Functional genomics
+
Data mining

BCH339N Systems Biology / Bioinformatics – Spring 2016
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Functional genomics

= field that attempts to use the vast data produced by genomic projects (e.g. genome sequencing projects) to describe gene (and protein) functions and interactions.

Focuses on dynamic aspects, e.g. transcription, translation, and protein–protein interactions, as opposed to static aspects of the genome such as DNA sequence or structures.

Adapted from Wikipedia
Functional genomics + Data mining

= field that attempts to computationally discover patterns in large data sets

Adapted from Wikipedia
We’re going to first learn about clustering algorithms & classifiers

**Clustering** = task of grouping a set of objects in such a way that objects in the same group (a **cluster**) are more similar (in some sense) to each other than to those in other groups (clusters).

Adapted from Wikipedia
We’re going to first learn about clustering algorithms & classifiers

**Classification** = task of categorizing a new observation, on the basis of a training set of data with observations (or instances) whose categories are known

Let’s motivate this with an example:

**Distinct types of diffuse large B-cell lymphoma identified by gene expression profiling**


Nature 2000
“Diffuse large B-cell lymphoma (DLBCL), the most common subtype of non-Hodgkin's lymphoma ... is one disease in which attempts to define subgroups on the basis of morphology have largely failed...”

“DLBCL ... is clinically heterogeneous: 40% of patients respond well to current therapy and have prolonged survival, whereas the remainder succumb to the disease.

We proposed that this variability in natural history reflects unrecognized molecular heterogeneity in the tumours.”

Refresher: Profiling mRNA expression with DNA microarrays

DNA molecules are attached to a solid substrate, then... probed with a labeled (usually fluorescent) DNA sequence

Wikipedia
Refresher: Profiling mRNA expression with DNA microarrays

Sample

Purification

RT

Coupling

Note that some arrays are 1-color, some are 2. Why?
Back to diffuse large B-cell lymphoma...

96 patient biopsies
(normal and malignant lymphocyte samples)

Extract mRNA from each sample

Perform DNA microarray experiment on each to
measure mRNA abundances (~1.8 million total gene
expression measurements)

Cluster samples by their expression patterns

Red = high expression
Green = low

(yes, I know it’s exactly backwards from what
you might expect.)

Hierarchical clustering of the gene
expression data
Genes can be found whose expression is specific to germinal centre B cells, and different across DLBCL’s

We can break up the DLBCL’s according the germinal B-cell specific gene expression:
What good is this? These molecular phenotypes predict clinical survival.

Kaplan-Meier plot of patient survival

Nature 2000

What good is this? These molecular phenotypes predict clinical survival.

Grouping patients by clinical prognostic index

Regrouping low risk patients by gene expression

Nature 2000
Gene expression, and other molecular measurements, provide far deeper phenotypes for cells, tissues, and organisms than traditional measurements.

Now, tons of work using these approaches to diagnose specific forms of disease, as well as to discover functions of genes and many other applications.

So, how does clustering work?

First, let’s think about the data, e.g. as for gene expression. From one sample, using DNA microarrays or RNA-seq, we get:

For yeast, \( N \sim 6,000 \)
For human, \( N \sim 22,000 \)

\( \text{i.e., a vector of } N \text{ numbers} \)
So, how does clustering work?

Every additional sample adds another column, giving us a matrix of data:

**$M$ samples**

<table>
<thead>
<tr>
<th>$N$ genes</th>
<th>$M$ samples</th>
</tr>
</thead>
<tbody>
<tr>
<td>Gene 1, sample 1</td>
<td>Gene 1, sample j</td>
</tr>
<tr>
<td>Gene 2, sample 1</td>
<td>Gene 2, sample j</td>
</tr>
<tr>
<td>.</td>
<td>.</td>
</tr>
<tr>
<td>Gene $i$, sample 1</td>
<td>Gene $i$, sample j</td>
</tr>
<tr>
<td>.</td>
<td>.</td>
</tr>
<tr>
<td>Gene $N$, sample 1</td>
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</tr>
</tbody>
</table>

For yeast, $N \sim 6,000$
For human, $N \sim 22,000$

i.e., a matrix of $N \times M$ numbers

So, how does clustering work?

Every gene has a **feature vector** of $M$ numbers associated with it.
So, how does clustering work?

<table>
<thead>
<tr>
<th>N genes</th>
<th>M samples</th>
</tr>
</thead>
<tbody>
<tr>
<td>Gene 1, sample 1</td>
<td>...</td>
</tr>
<tr>
<td>Gene 2, sample 1</td>
<td>...</td>
</tr>
<tr>
<td>...</td>
<td>...</td>
</tr>
<tr>
<td>Gene N, sample 1</td>
<td>...</td>
</tr>
</tbody>
</table>

Similarly, every sample has a **feature vector** of \( N \) numbers associated with it.

The first clustering method we’ll learn about simply groups the objects (samples or genes) in a hierarchy by the similarity of their feature vectors.
A hierarchical clustering algorithm

Start with each object in its own cluster

Until there is only one cluster left, repeat:
  Among the current clusters, find the two most similar clusters
  Merge those two clusters into one

We can choose our measure of similarity and how we merge the clusters

Hierarchical clustering

*Conceptually*

Data points on an X-Y plane

Dendrogram (grouped by closeness)
We’ll need to measure the similarity between feature vectors. Here are a few (of many) common distance measures used in clustering.

<table>
<thead>
<tr>
<th>Names</th>
<th>Formula</th>
</tr>
</thead>
<tbody>
<tr>
<td>Euclidean distance</td>
<td>$| a - b |_2 = \sqrt{\sum_i (a_i - b_i)^2}$</td>
</tr>
<tr>
<td>Manhattan distance</td>
<td>$| a - b |_1 = \sum_i</td>
</tr>
<tr>
<td>cosine similarity</td>
<td>$\frac{a \cdot b}{|a| |b|}$</td>
</tr>
</tbody>
</table>

Back to the B cell lymphoma example

**Hierarchical clustering**

Similarity measure = Pearson correlation coefficient between gene expression vectors

Similarity between clusters = average similarity between individual elements of each cluster (also called average linkage clustering)
K-means clustering is a common alternative clustering approach *mainly because it’s easy and can be quite fast!*

The basic algorithm:
1. Pick a number \((k)\) of cluster centers
2. Assign each gene to its nearest cluster center
3. Move each cluster center to the mean of its assigned genes
4. Repeat steps 2 & 3 until convergence

*See the K-means example posted on the web site*
A 2-dimensional example: hierarchical

A 2-dimensional example: \( k \)-means
Some features of K-means clustering

• Depending on how you seed the clusters, it may be stochastic. You may not get the same answer every time you run it.
• Every data point ends up in exactly 1 cluster (so-called hard clustering)
• Not necessarily obvious how to choose \( k \)
• Great example of something we’ve seen already: Expectation-Maximization (E-M) algorithms

EM algorithms alternate between assigning data to models (here, assigning points to clusters) and updating the models (calculating new centroids)
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- **Let’s think about this aspect for a minute.**
  
  Why is this good or bad? How could we change it?

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\[ k\text{-means} \]

The basic algorithm:

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2. Assign each gene to its nearest cluster center
3. Move each cluster center to the mean of its assigned genes
4. Repeat steps 2 & 3 until convergence
Fuzzy $k$-means

The basic algorithm:
1. Choose $k$. Randomly assign cluster centers.
2. Fractionally assign each gene to each cluster:
   \[ \text{e.g. occupancy (} g_i, m_j \text{)} = \frac{e^{-|g_i - m_j|^2}}{\sum_j e^{-|g_i - m_j|^2}} \]
   Note: $||x||$ is just shorthand for the length of the vector $x$.
   $g_i$ = gene $i$
   $m_j$ = centroid of cluster $j$
3. For each cluster, calculate weighted mean of genes to update cluster centroid
4. Repeat steps 2 & 3 until convergence
Iterating fuzzy k-means
A fun clustering strategy that builds on these ideas: Self-organizing maps (SOMs)

- Combination of clustering & visualization
- Invented by Teuvo Kohonen, also called Kohonen maps

SOMs have:

1. your data (points in some high-dimensional space)
2. a grid of nodes, each node also linked to a point someplace in data space

1. First, SOM nodes are arbitrarily positioned in data space. Then:
2. Choose a training data point. Find the node closest to that point.
3. Move its position closer to the training data point.
4. Move its grid neighbors closer too, to a lesser extent.

Repeat 2-4. After many iterations, the grid approximates the data distribution.
Here’s an example using colors. Each color has an RGB vector. Take a bunch of random colors and organize them into a map of similar colors:

Here’s the input color data → …

Each SOM node lives in RGB space →

Here’s the SOM →

Iteratively test new colors, update the map using some rule

\[ m_i(t+1) = m_i(t) + \alpha(t)[x(t) - m_i(t)] \]

for each \( i \in N_i(t) \),

The weight and node neighborhoods shrink with time (iterations)

Over time, the map self-organizes to show clusters of like colors.

http://www.generation5.org/content/2004/kohonenApplications.asp
http://users.ics.aalto.fi/tho/thesis/
A SOM of U.S. Congress voting patterns

Exploratory Analysis of CIA Factbook Data Using
Kohonen Self-Organizing Maps

CS-BIGS 3(1): 48-59
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Exploratory Analysis of CIA Factbook Data Using Kohonen Self-Organizing Maps

SOM of Wikipedia (from Wikipedia, naturally)
(data = wiki article word frequency vectors)
SOMs can accommodate unusual data distributions

One-dimensional SOM

Data points

Wikipedia

A biological example, analyzing mRNA expression

Proc. Natl. Acad. Sci. USA
Vol. 96, pp. 2807-2812, March 1999
Genetics

Interpreting patterns of gene expression with self-organizing maps: Methods and application to hematopoietic differentiation

Pablo Tamayo*, Donna Slonim*, Jill Mesirov*, Qing Zhu¹, Suttipon Kitareewan, Ethan Dmitrovsky¹, Eric S. Lander*², and Todd R. Golub*²

Vol. 96, pp. 2807-2812, March 1999
Genetics
A biological example, analyzing mRNA expression

Yeast cell division cycle
- Synchronized cells
- Collect mRNAs at time points
- DNA microarrays