Loyola Genomics Facility

Michael J. Zilliox
Loyola Genomics Facility

- Loyola Genomics Facility (Google “Loyola Genomics”)
- genomics.luc.edu
- Research Channel in Loyola Wired
- Ion Torrent Personal Genome Machine
- 2 Illumina MiSeq Sequencers
- Gina Kuffel- Lab Manager

- Funding:
  - P01- Nishimura
  - R01- Le Poole
  - R56- Brubaker
  - P20- Wolfe
  - RFC- Hutchens
  - Astellas
  - Kimberly-Clark
Collaborating Facilities

• University of Chicago
  – Illumina microarrays
  – RNA-Seq

• Notre Dame
  – RNA-Seq
  – Proteomics

• Johns Hopkins
  – Affymetrix microarrays
Protocols

• Amplicon Sequencing
  – Variant analysis
  – 16S rRNA sequencing
    (microbiome, virome, fungiome)

• Whole Genome Sequencing
  – Bacterial genomes
  – Viral genomes

• Gene Expression Analysis
  – Affymetrix, Illumina bead arrays,
    Illumina RNA-Seq, NanoString,
    bacterial RNA-seq,
  – miRNA-seq
Beyond Heatmaps
Classic Gene Expression Analysis
Classic Gene Expression Analysis

Control

Experimental Sample

Up-regulated

Down-regulated
New Gene Expression Analysis

Control

Experimental Sample

Up-regulated

No Change

Down-regulated
New Gene Expression Analysis

Control

Experimental Sample

Up-regulated

No Change
Why???

• Determine the components of normal cells
• Discover genes missed due to variation
• Find genes that are potentially co-regulated
• Discover biomarkers/make clinical predictions
Example 1- Naive, Normal Components
# Human Immune Cell Transcriptomes

<table>
<thead>
<tr>
<th>Cell Type</th>
<th>N</th>
<th>Genes Expressed</th>
<th>Immune-specific</th>
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<tbody>
<tr>
<td>Broadly Expressed</td>
<td>3212</td>
<td>1319</td>
<td>0</td>
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<tr>
<td>CD8+ T cells</td>
<td>4</td>
<td>4510</td>
<td>68</td>
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<tr>
<td>CD4+ T cells</td>
<td>9</td>
<td>4083</td>
<td>37</td>
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<tr>
<td>B cells</td>
<td>4</td>
<td>5066</td>
<td>192</td>
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<tr>
<td>CD14+ monocytes</td>
<td>13</td>
<td>3652</td>
<td>42</td>
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<tr>
<td>Alveolar macrophages</td>
<td>11</td>
<td>4465</td>
<td>178</td>
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</table>
Human Naïve CD8+ T Cell


*Rough ER and Smooth ER are combined

Image from Wikimedia Commons: Authors MesserWoland and Szczepan1990
Proteome Comparison

- B Cells
- CD4 T Cells
- CD8 T Cells
Example 2- Discover genes missed due to variation
Finding Variable Genes

CD82

MAL2
Classic Analysis

Up-regulated

Classic

Barcode

321
781
547
Example 3 - Find genes that are potentially co-regulated
New Gene Expression Analysis

Control → Enhancer? → Experimental Sample

Control → Transcription Factor? → Experimental Sample

Control → No Change
Example 4 - Discover Biomarkers
Biomarker Discovery

Gene 1 - Up-regulated 2 fold
Gene 2 - Off in whole cell/On in tumor
Survival

William Adams
## Models

<table>
<thead>
<tr>
<th></th>
<th>Hazard Ratio</th>
<th>95% CI</th>
<th>P value</th>
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<tbody>
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<td><strong>Model 1</strong></td>
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<tr>
<td>Spectrin</td>
<td>4.29</td>
<td>1.60-11.51</td>
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<tr>
<td>CAND1</td>
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<td>0.26-3.82</td>
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<td>HNRDL</td>
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<td>0.91-18.67</td>
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<td>Spectrin</td>
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<td>1.37-8.57</td>
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<tr>
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<td>0.001</td>
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<tr>
<td><strong>Model 4</strong></td>
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<td>Spectrin</td>
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<td>1.52-9.76</td>
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<td>Stage III and IV (vs I and II)</td>
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<td>ECE</td>
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Acknowledgements

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• Katherine Radek

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• Mark Rubinstein
• Elizabeth Garrett-Mayer

Others
• Rafael Irizarry
• Matt McCall
• Harris Jaffee

Barcode website: Google “Gene Expression Barcode”
barcode.luhs.org
The End