

Today.

Modelling.

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An Analysis of the Power of PCA.

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An Analysis of the Power of PCA.

Musing (rant?) about algorithms in the real world.

# Two populations.

DNA data:

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human1: A ... C ... T ... A

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Single Nucleotide Polymorphism.

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Model: same population breeds.

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Population 1: snp 843:  $\Pr[A] = .4$  ,  $\Pr[T] = .6$

Population 2: snp 843:  $\Pr[A] = .6$  ,  $\Pr[T] = .4$

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Individual:  $x_1, x_2, x_3, \dots, x_n$ .

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E.g., republican/democrat, shopper/saver.

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Population 1: snp  $i$ :  $\Pr[x_i = 1] = p_i^{(1)}$

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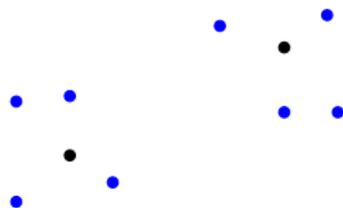
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Need  $d \gg \sigma^4/\varepsilon^4$ .

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Std deviation is  $\sigma^2$ !

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Std deviation is  $\sigma^2$ ! versus  $\sqrt{d}\sigma^2$ !

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No loss in signal!

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$$d\varepsilon^2 \gg \sigma^2.$$

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$$d\varepsilon^2 \gg \sigma^2.$$

$$\rightarrow d \gg \sigma^2/\varepsilon^2$$

Versus  $d \gg \sigma^4/\varepsilon^4$ .

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Std deviation is  $\sigma^2$ ! versus  $\sqrt{d}\sigma^2$ !

No loss in signal!

$$d\varepsilon^2 \gg \sigma^2.$$

$$\rightarrow d \gg \sigma^2/\varepsilon^2$$

Versus  $d \gg \sigma^4/\varepsilon^4$ .

A quadratic difference in amount of data!

Don't know much about...

Don't know  $\mu_1$  or  $\mu_2$ ?

# Without the means?

Sample of  $n$  people.

## Without the means?

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Some (say half) from population 1,

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**Near Neighbors Approach**

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### **Near Neighbors Approach**

Compute Euclidean distance squared.

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### **Near Neighbors Approach**

Compute Euclidean distance squared.

Cluster using threshold.

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### **Near Neighbors Approach**

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Signal  $E[d(x_1, x_2)] - E[d(x_1, y_1)]$

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### **Near Neighbors Approach**

Compute Euclidean distance squared.

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Signal  $E[d(x_1, x_2)] - E[d(x_1, y_1)]$   
should be larger than noise in  $d(x, y)$

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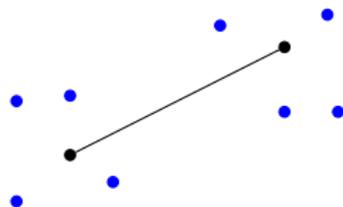
Best one can do?

# Principal components analysis.

Remember Projection!

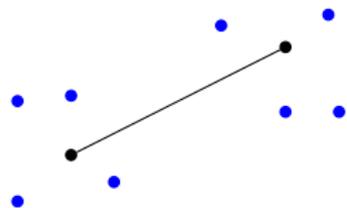
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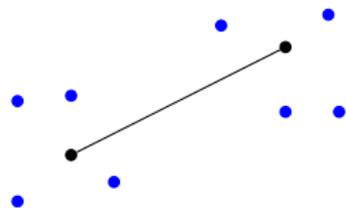
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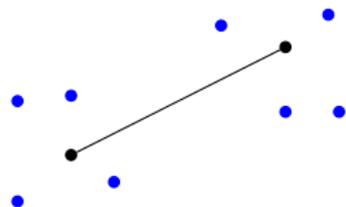


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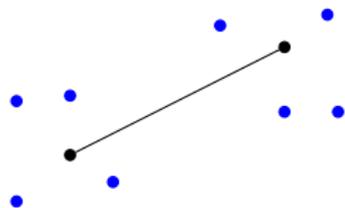
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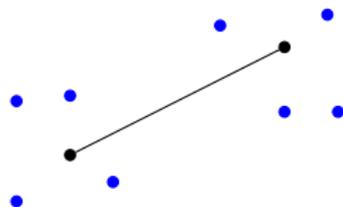
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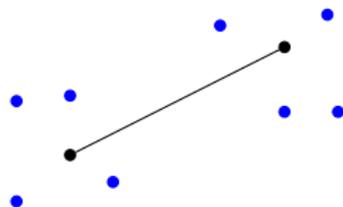
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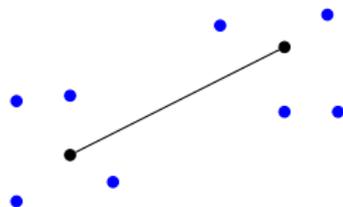
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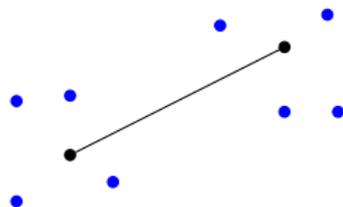
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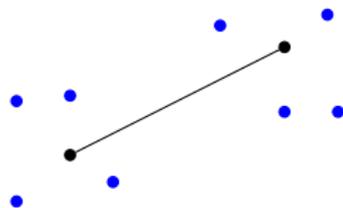
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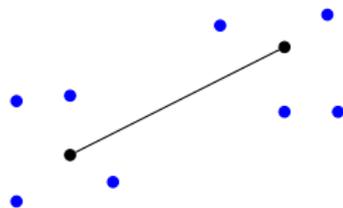
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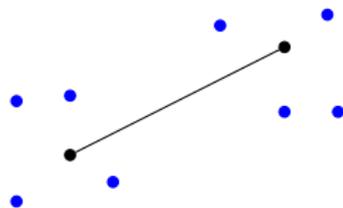
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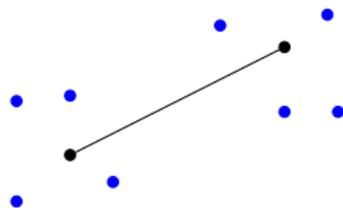
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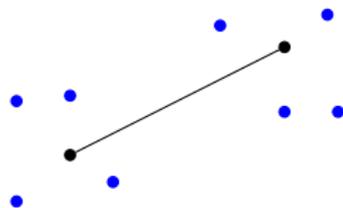
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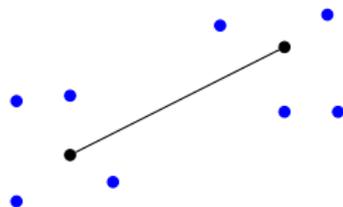
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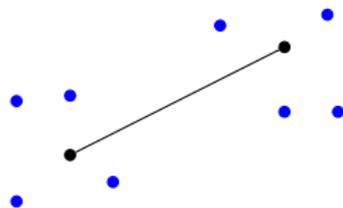
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PCA can reduce  $d$  to “knowing centers” case, with reasonable number of sample points.

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$x$  is composed of possibly smaller eigenvalue vectors.

## PCA calculation.

Matrix  $A$  where rows are points.

First eigenvector of  $B = A^T A$  is maximum variance direction.

$Av$  are projections onto  $v$ .

$$vBv = (vA)^T (Av) \text{ is } \sum_x (x \cdot v)^2.$$

First eigenvector,  $v$ , of  $B$  maximizes  $x^T Bx$ .

$$Bv = \lambda v \text{ for maximum } \lambda.$$

$$\rightarrow vBv = \lambda \text{ for unit } v.$$

Eigenvectors form orthonormal basis.

Any other vector  $av + x$ ,  $x \cdot v = 0$

$x$  is composed of possibly smaller eigenvalue vectors.

$$\rightarrow vBv \geq (av + x)B(av + x) \text{ for unit } v, av + x.$$

# Computing eigenvalues.

Power method:

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Choose random  $x$ .

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Repeat: Let  $x = Bx$ . Scale  $x$  to unit vector.

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Cluster Algorithm:

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Cluster Algorithm:

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Cluster Algorithm:

Choose random partition.

Repeat: Compute means of partition. Project, cluster.

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Choose random partition.

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Choose random  $+1/-1$  vector.

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Repeat: Compute means of partition. Project, cluster.

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Choose random partition.

Repeat: Compute means of partition. Project, cluster.

Choose random  $+1/-1$  vector. Multiply by  $A^T$  (direction between means), multiply by  $A$  (project points), cluster (round to  $+1/-1$  vector.)

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Choose random partition.

Repeat: Compute means of partition. Project, cluster.

Choose random  $+1/-1$  vector. Multiply by  $A^T$  (direction between means), multiply by  $A$  (project points), cluster (round to  $+1/-1$  vector.)

Sort of repeatedly multiplying by  $AA^T$ . Power method.

Sum up.

Clustering mixture of gaussians.

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Generic clustering algorithm is rounded version of power method.

See you on Tuesday.