

Welcome back.

Projects comments available on Glookup!

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Turn in homework!

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I am away April 15-20.

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Midterm out when I get back.

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Few days takehome.

Shiftable.

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Have handle on projects before that.

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Turn in homework!

I am away April 15-20.

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Few days takehome.

Shiftable.

Have handle on projects before that.

Progress report due Monday.

Two populations.

DNA data:

Two populations.

DNA data:

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

Two populations.

DNA data:

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

human2: C ... C ... A ... T

Two populations.

DNA data:

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

human2: C ... C ... A ... T

human3: A ... G ... T ... T

Two populations.

DNA data:

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

human2: C ... C ... A ... T

human3: A ... G ... T ... T

Single Nucleotide Polymorphism.

Two populations.

DNA data:

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

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Single Nucleotide Polymorphism.

Same population?

Two populations.

DNA data:

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

human2: C ... C ... A ... T

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Single Nucleotide Polymorphism.

Same population?

Model: same population breeds.

Two populations.

DNA data:

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

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Single Nucleotide Polymorphism.

Same population?

Model: same population breeds.

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

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

Two populations.

DNA data:

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

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Single Nucleotide Polymorphism.

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

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

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

Two populations.

DNA data:

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

human2: C ... C ... A ... T

human3: A ... G ... T ... T

Single Nucleotide Polymorphism.

Same population?

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

Which population?

Two populations.

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

Which population?

Comment: snps could be movie preferences, populations could be types.

Two populations.

DNA data:

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

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Which population?

Comment: snps could be movie preferences, populations could be types.

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

Which population?

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

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Which population?

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Which population?

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

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

Population 2: snp i : $\Pr[x_i = 0] = p_i^{(2)}$

Which population?

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

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Simpler Calculation:

Which population?

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Simpler Calculation:

Population 1: Gaussian with mean $\mu_1 \in R^d$, variance σ in each dim.

Population 2: Gaussian with mean $\mu_2 \in R^d$, variance σ in each dim.

Which population?

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

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

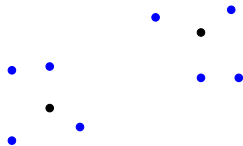
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Gaussians

Population 1: Gaussian with mean $\mu_1 \in R^d$, std deviation σ in each dim.

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Difference between humans σ per snp.

Difference between populations ε per snp.

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How many snps to collect to determine population for individual x ?

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$$E[(x - \mu_1)^2] = d\sigma^2$$

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$$E[(x - \mu_1)^2] = d\sigma^2$$

$$E[(x - \mu_2)^2] \geq (d - 1)\sigma^2 + (\mu_1 - \mu_2)^2.$$

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If $(\mu_1 - \mu_2)^2 = d\varepsilon^2 \gg \sigma^2$, then different.

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Variance of estimator?

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Variance of estimator?

Roughly $d\sigma^4$.

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Roughly $d\sigma^4$.

Signal is difference between expectations.

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Roughly $d\sigma^4$.

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roughly $d\varepsilon^2$

Signal \gg Noise. $\leftrightarrow d\varepsilon^2 \gg \sqrt{d}\sigma^2$.

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Roughly $d\sigma^4$.

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Signal \gg Noise. $\leftrightarrow d\varepsilon^2 \gg \sqrt{d}\sigma^2$.

Need data $\approx 4/\varepsilon^2$

Projection

Population 1: Gaussian with mean $\mu_1 \in \mathbb{R}^d$, variance σ in each dim.

Population 2: Gaussian with mean $\mu_2 \in \mathbb{R}^d$, variance σ in each dim.

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Project x onto unit vector v in direction $\mu_2 - \mu_1$.

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Project x onto unit vector v in direction $\mu_2 - \mu_1$.

$E[((x - \mu_1) \cdot v)^2] = 0$ if x is population 1.

Projection

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Project x onto unit vector v in direction $\mu_2 - \mu_1$.

$E[((x - \mu_1) \cdot v)^2] = \sigma$ if x is population 1.

$E[((x - \mu_2) \cdot v)^2] \geq \varepsilon$ if x is population 2.

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Std deviation is $\sqrt{\sigma}$!

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$E[((x - \mu_1) \cdot v)^2] = 0$ if x is population 1.

$E[((x - \mu_2) \cdot v)^2] \geq (\mu_1 - \mu_2)^2$ if x is population 2.

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

Projection

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

No loss in signal!

Projection

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

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

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

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

No loss in signal!

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

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

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

Projection

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

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

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

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

A quadratic difference in amount of data!

Don't know much about...

Don't know μ_1 or μ_2 ?

Without the means?

Sample of n people.

Without the means?

Sample of n people.

Some (say half) from population 1,

Without the means?

Sample of n people.

Some (say half) from population 1,
some from population 2.

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Which are which?

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Near Neighbors Approach

Without the means?

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Which are which?

Near Neighbors Approach

Compute Euclidean distance squared.

Without the means?

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Near Neighbors Approach

Compute Euclidean distance squared.

Cluster using threshold.

Without the means?

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Near Neighbors Approach

Compute Euclidean distance squared.

Cluster using threshold.

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

Without the means?

Sample of n people.

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Which are which?

Near Neighbors Approach

Compute Euclidean distance squared.

Cluster using threshold.

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

Without the means?

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Where x 's from one population, y 's from other.

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Signal is proportional $d\epsilon^2$.

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Noise is proportional to $\sqrt{d}\sigma^2$.

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$d \gg \sigma^4/\varepsilon^4 \rightarrow$ same type people closer to each other.

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$d \gg (\sigma^4/\varepsilon^4) \log n$ suffices for threshold clustering.

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$d \gg (\sigma^4/\varepsilon^4) \log n$ suffices for threshold clustering.

$\log n$ factor for union bound over $\binom{n}{2}$ pairs.

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Compute Euclidean distance squared.

Cluster using threshold.

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

should be larger than noise in $d(x, y)$

Where x 's from one population, y 's from other.

Signal is proportional $d\varepsilon^2$.

Noise is proportional to $\sqrt{d}\sigma^2$.

$d \gg \sigma^4/\varepsilon^4 \rightarrow$ same type people closer to each other.

$d \gg (\sigma^4/\varepsilon^4) \log n$ suffices for threshold clustering.

$\log n$ factor for union bound over $\binom{n}{2}$ pairs.

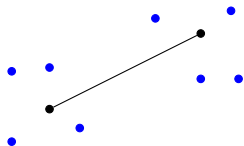
Best one can do?

Principal components analysis.

Remember Projection!

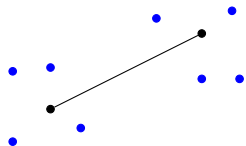
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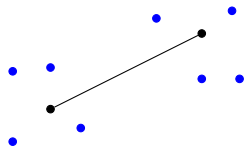
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Don't know μ_1 or μ_2 ?

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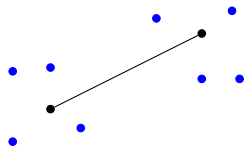


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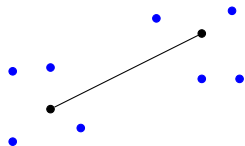
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Principal component analysis:

Find direction, v , of maximum variance.

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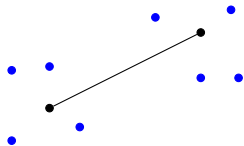
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Maximize $\sum(x \cdot v)^2$ (zero center the points)

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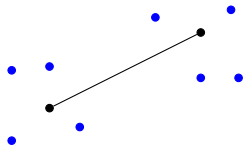
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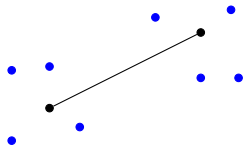
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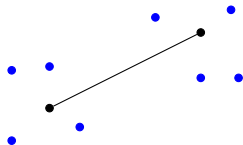
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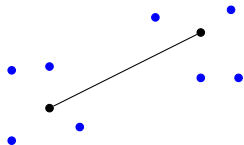
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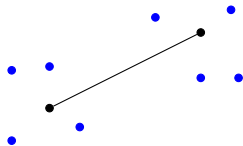
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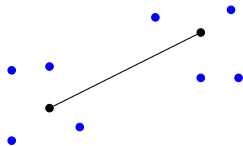
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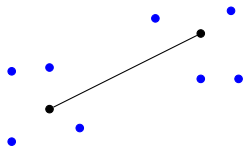
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When will PCA pick correct direction with good probability?

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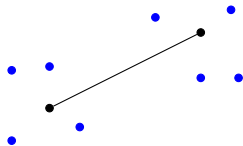
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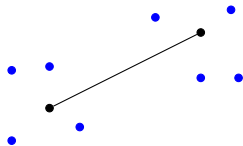
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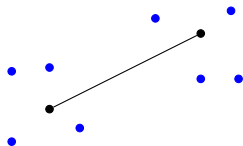
When will PCA pick correct direction with good probability?

Union bound over directions. How many directions?

Infinity

Principal components analysis.

Remember Projection!



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When will PCA pick correct direction with good probability?

Union bound over directions. How many directions?

Infinity and beyond!

Nets

“ δ - Net”.

Nets

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Set \mathcal{D} of directions

Nets

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where all others, v , are close to $x \in \mathcal{D}$.

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

PCA calculation.

Matrix A where rows are points.

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

Computing eigenvalues.

Power method:

Computing eigenvalues.

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Choose random x .

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

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$$x = a_1 v_1 + a_2 v_2 + \dots$$

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$$x_t \propto B^t x = a_1 \lambda_1^t v_1 + a_2 \lambda_2^t v_2 + \dots$$

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Mostly v_1 after a while since $\lambda_1^t \gg \lambda_2^t$.

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Cluster Algorithm:

Choose random partition.

Computing eigenvalues.

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Cluster Algorithm:

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Repeat: Compute means of partition. Project, cluster.

Computing eigenvalues.

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Cluster Algorithm:

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Repeat: Compute means of partition. Project, cluster.

Choose random $+1/-1$ vector.

Computing eigenvalues.

Power method:

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Cluster Algorithm:

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Repeat: Compute means of partition. Project, cluster.

Choose random $+1/-1$ vector. Multiply by A^T (direction between means),

Computing eigenvalues.

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Computing eigenvalues.

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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 .

Computing eigenvalues.

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

$$x = a_1 v_1 + a_2 v_2 + \dots$$

$$x_t \propto B^t x = a_1 \lambda_1^t v_1 + a_2 \lambda_2^t v_2 + \dots$$

Mostly v_1 after a while since $\lambda_1^t \gg \lambda_2^t$.

Cluster Algorithm:

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.

Sum up.

Clustering mixture of gaussians.

Near Neighbor works with sufficient data.

Sum up.

Clustering mixture of gaussians.

Near Neighbor works with sufficient data.

Projection onto subspace of means is better.

Sum up.

Clustering mixture of gaussians.

Near Neighbor works with sufficient data.

Projection onto subspace of means is better.

Principal component analysis can find subspace of means.

Sum up.

Clustering mixture of gaussians.

Near Neighbor works with sufficient data.

Projection onto subspace of means is better.

Principal component analysis can find subspace of means.

Power method computes principal component.

Sum up.

Clustering mixture of gaussians.

Near Neighbor works with sufficient data.

Projection onto subspace of means is better.

Principal component analysis can find subspace of means.

Power method computes principal component.

Generic clustering algorithm is rounded version of power method.

See you on Thursday.