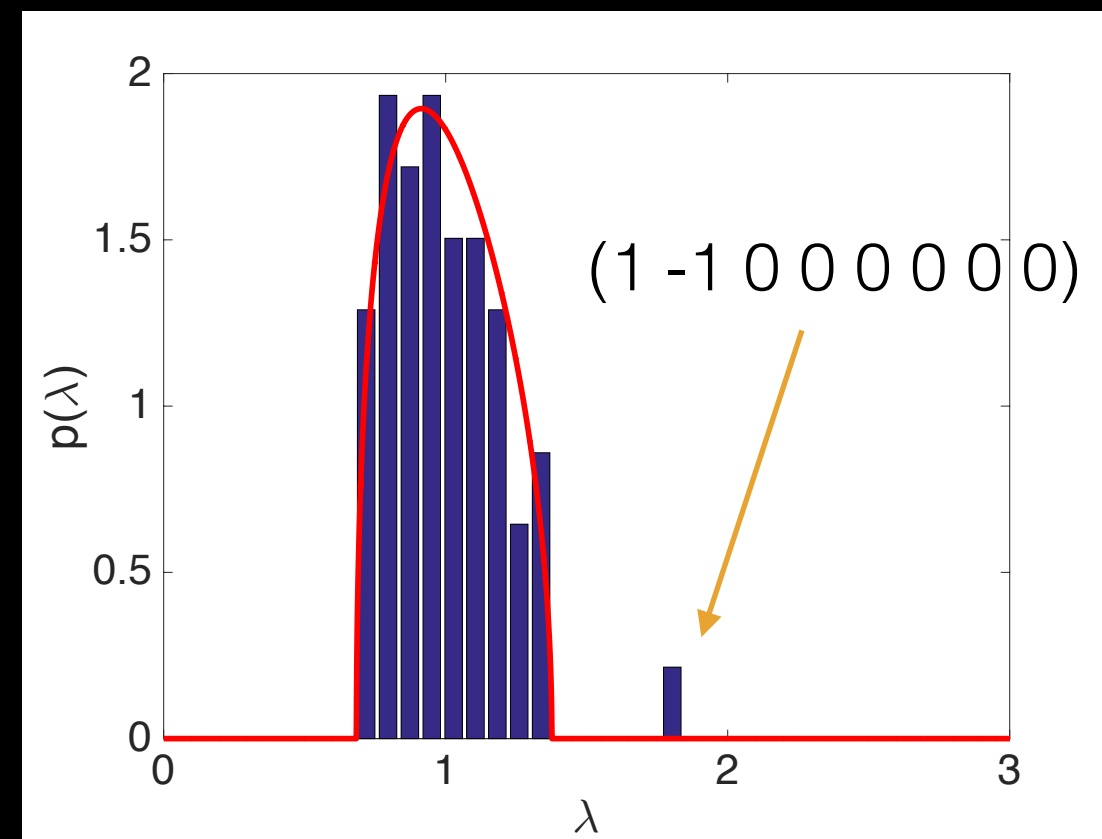
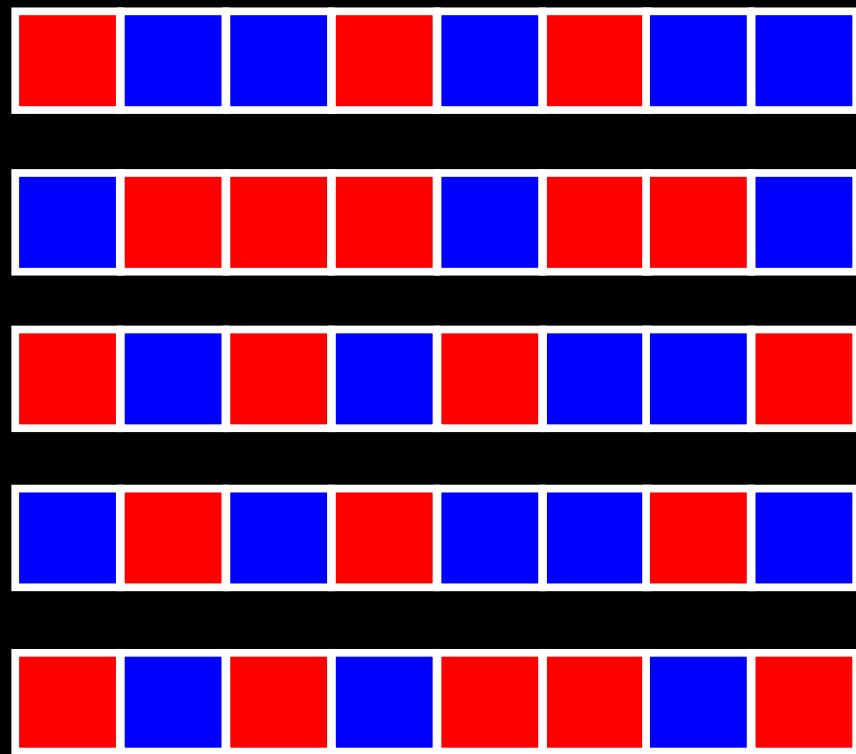
- Null model: the lattice sites are randomly coloured
- The eigenvalue distribution of the null model can be computed analytically



E. T. Jaynes, *Physical Review*, 106, 620 (1957)

V. A. Macherenko, L. A. Pastur, *Math. USSR Sb.*, 1, 457 (1967)

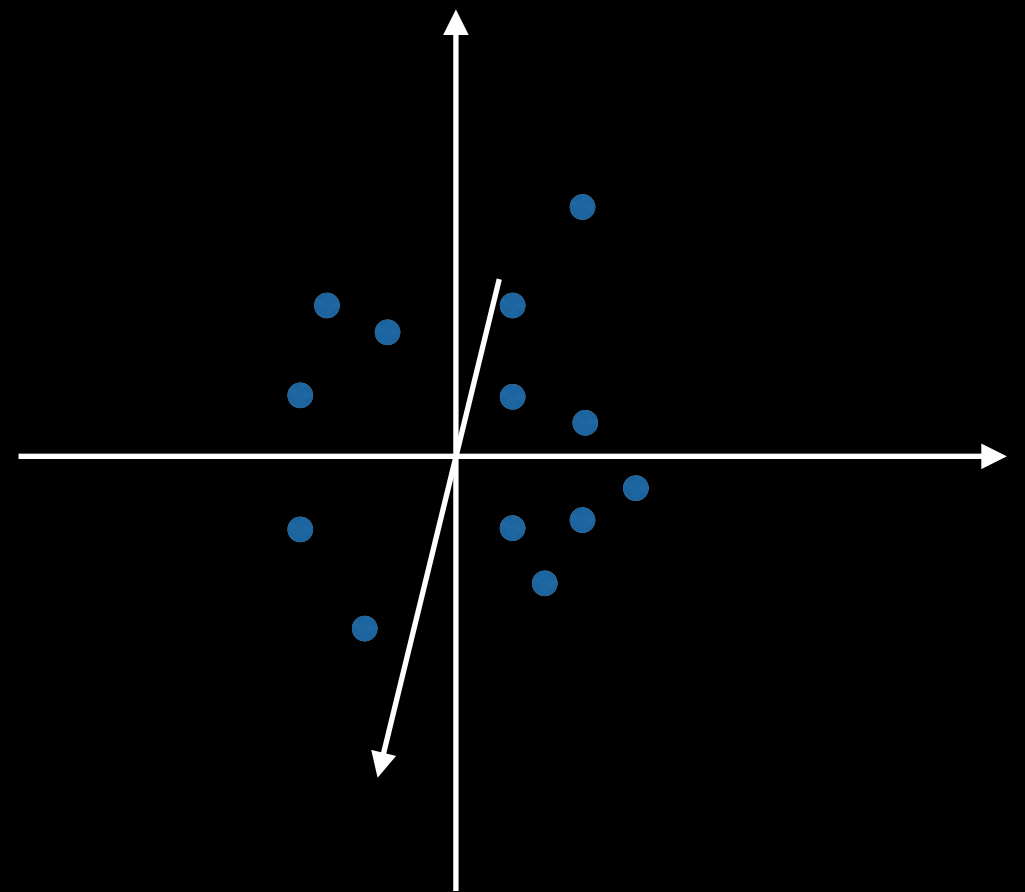
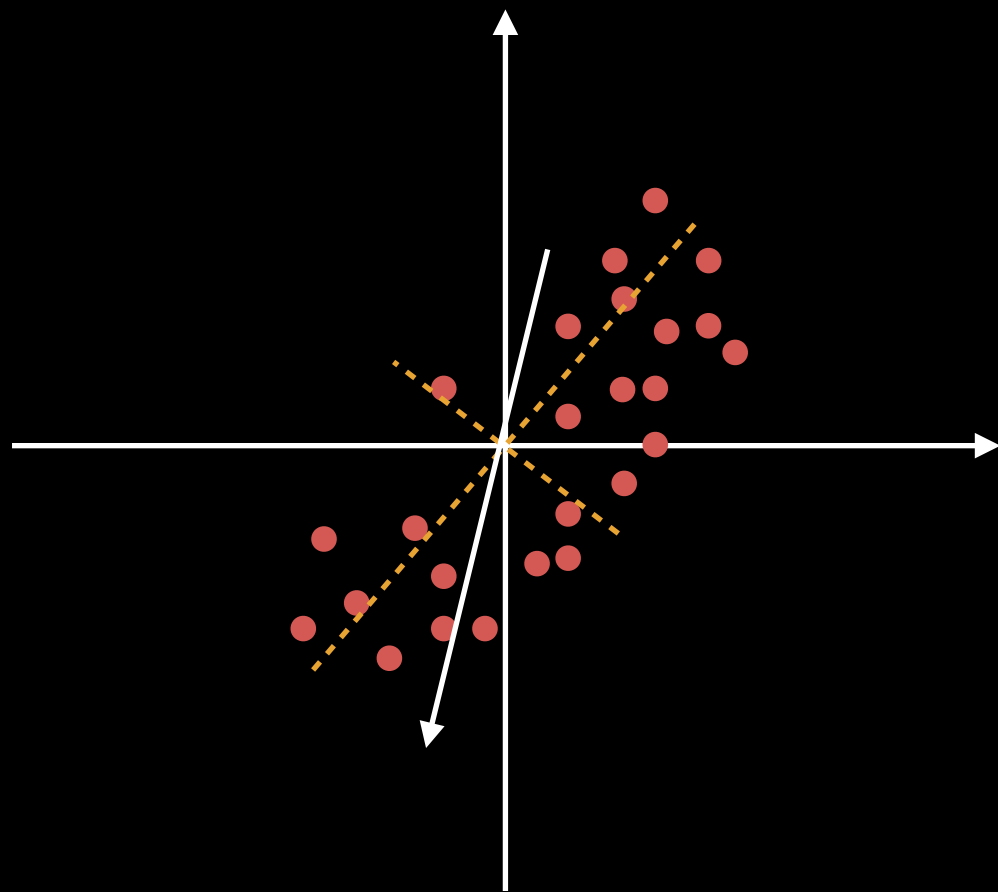
Random matrix theory



E. T. Jaynes, *Physical Review*, 106, 620 (1957)

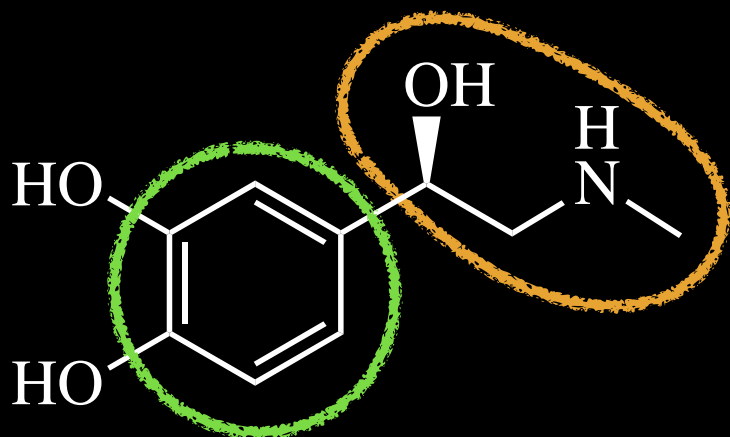
V. A. Makhenko, L. A. Pastur, *Math. USSR Sb.*, 1, 457 (1967)

Connection to PCA

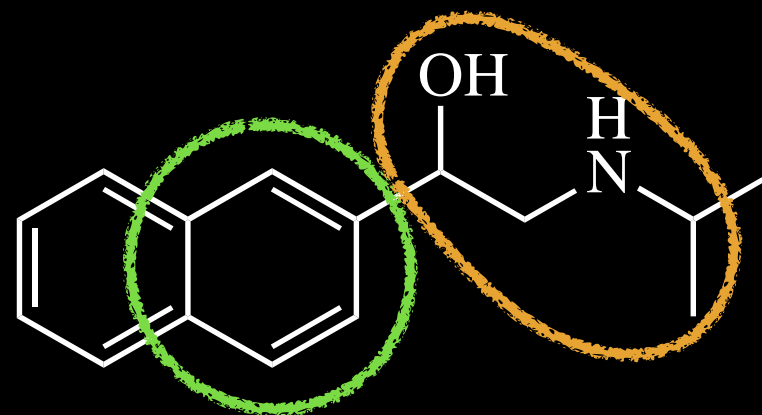


Chemical similarity

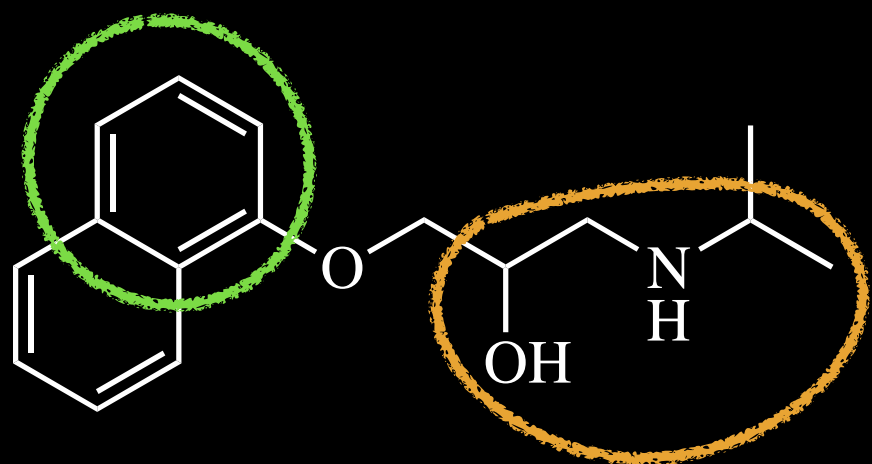
Suppose we want to design an ADRB1 antagonist



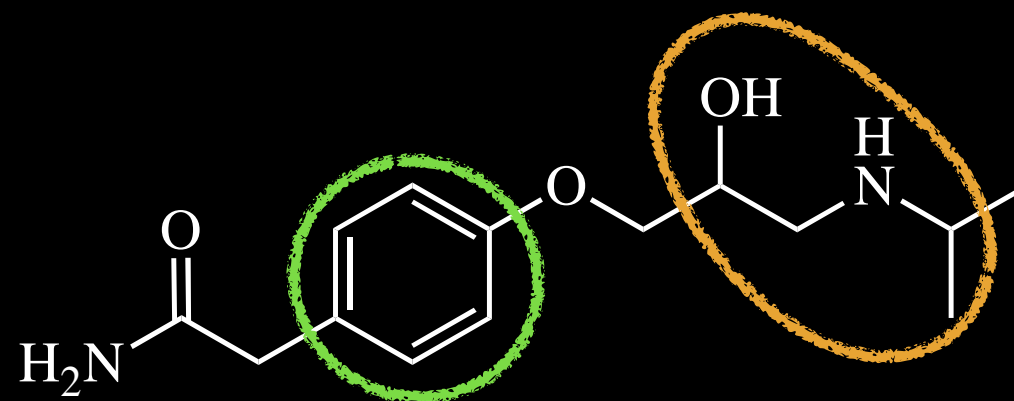
Adrenaline



Pronethalol

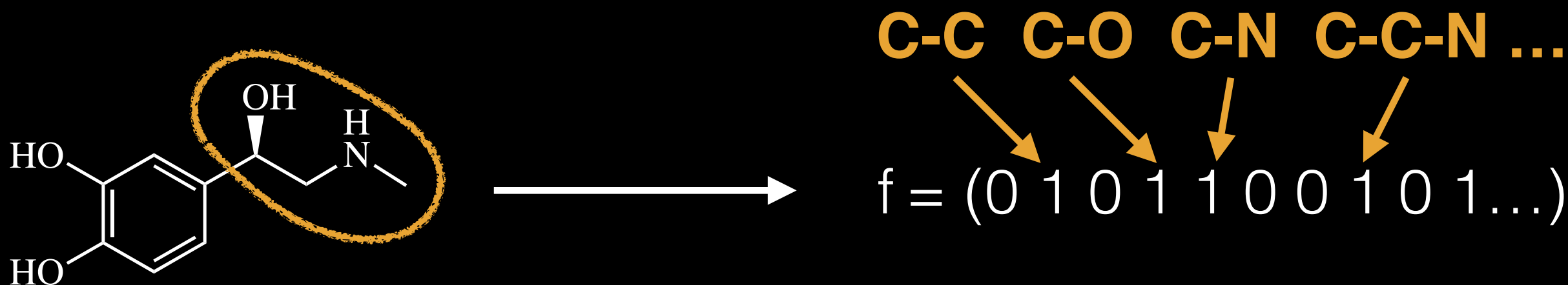


Propranolol



Atenolol

How to extracting relevant chemical features?



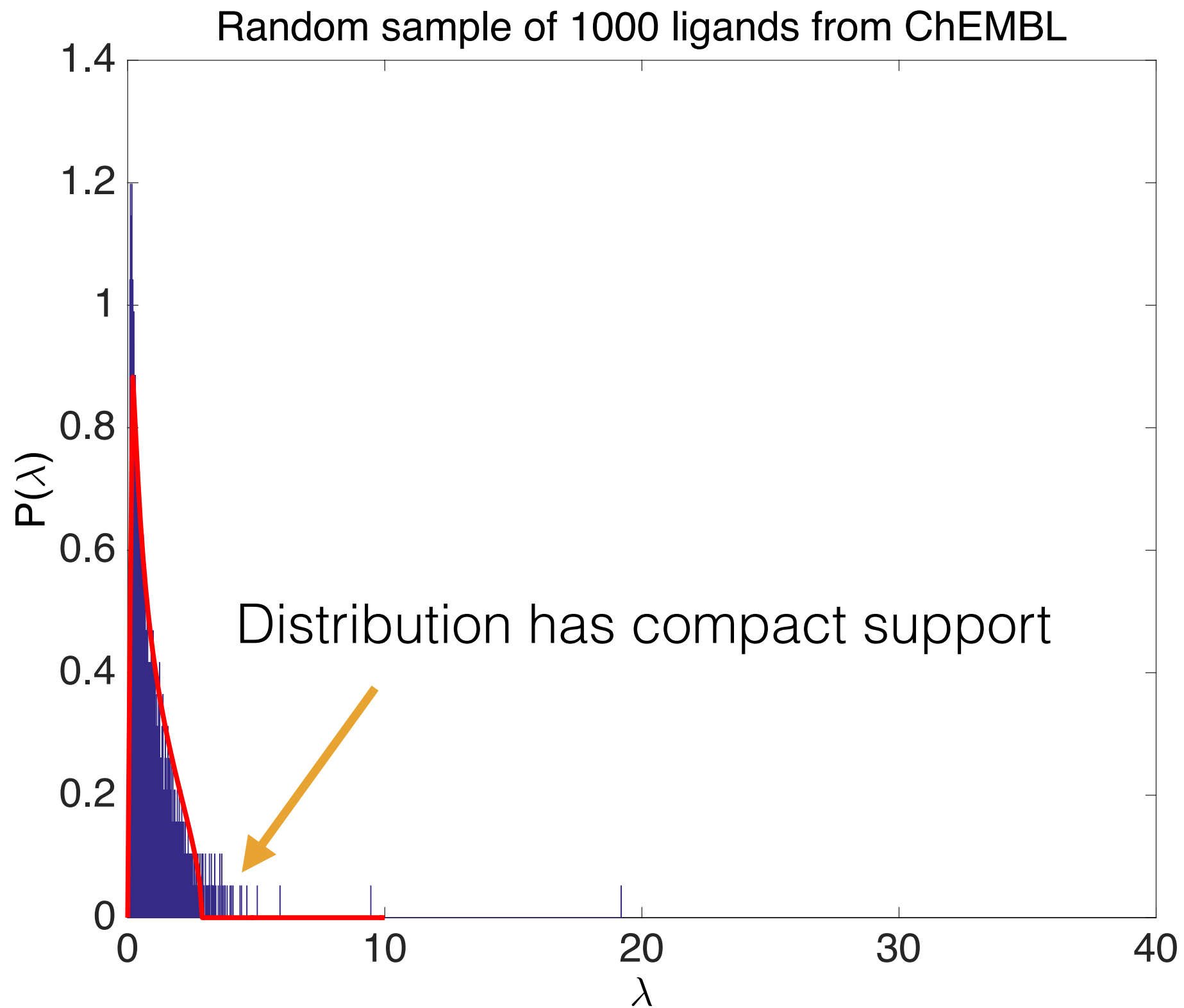
- Intuitively, there are only a few combinations chemical bonds (variables in the vector) that are important
- Many variables but often not many samples - data corrupted by finite sampling noise
- How do we get rid of the noise?

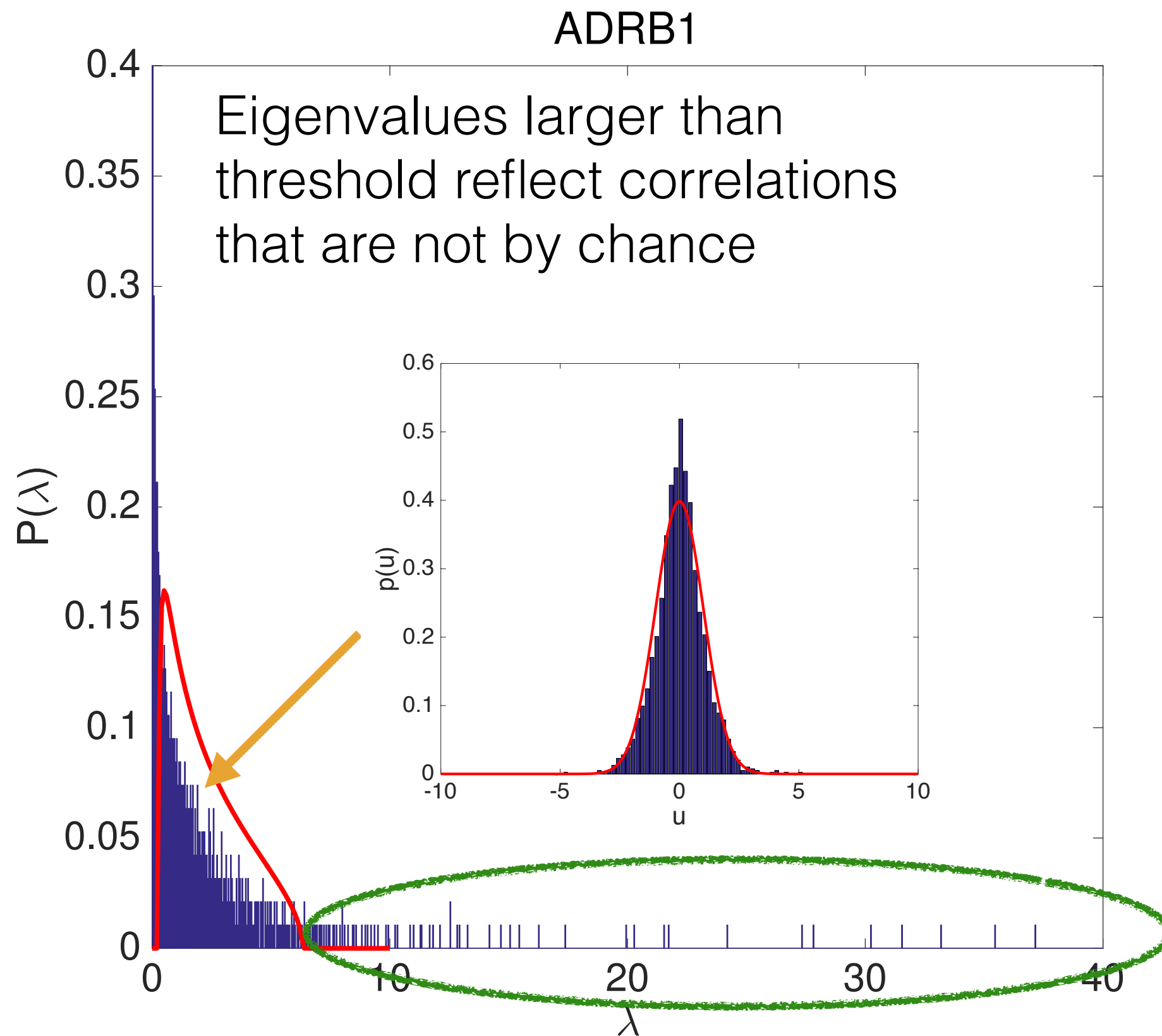
H. L. Morgan, *J. Chem. Doc.*, 5, 107 (1965)

Daylight Chemical Information Systems, Inc (since 1987)

A. Bender et al, *J. Chem. Inf. Comput. Sci.*, 44, 170 (2004)

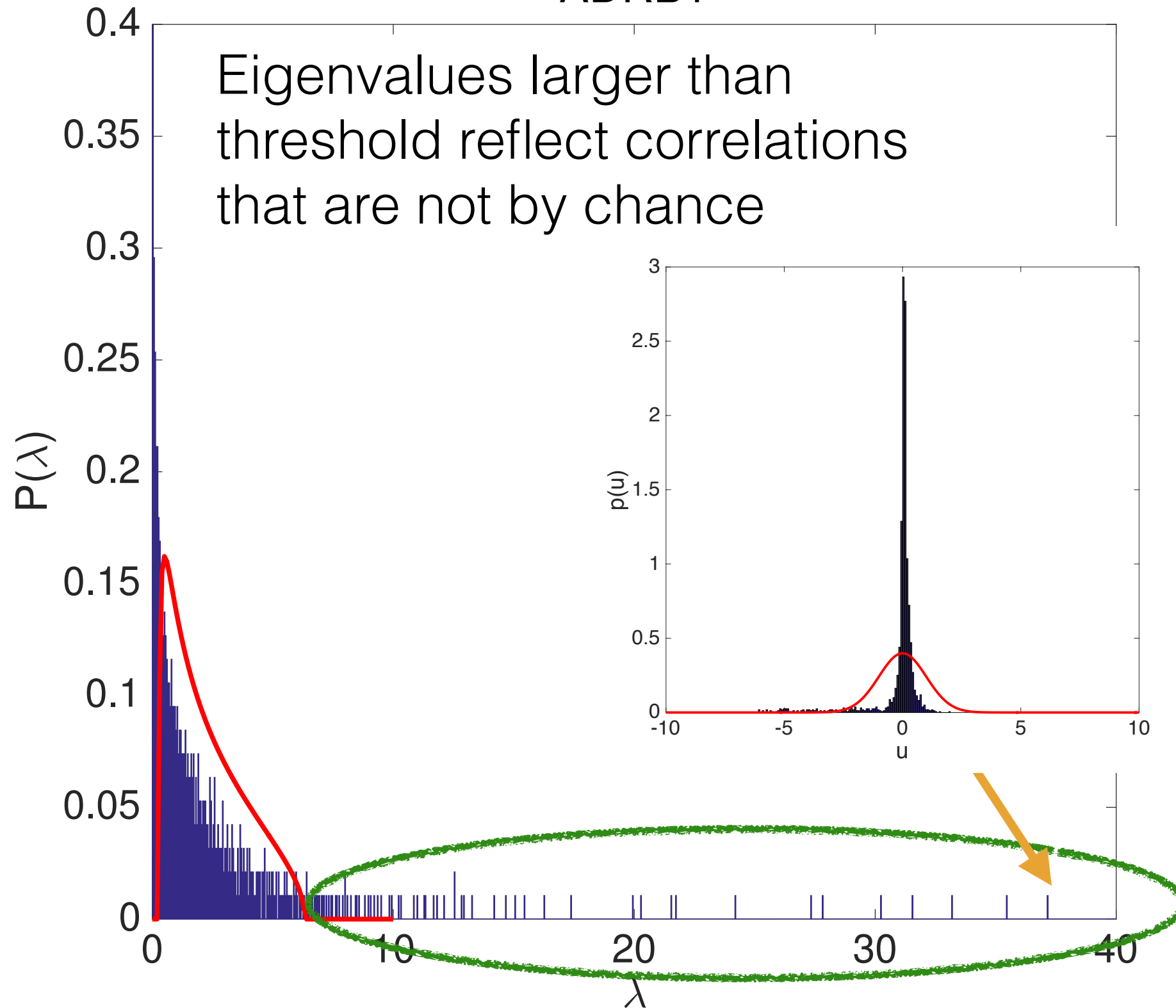
D. Rogers and M. Hahn, *J. Chem. Inf. Model.*, 50, 742 (2010)



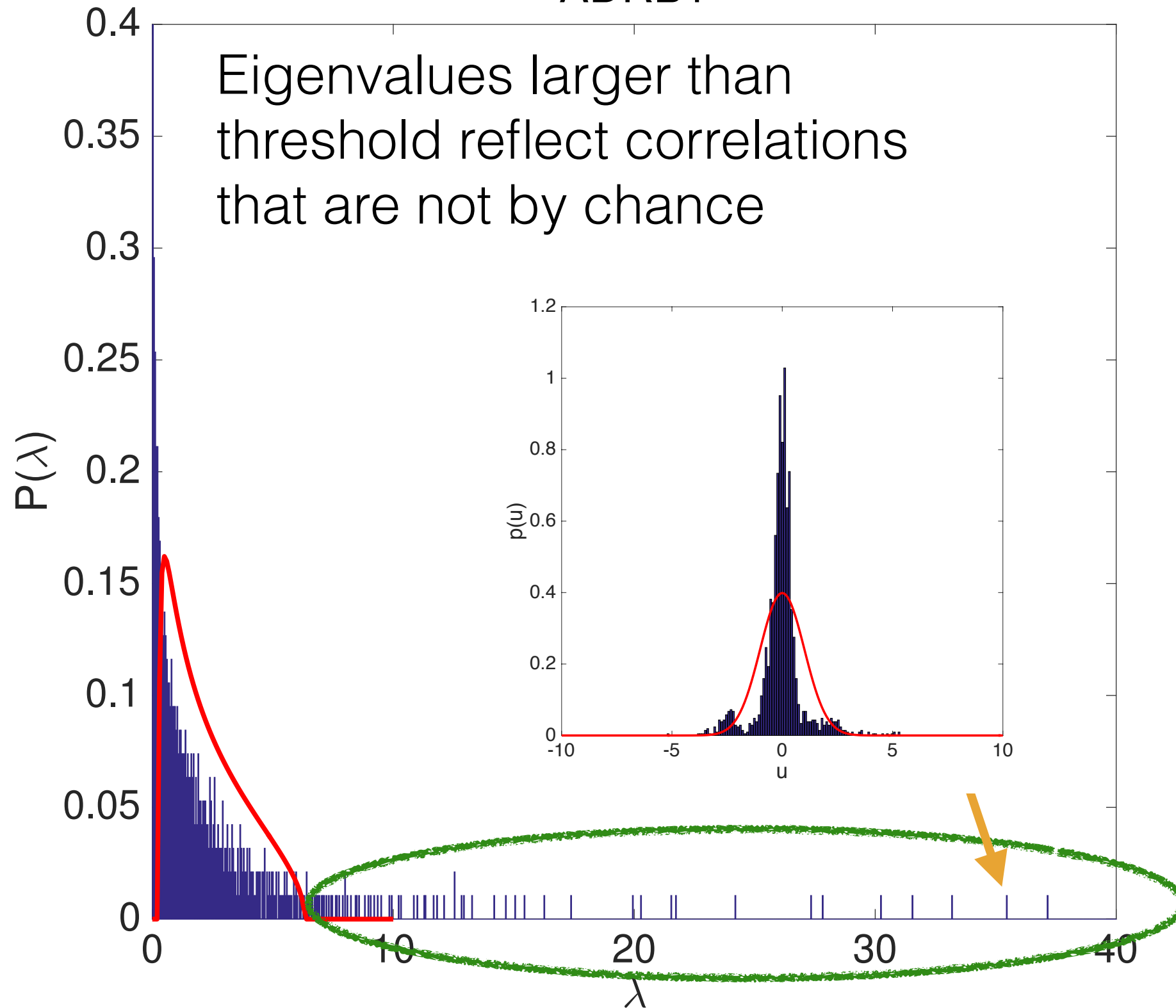


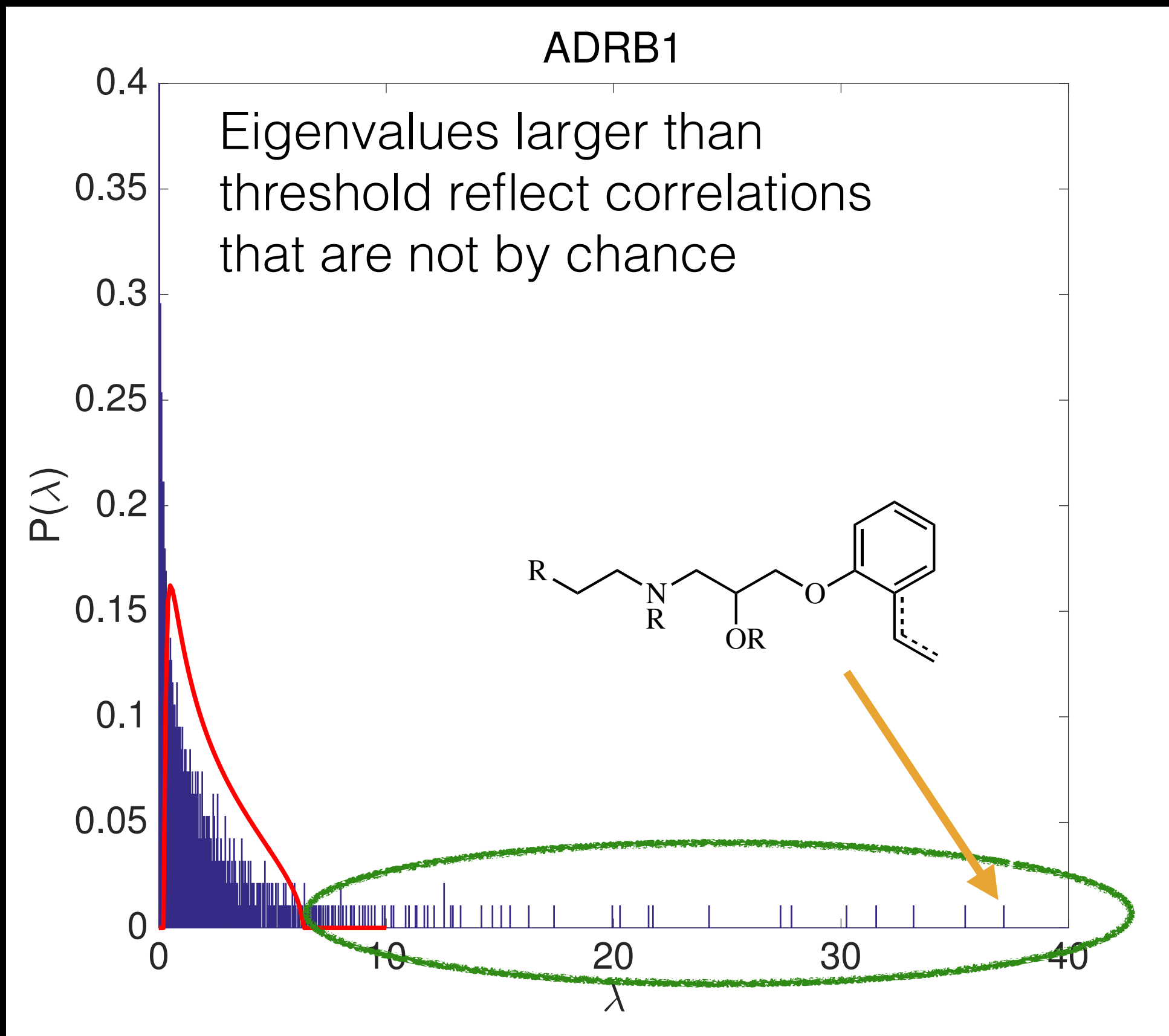
c.f. M. Turk, A. Pentland, *J. Cognitive Neurosci.*, 3, 71 (1991)
L. Laloux et al., *Phys. Rev. Lett.*, 83, 1467 (1999)

ADRB1



ADRB1



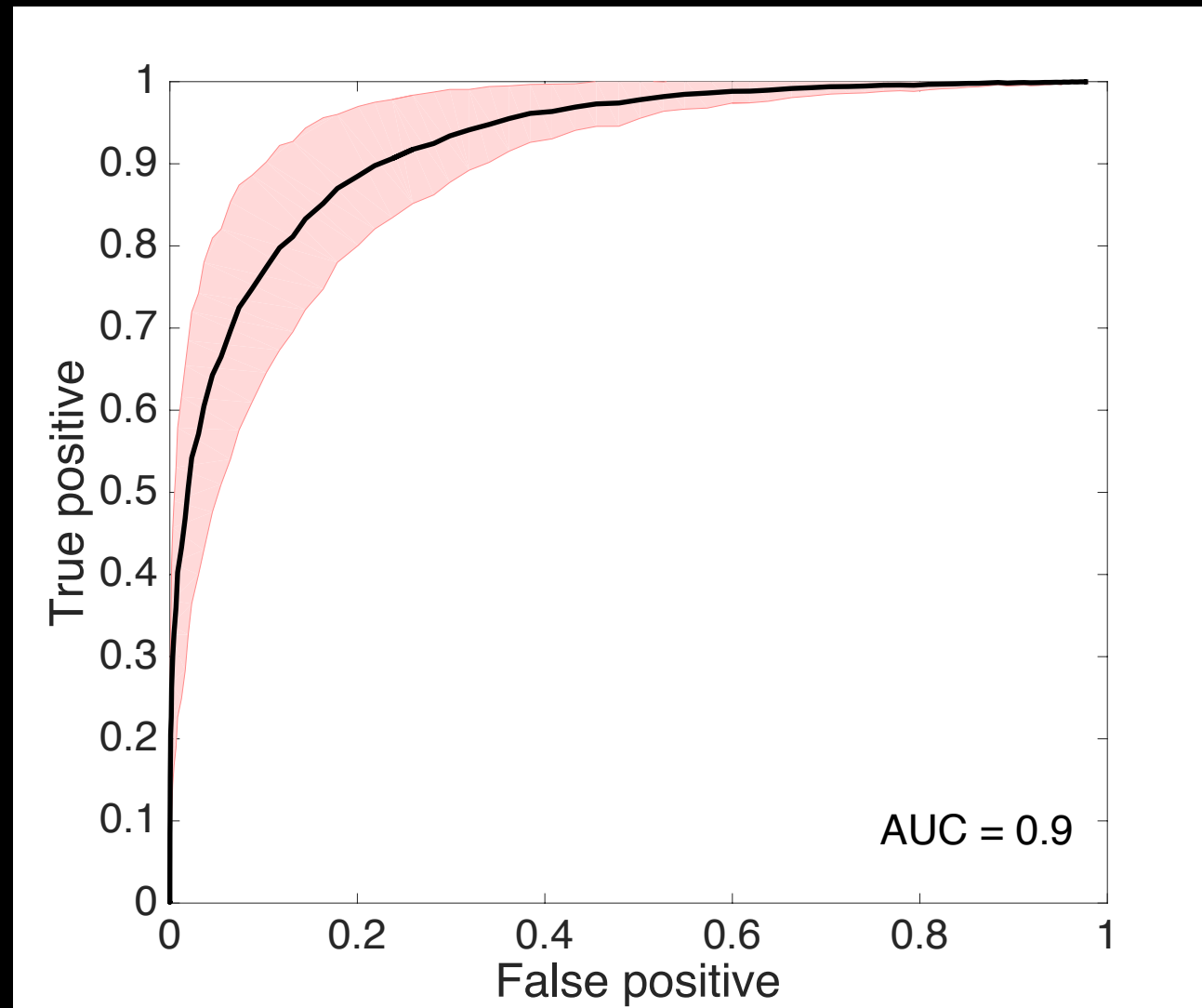


Predicting protein-ligand affinity

1. Let $\{v_i\}_{i=1}^q$ be eigenvectors with eigenvalues above threshold
2. Convert unknown molecules into vector u
3. Compute how “close” is u to $\text{span}\{v_i\}_{i=1}^q$

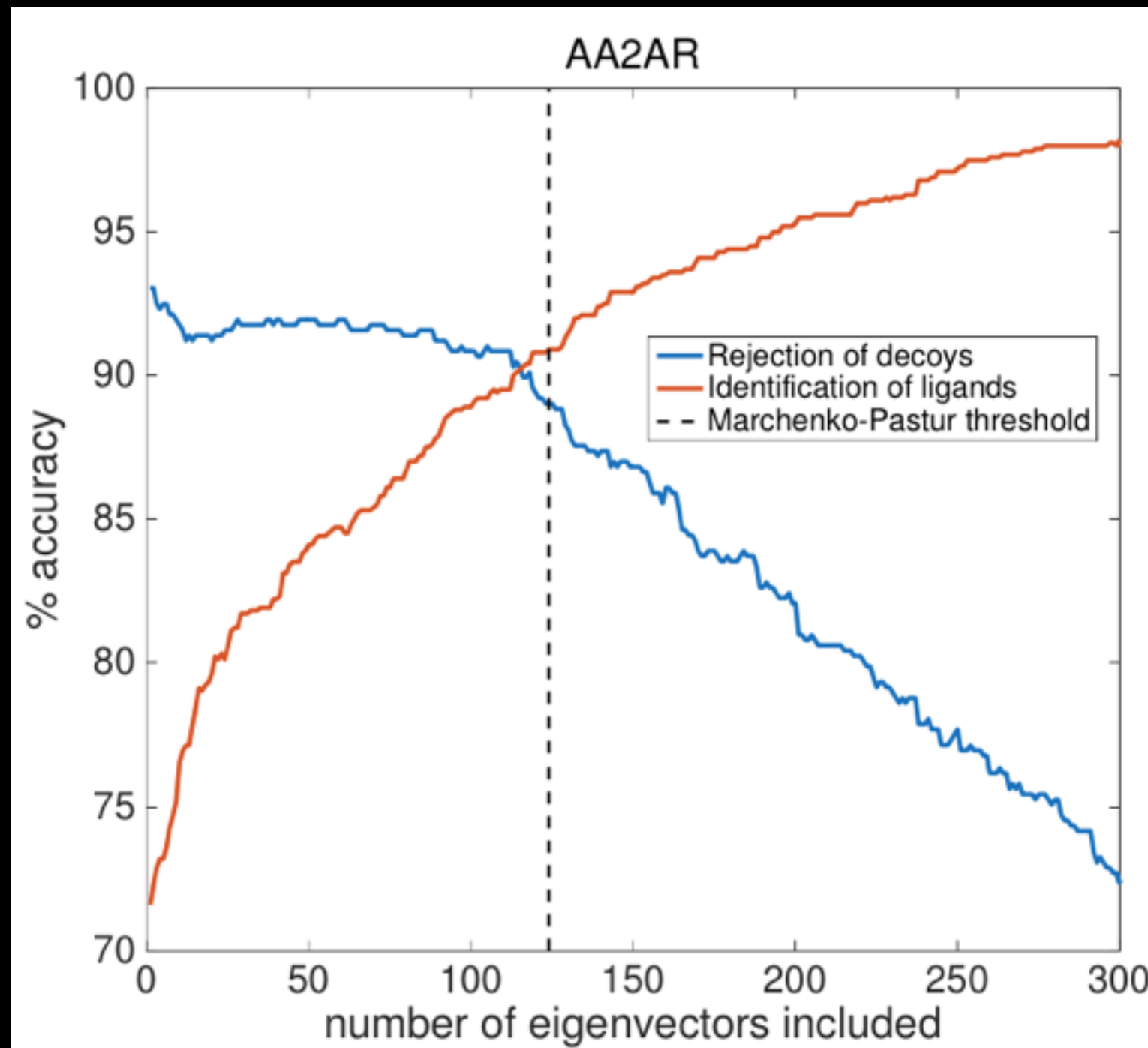
Criterion for binding $\left\| u - \sum_{i=1}^q (u \cdot v_i) v_i \right\|_2 < \epsilon$

Performance of classification algorithm



The algorithm outperforms all algorithms that we are aware of

Near optimality of random matrix bound



Many shades of grey: Turning classification into regression

- It is costly to do measurements precisely!
- It is often much easier to measure whether the property of a compound is above/below a threshold

molecule ₁	soluble		molecule _j	s = 1 mol/L	
molecule ₂	soluble		molecule _{j+1}	s = 0.1 mol/L	
molecule ₃	insoluble	+	molecule _{j+2}	s = 0.5 mol/L	= ?
molecule ₄	insoluble		molecule _{j+3}	s = 0.01 mol/L	
...			...		

Back to correlation analysis

We know that there are chemical functional groups contributing to a molecule being soluble/insoluble

Soluble molecules

```
1001100111...  
1101100101...  
0101101101...  
0101101111...  
...
```



Fragments

Insoluble molecules

```
1000100100...  
0001100101...  
0100001101...  
0101101101...  
...
```



Fragments

Combining imprecise and precise measurements

Posit a quadratic model:

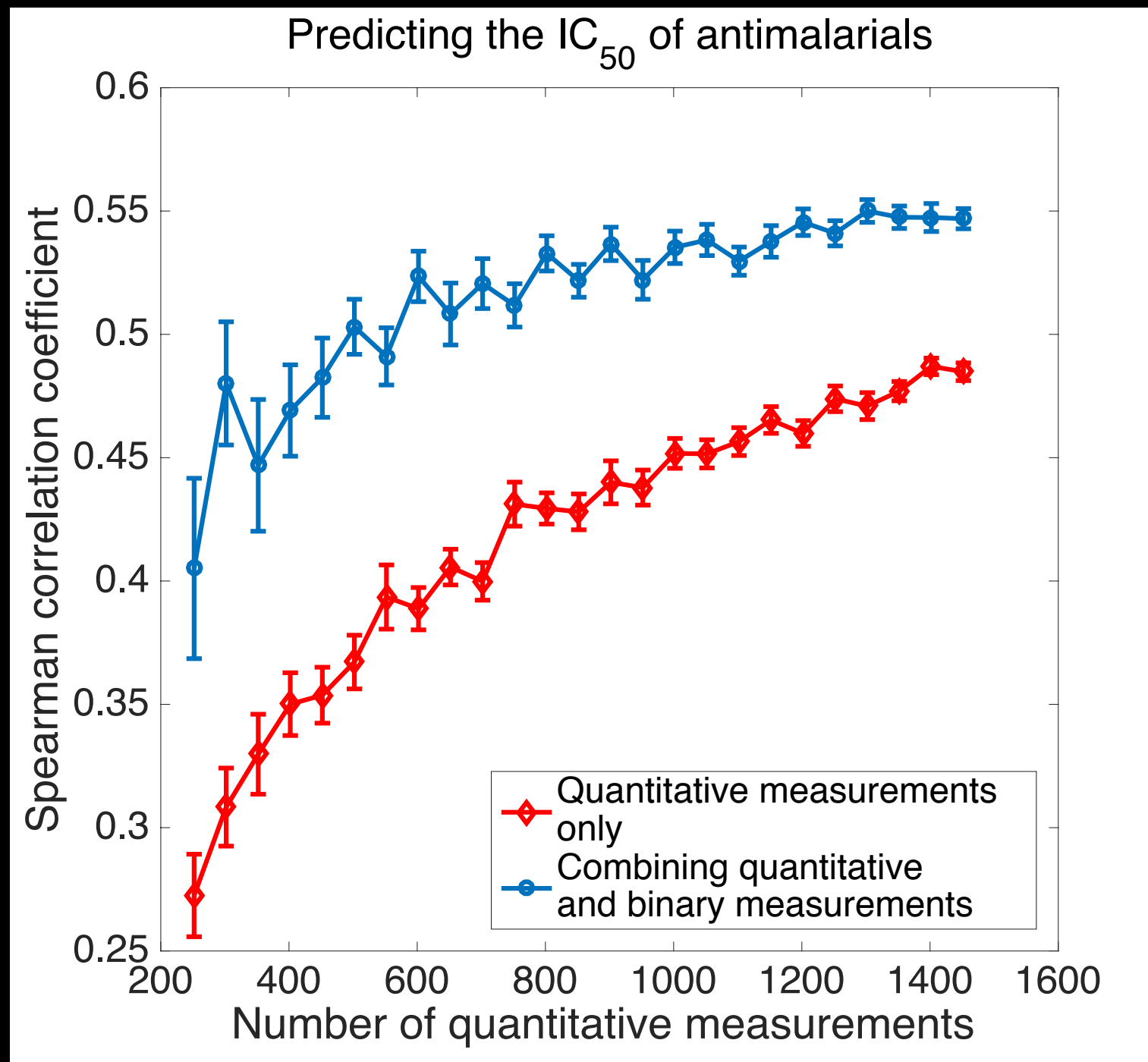
$$y_i = \mathbf{h}^T \mathbf{f}_i + \mathbf{f}_i^T J \mathbf{f}_i + \epsilon_i$$

Let $\{\mathbf{u}^\pm\}$ be the set of eigenvectors of the correlation matrix of soluble/insoluble molecules

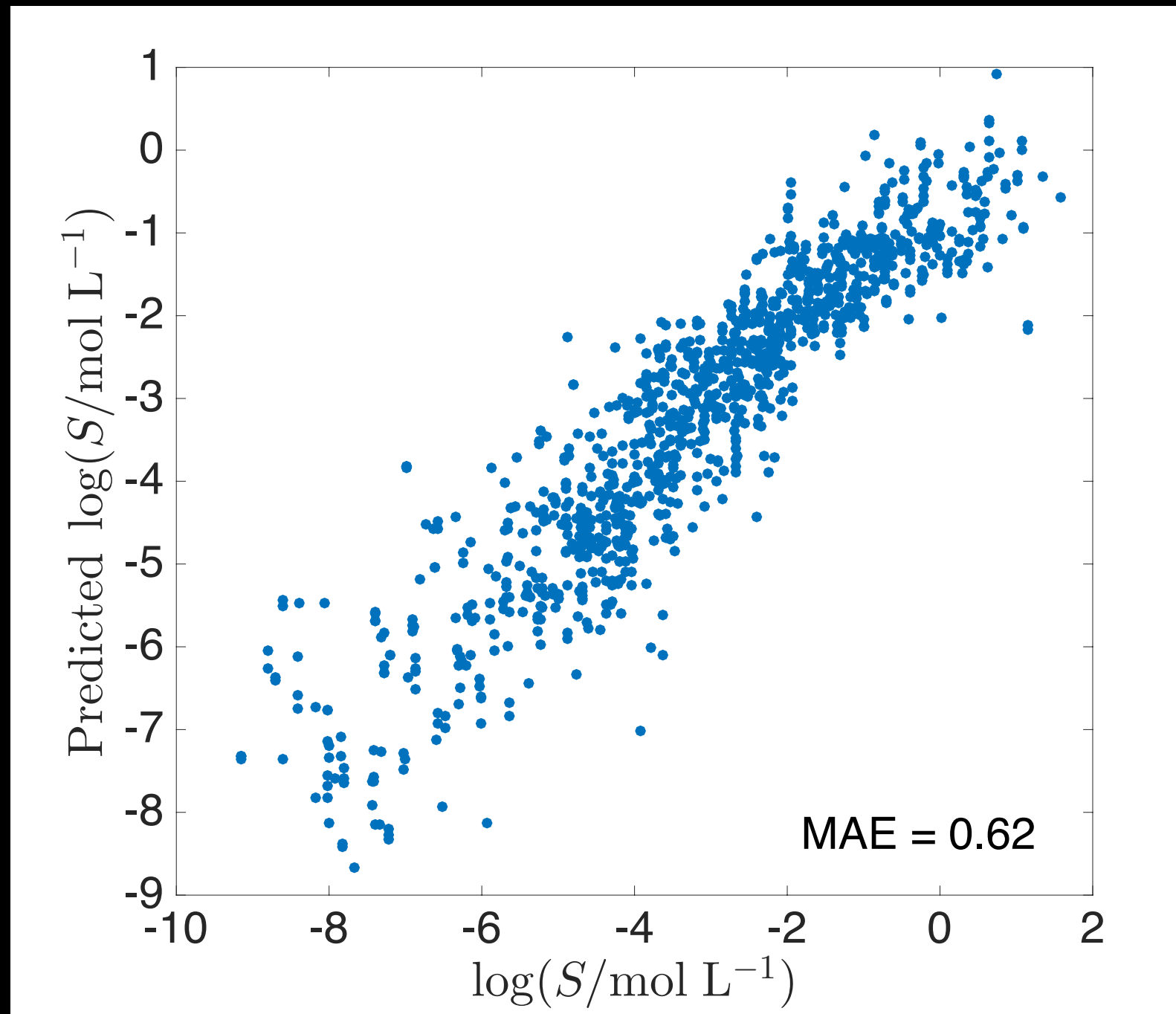
$$J = \sum_{i=1}^{\hat{p}_+} c_i^+ \mathbf{u}_i^+ \otimes \mathbf{u}_i^+ + \sum_{i=1}^{\hat{p}_-} c_i^- \mathbf{u}_i^- \otimes \mathbf{u}_i^-$$

Use regression to find $\{\mathbf{h}, \mathbf{c}^+, \mathbf{c}^-\}$

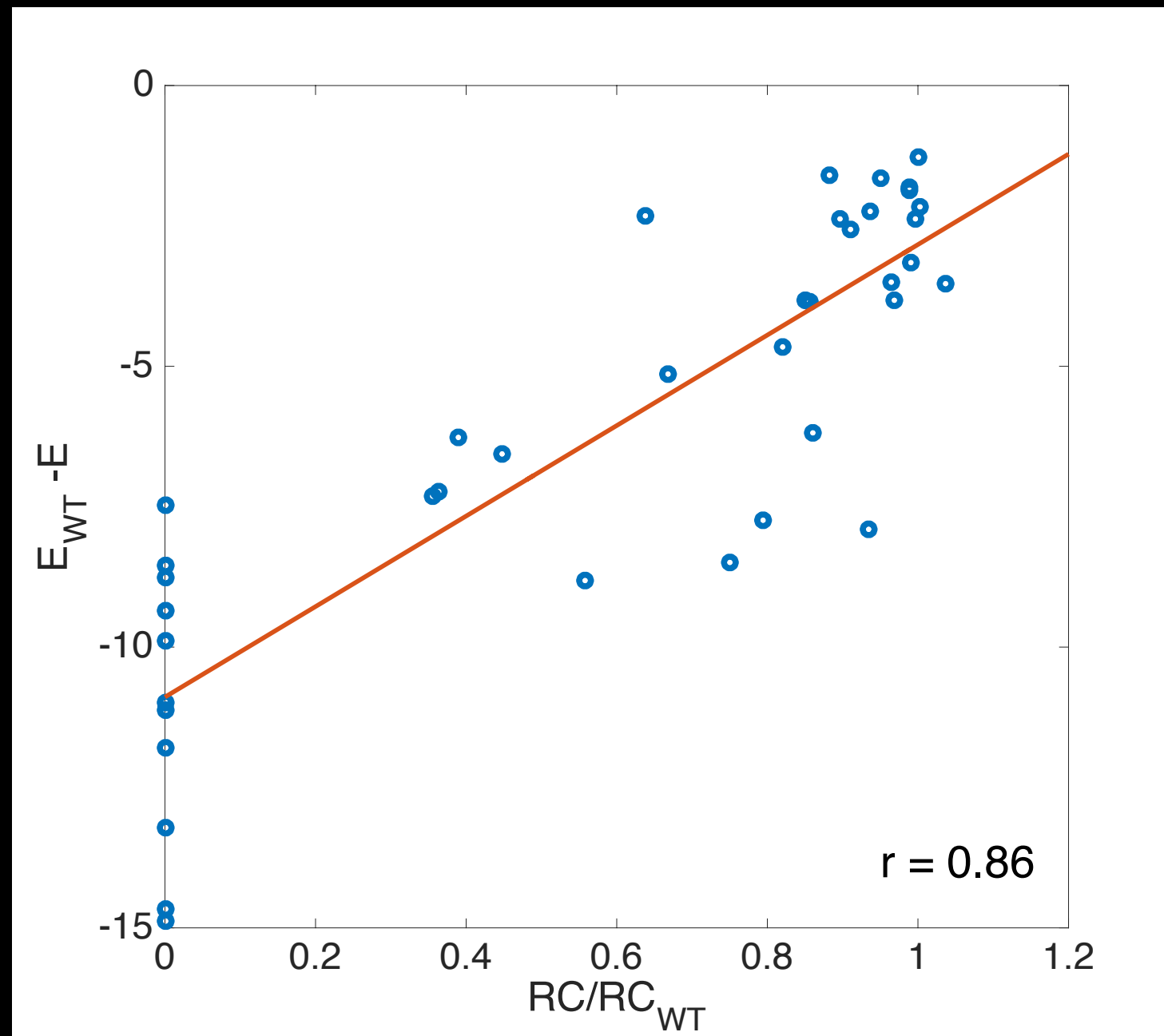
The malaria TDT challenge



Solubility prediction



Fitness landscape of HIV-1 Gag



Conclusion

- Finite data effects are prevalent in chemical space exploration
- Random matrix theory provides a useful null model to undress sampling noise
- Precise and imprecise measurements can be combined to yield a predictive model

We are hiring!



contact me: aal44@cam.ac.uk