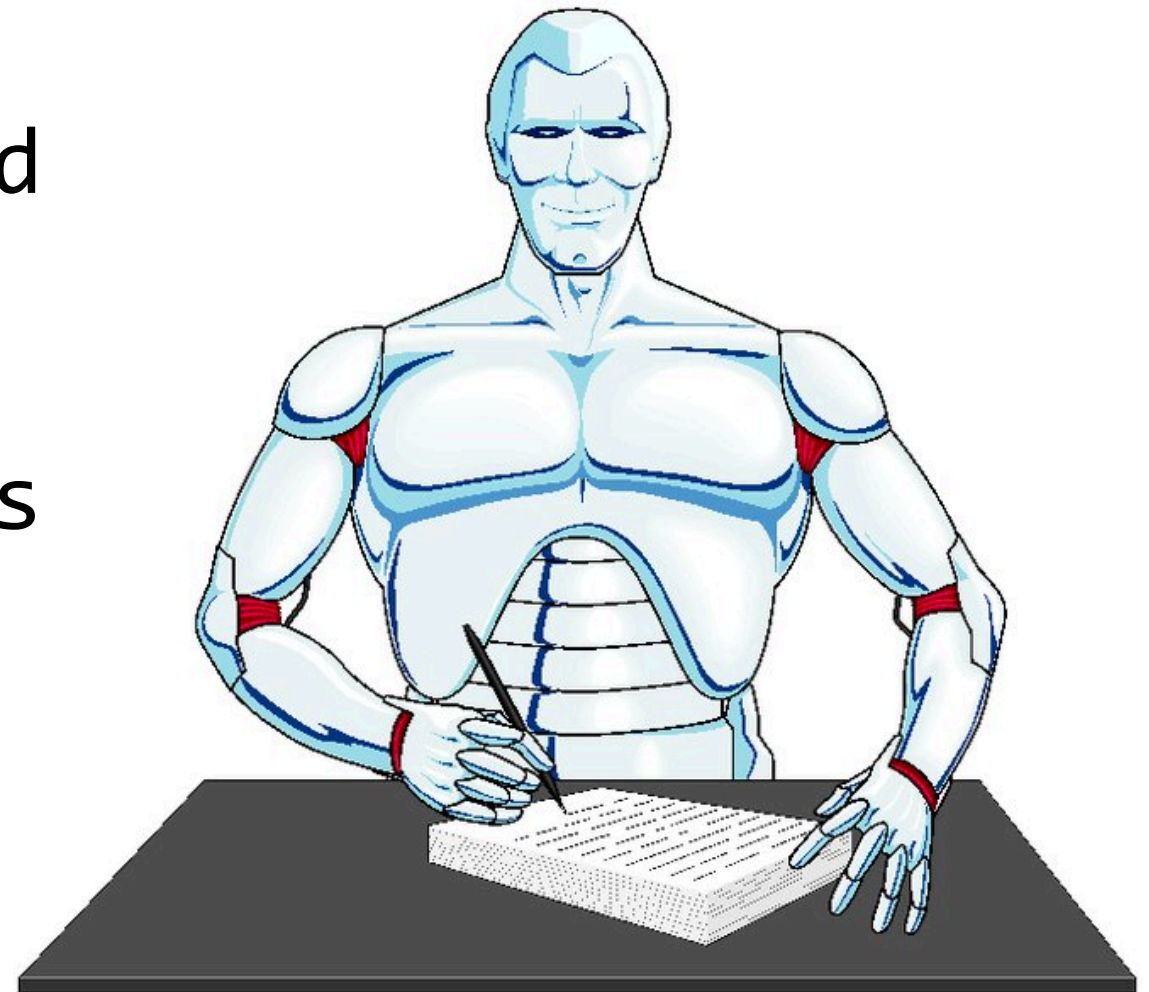


PRINCIPAL COMPONENTS ANALYSIS

11.30.2020

FINAL

- * the final will be posted **next monday** (Dec. 7)
- * it will be due (and this is a **HARD** deadline) on Monday, December 14 at 10:59 AM



FINAL

- * the final will be SELF-TIMED (*honor system!*) for 4 hours (no proctorio, etc.)
- * your time starts when you first look at it, and you should stop working on it (& turn it in) 4 hours later
- * it is **OPEN BOOK, OPEN DOCUMENTATION, & OPEN INTERNET**
- * but don't discuss it with anyone else until you have both finished it

FINAL

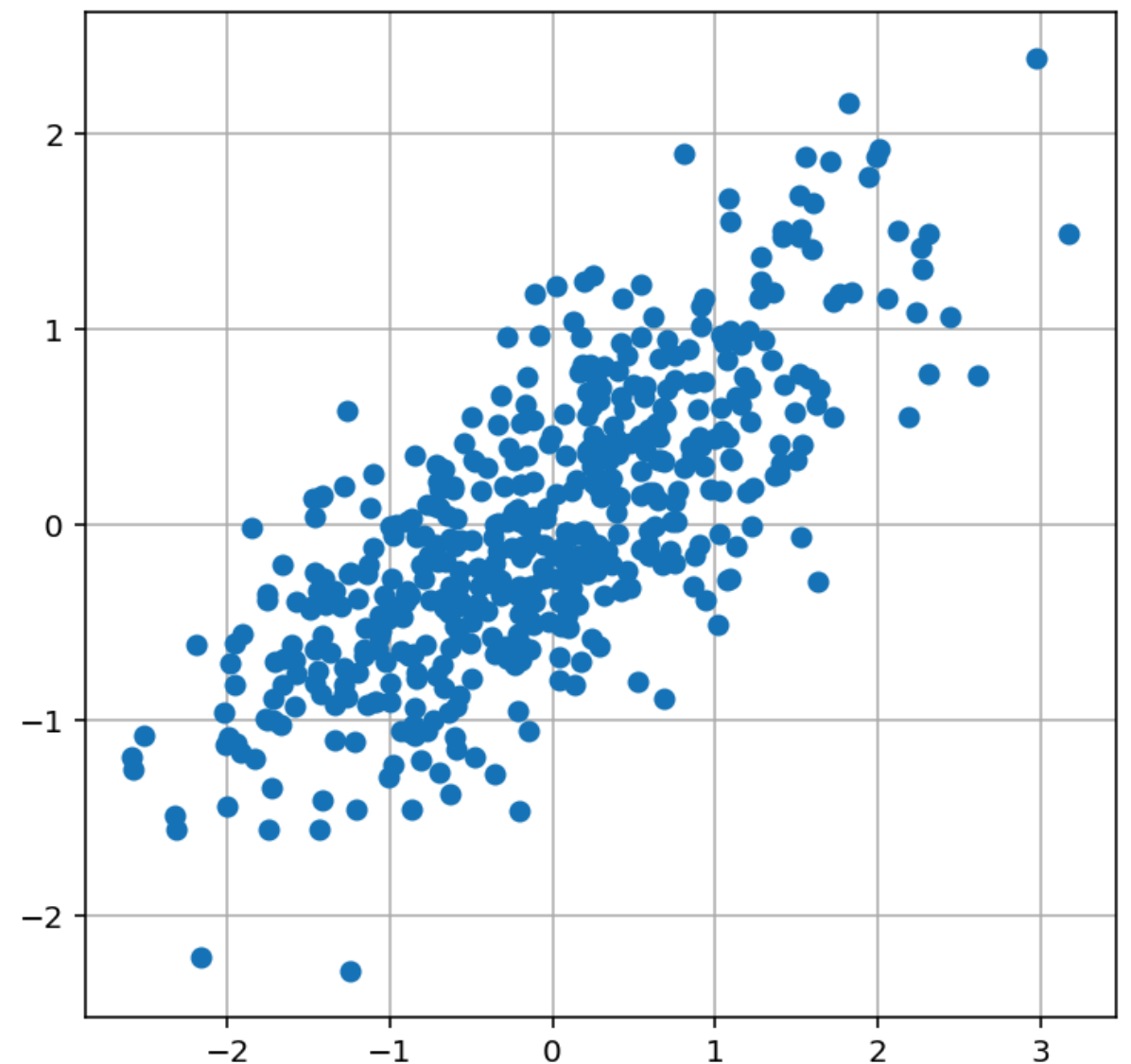
- * the final will cover all the topics we've touched on in class
- * it will be EASIER THAN THE HOMEWORKS
 - * i.e. the vast majority of you should finish in 4 hours
- * good luck :)

PCA

- * **Principal Components Analysis** is an *unsupervised* method for finding structure in datasets
- * (This is different from regression & classification, which are examples of *supervised Learning*. They learn a function $f(X)=y$. Here we only have X !)

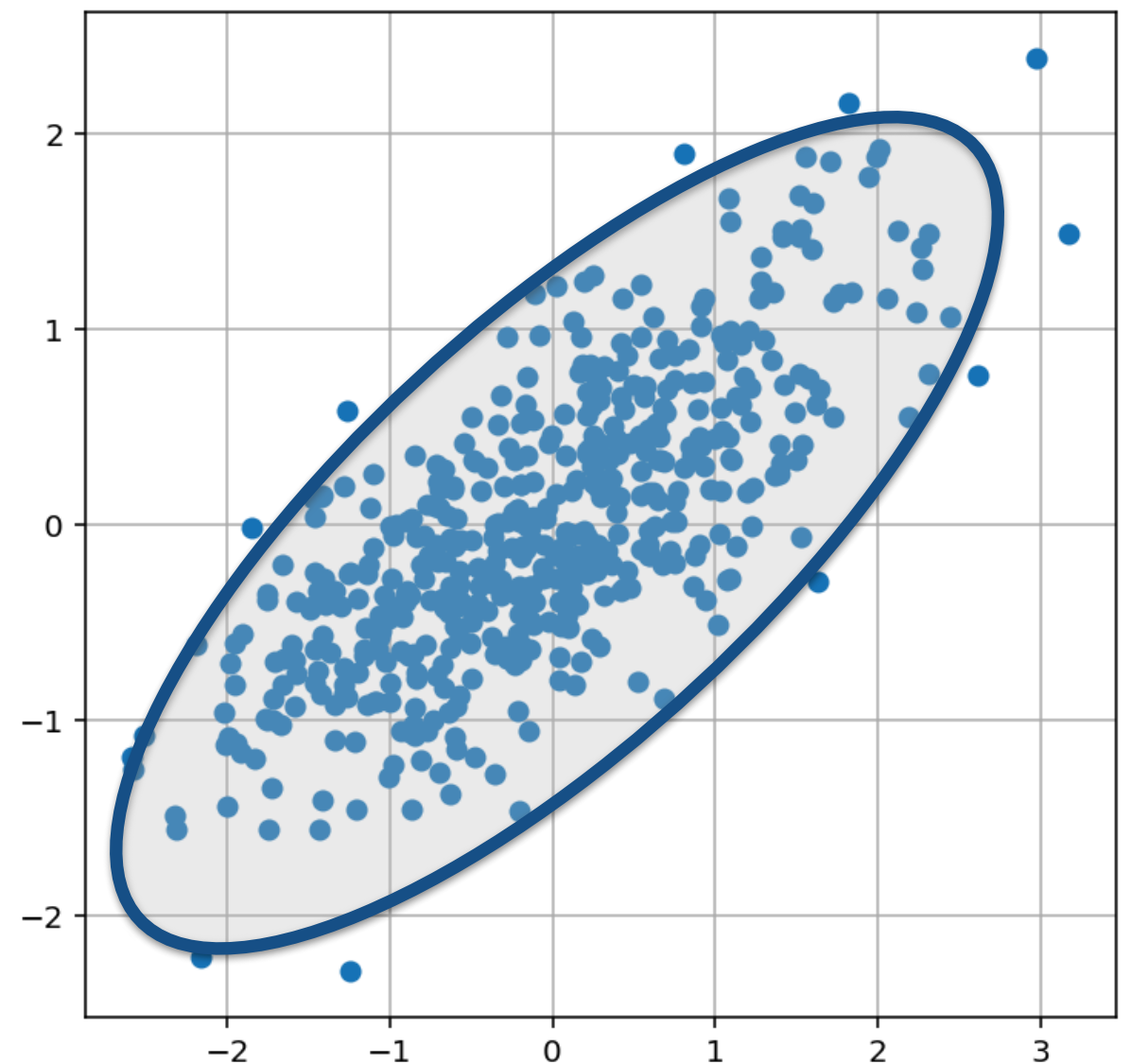
PCA

- * The typical explanation of PCA:
- * PCA “fits an ellipse” to a cloud of datapoints



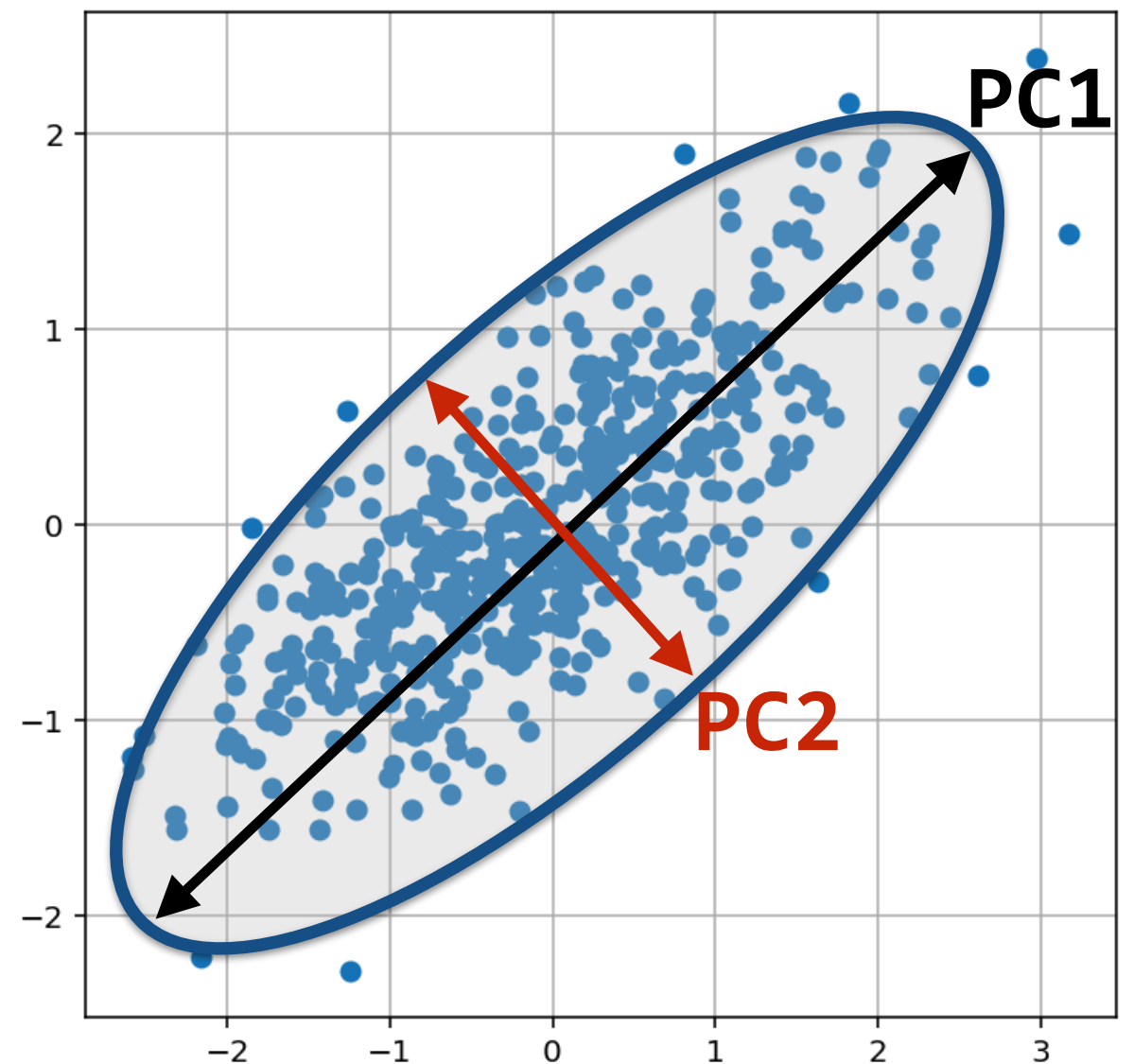
PCA

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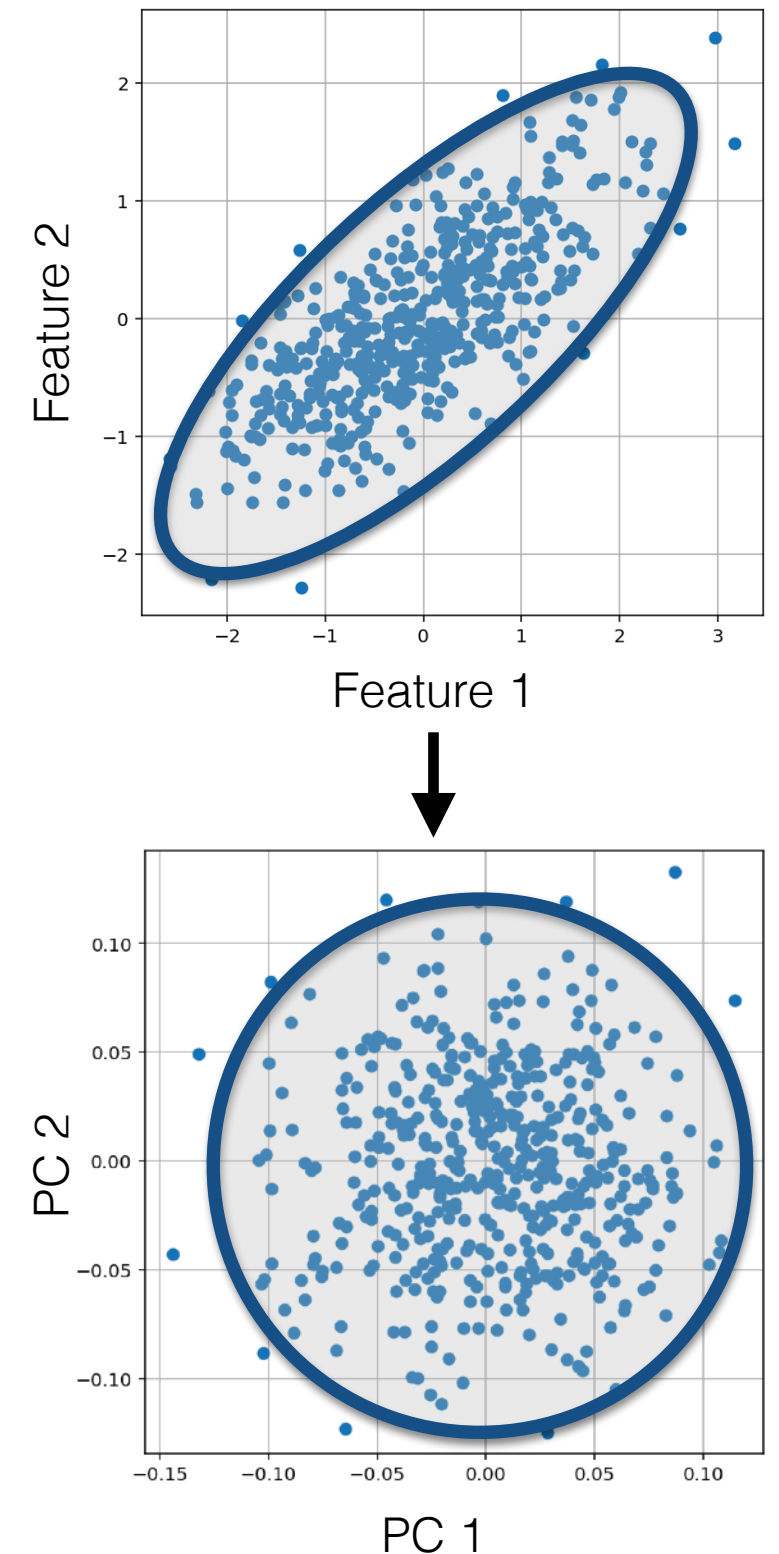
PCA

- * The axes of the ellipse are the “principal components”



PCA

- * It also gives you a way to *transform* the data so that the ellipse becomes a perfect circle

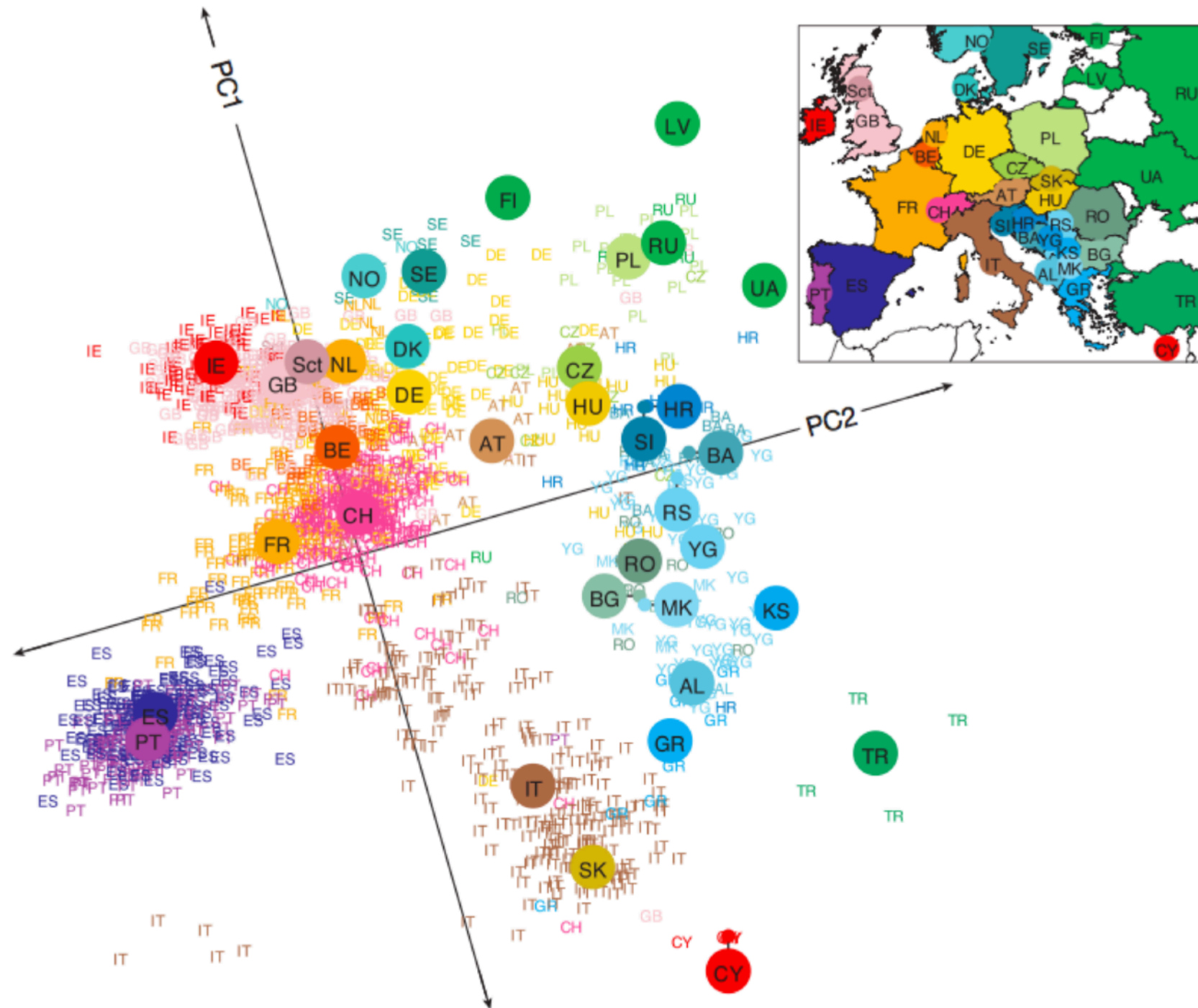


PCA

- * But the key use case of PCA is *dimensionality reduction*
- * If your data has lots of dimensions, PCA finds new dimensions along which the data vary a lot (the long axis of the ellipse)
- * and dimensions along which the data don't vary much at all, and can be ignored (the short axis)

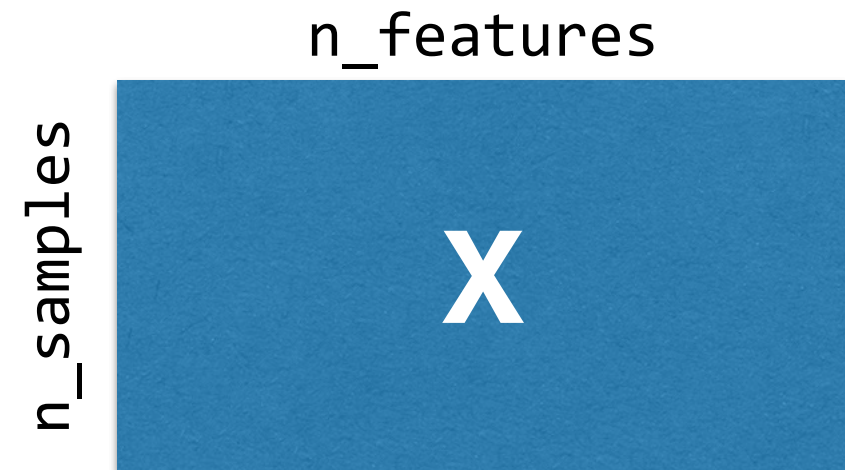
EXAMPLE : HUMAN GENETICS

- * Hundreds of Europeans are genotyped for thousands of genes
- * This info is reduced to 2 dimensions using PCA



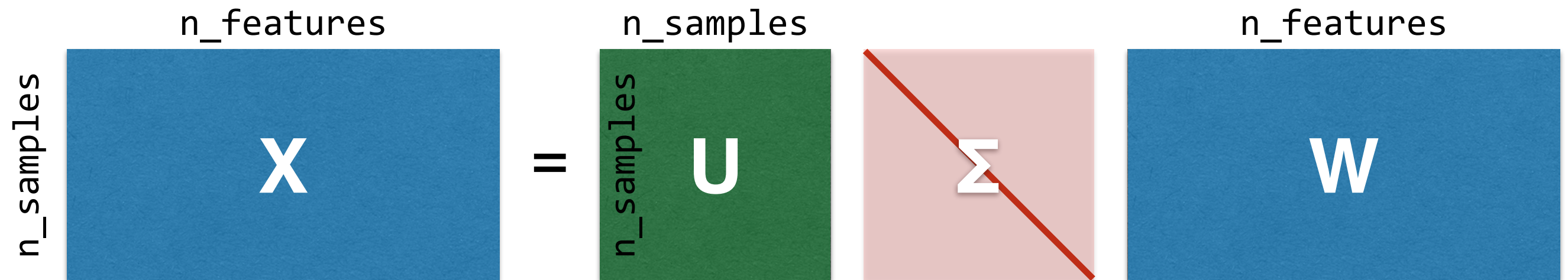
HOW DO YOU USE IT

- * The input to PCA is a matrix X with shape $(n_samples, n_features)$
- * (Assume that each column of X has zero mean. If this isn't true, you can make it true!)



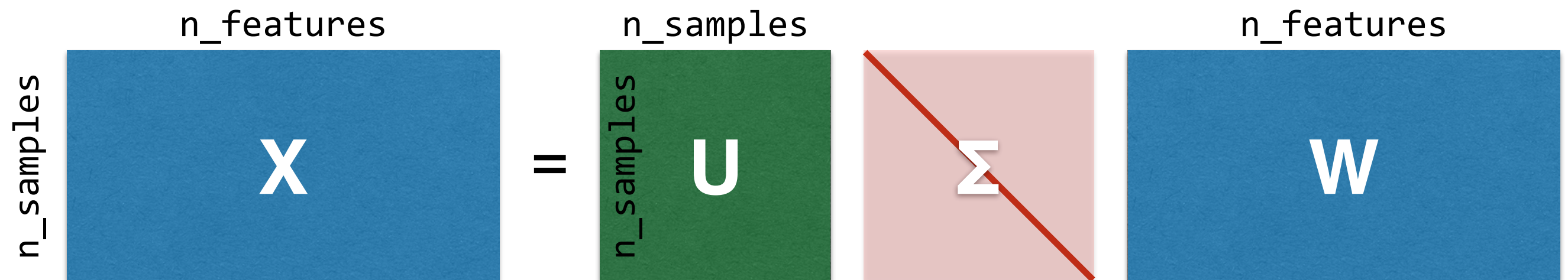
HOW DO YOU USE IT

- * PCA represents X as a product of 3 matrices: U , Σ , and W
- * (Here assuming that $n_features > n_samples$)



HOW DO YOU USE IT

- * **W** contains the **principal components** (each row is one)
- * **U** is the **score matrix**, which tells you how much of each PC is in each sample
- * **Sigma** is a diagonal matrix of **singular values**, which tell you how “big” (or important) each PC is

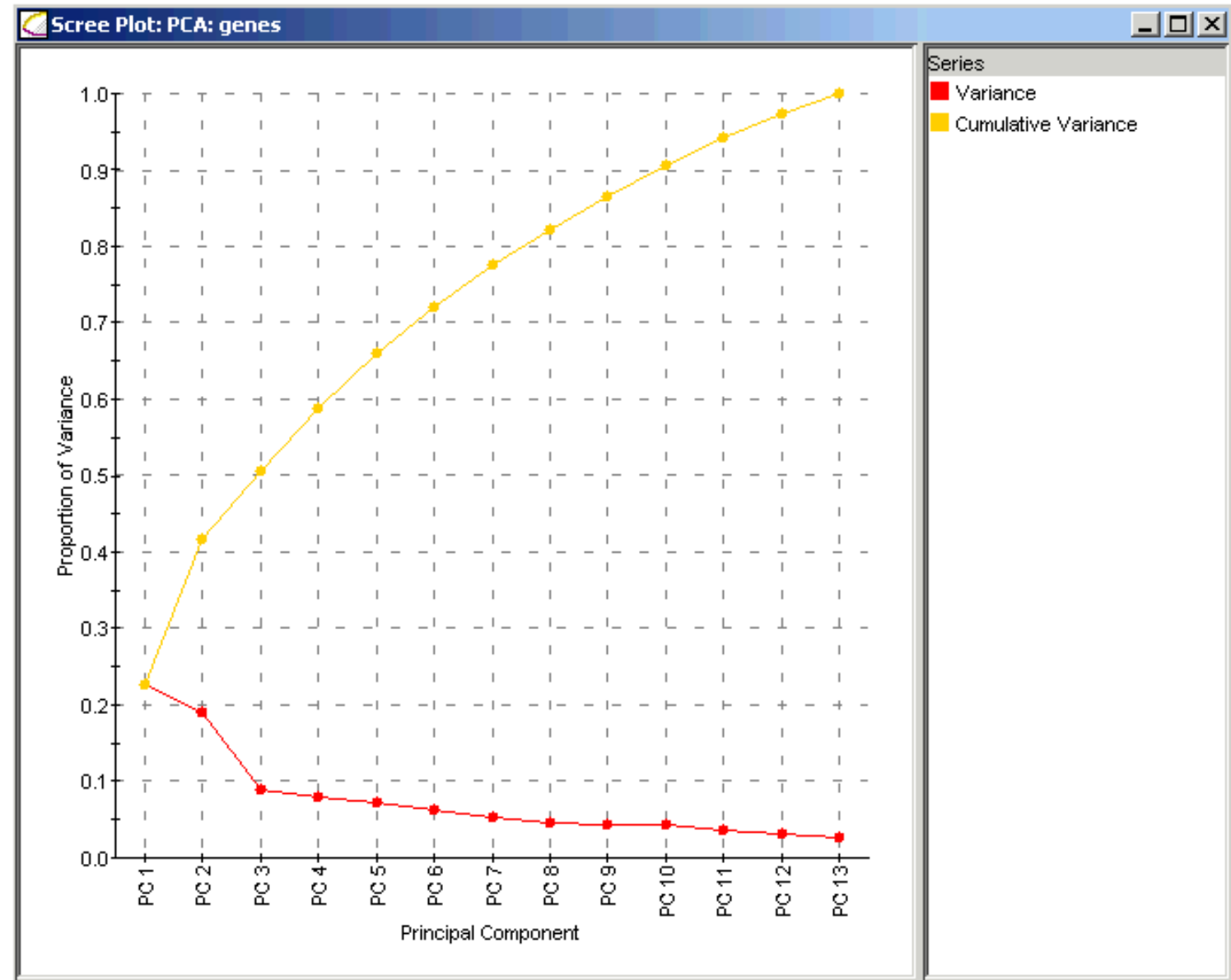


HOW DO YOU USE IT

- * You can then visualize the scores (data projected onto PCs), the PCs themselves, and the singular values

HOW DO YOU USE IT

- * Singular values are typically visualized as a “Scree plot”
- * this shows how much **variance** each component accounts for in the dataset



HOW DO YOU USE IT

- * (If you're familiar with the **singular value decomposition** (SVD), this is exactly the same thing)
- * you can use the SVD directly with **`np.linalg.svd`**

HOW DO YOU USE IT

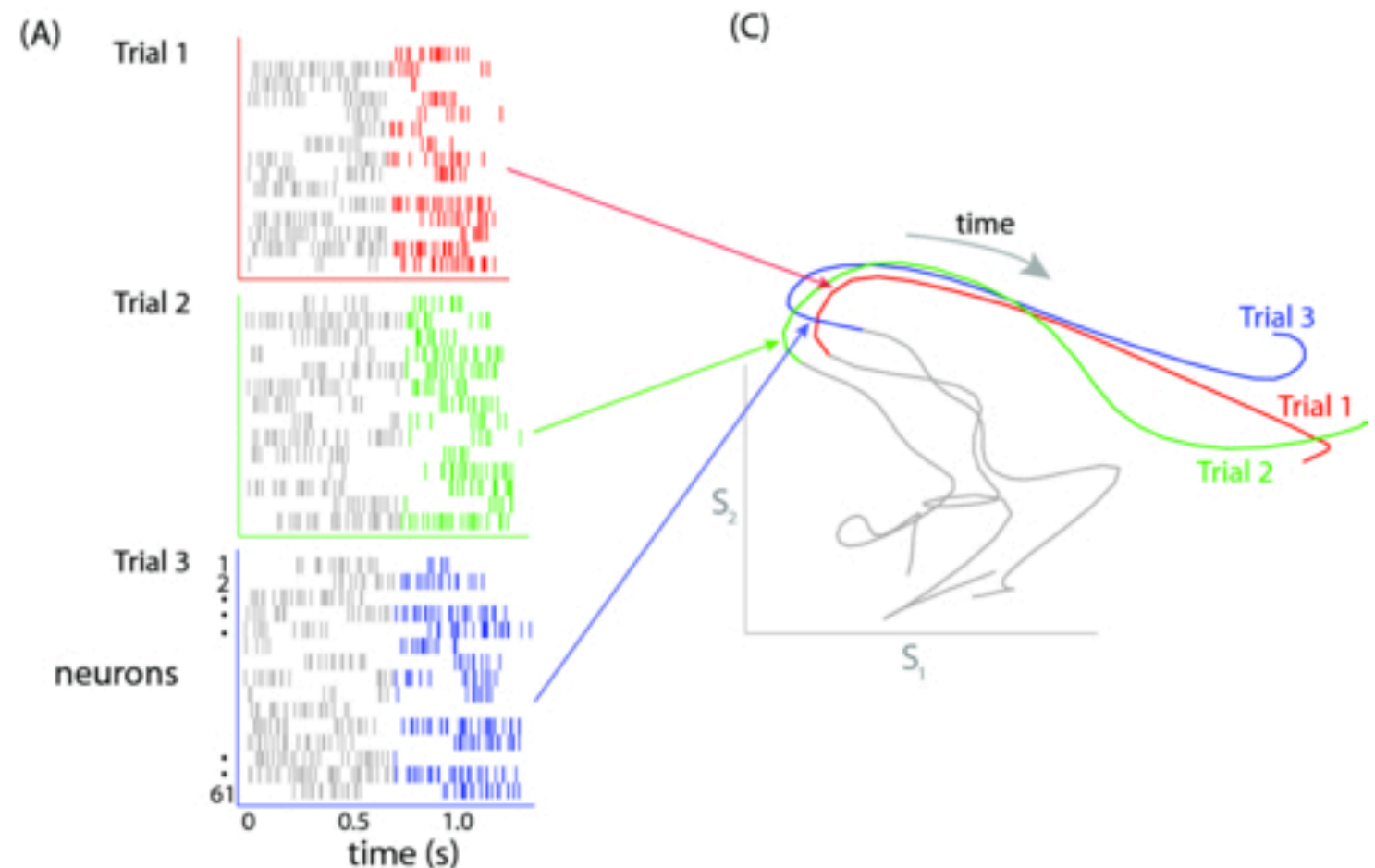
- * But it's better to do PCA through scikit-learn with `sklearn.decomposition.PCA`
- * (This has more options, and will do nice things like subtract the column means for you.)

PCA APPLICATIONS

- * PCA can be used for either *data analysis* or *data visualization* (and often both)
- * It should probably be your #1 go-to visualization tool whenever you have lots of features and don't know how to look at them

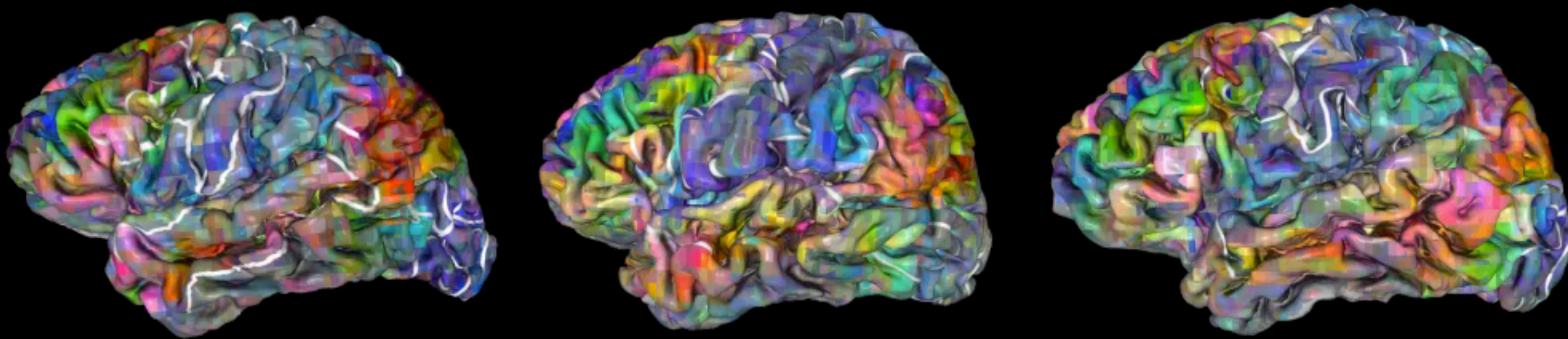
PCA APPLICATIONS

- * population analyses of neural activity
- * PCA gives a “neural state space”



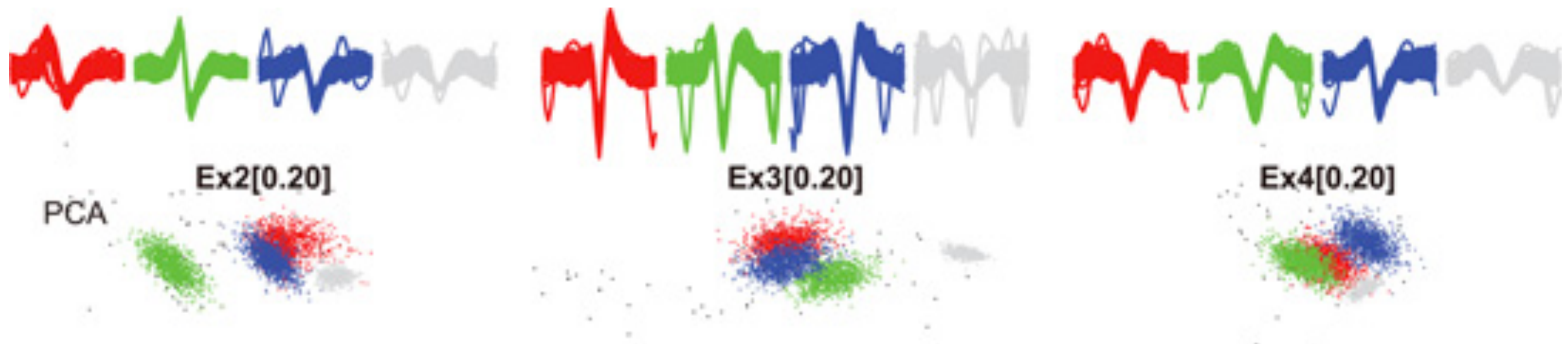
PCA APPLICATIONS

- * visualization of high-dimensional regression models



PCA APPLICATIONS

* spike sorting!

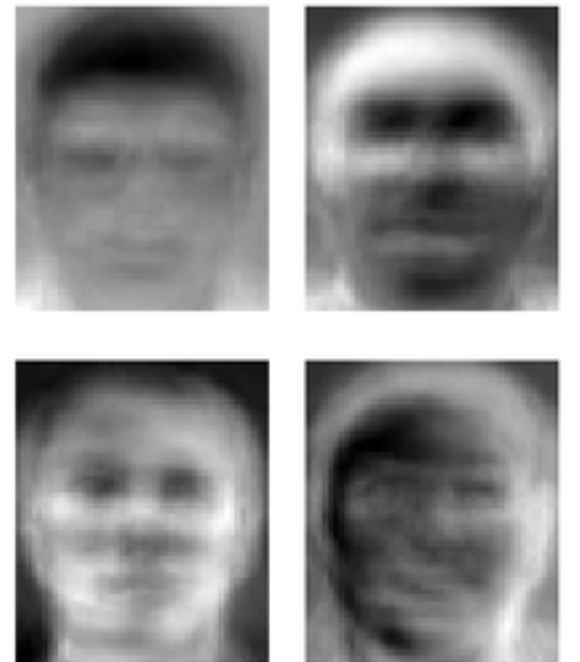


PCA APPLICATIONS

- * it's almost certain that PCA is something that *individual neurons do*
- * Hebbian learning (“neurons that fire together wire together”) results in a neuron learning the **first principal component** of its inputs

PCA APPLICATIONS

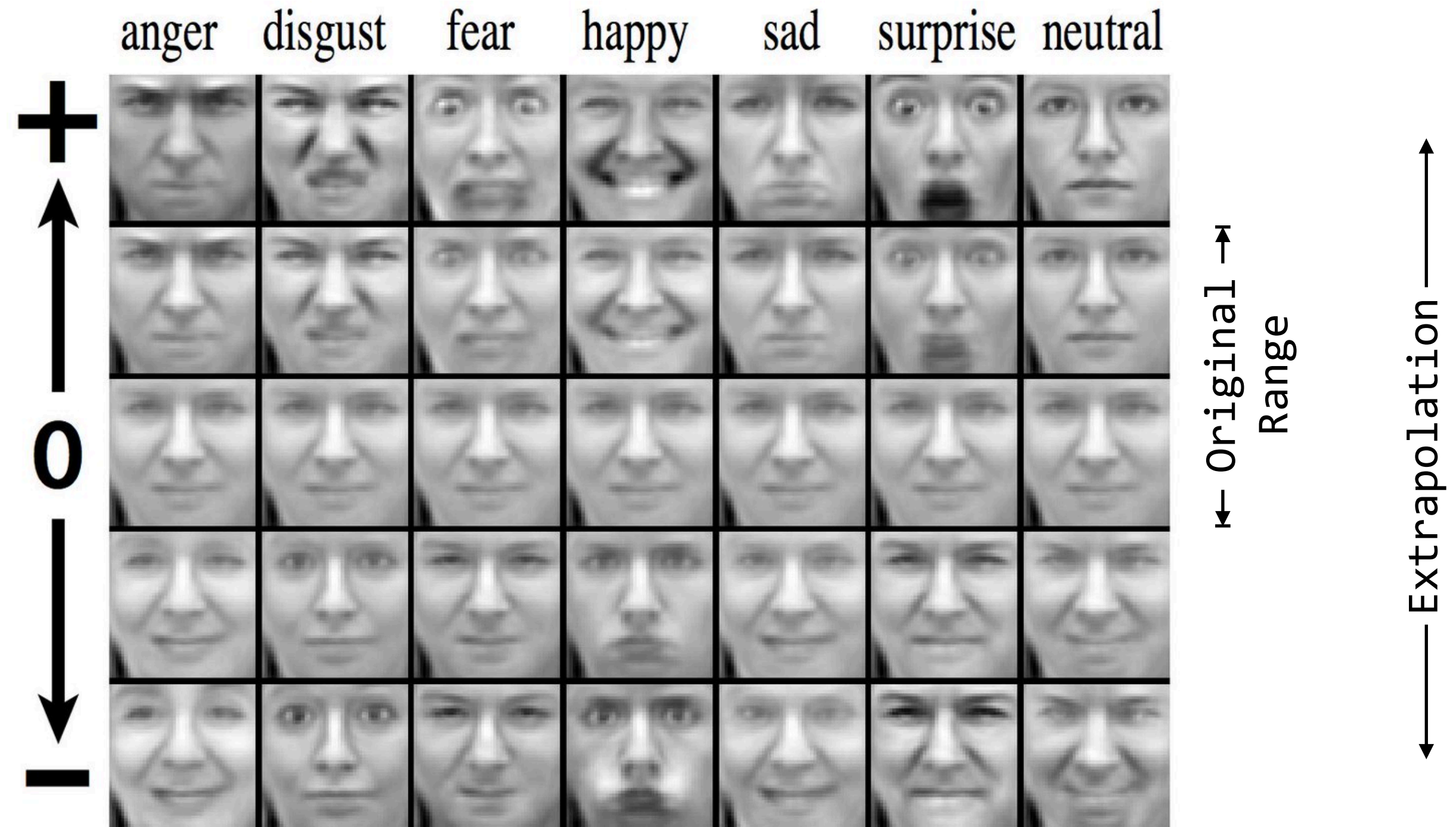
- * do PCA on a whole bunch of (aligned) face images to get “eigenfaces” – basis functions that all face images are built out of
- * it turns out this might be fundamental to how individual neurons represent faces! (Chang & Tsao, *Cell* 2017)



PCA EXTENSIONS: AUTOENCODERS

- * autoencoders are artificial neural networks that push each sample through a “bottleneck layer” and then try to reconstruct the original sample
- * simple (linear) autoencoders compute exactly PCA
- * more complicated ones can do very cool stuff

PCA EXTENSIONS: AUTOENCODERS



from Cheung, Livezey, Bansal, & Olshausen (2015)

MORE RESOURCES

- * If you want to learn more about PCA, see this great chapter from PDSH:
<https://jakevdp.github.io/PythonDataScienceHandbook/05.09-principal-component-analysis.html>

THANK YOU!