Everything you wanted to know about RNAseq

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Overview

- RNAseq
 - Goals
 - Introduction
 - Central Dogma
 - Measuring RNA
- Project Groups

Today's Goals

- How does RNAseq work?
- What are the benefits?
- What are the challenges?
- Meet your group!

Dotstorming

- What questions did you have?
- Dotstorming Board
- Write your question
- Vote on others
- (Take 5 mins)

 Steve and Susan wanted to know how water affects plant growth



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- They decide to grow the same vine in 6 different pots by the window in their classroom



 Each day they give the pots 2 cups of water



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- At the end of 3 months they measure the length of the vine



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- At the end of 3 months they measure the length of the vine
- What is wrong with this "experiment"?



Central Dogma

DNA codes for

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- RNA codes for

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- Protien

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- A written record of selection over time
 - (or population size changes)
 - (or species histories)

RNA

Dynamic, ever-changing

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- Transcribed "as needed" from DNA

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- Only exons, introns are spliced out

Protein

Final product of central dogma

Protein

- Final product of central dogma
- "Action item" from the list

Protein

- Final product of central dogma
- "Action item" from the list
- Performs a task within the cell

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 - Unstable
 - Difficult to collect and quantify

Measuring RNA

Generate cDNA

Measuring RNA

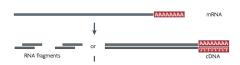
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- Prepare a sequencing library

Measuring RNA

- Generate cDNA
- Prepare a sequencing library
- (Next-Gen) Sequence!!!

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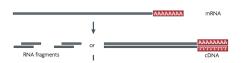
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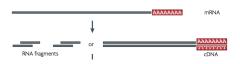
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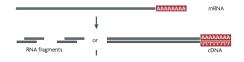
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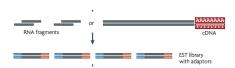
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 - Can be kept with labeling



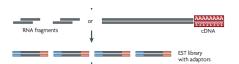
prepare a sequencing library

 Take the now-cDNA into a standard library prep



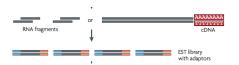
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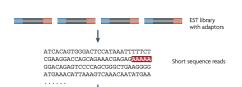
- Take the now-cDNA into a standard library prep
- Add adapters
- Amplify (with PCR) and sequence



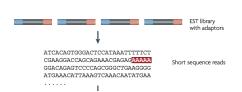
Single-end or paired-end



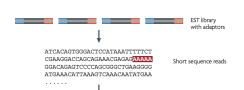
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- "fastq" format



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- Sequence content bases

@HWI-EAS209_0006_FC706VJ;5:58:5894:21141#ATCACG/1
TTAATTGGTAAATAAATCACTTCCAATAGGTTAGATNTTACCTTHNNNNNNNNTAGTTTC:
+WHI-EAS209_0006_FC706VJ:5:58:5894:21141#ATCACG/1
efcfffffcfeefffcfffffddf^feed]^]_Ba_^_[YBBBBBBBBBTT\]]][

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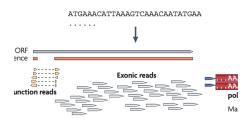
@HMI-EAS209_0006_FC706VJ;5;58;5894:21141#ATCACG/1
TTAATTGGTAAATAAATCACTTACATTTGCTTHANNNNNNNTAGTTTC:
+HMT-EAS209_0006_FC706VJ;5;58;5894:21141#ATCACG/1
efcfffffcfeefffcfffffddf^feed]^]_Ba_^_[YBBBBBBBBBRTT\]][

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@BHT-EAS209_0006_FC706V1:5:58:5894:21141#ATCACG/1
TTAATTGGTAATAAATCTCTAATAGCTTAGATNTTACCTTNNNNNNNNTAGTTTC:
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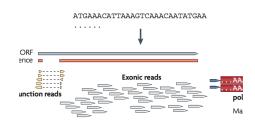
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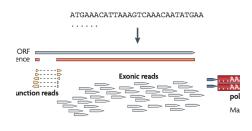
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Now what do we do?

- Map reads to a genome/annotation
 - (or not! de novo)
- Count depth of reads at each gene
- Infer amount of RNA (and thus protein) in the cells



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 - Poisson distribution



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- Recent feud between kallisto and salmon authors

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 - Help annotation (listing exons and introns) of new genomes

What can RNAseq tell us?

- Which genes are being transcribed
 - What genes/proteins are involved in specific functions
 - How those genes change with conditions
- Allele-Specific Expression (ASE)
 - Which version of a gene is being expressed more
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- Where the genes are in a genome?
 - Help annotation (listing exons and introns) of new genomes
 - Quick way to analyze functional portion of the genome, target of selection

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- Strand specificity (also fixable)

"New" Insights

(from the 2009 paper)

Mapping genes and exons

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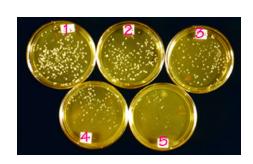
- Mapping genes and exons
- Catalog transcript complexity

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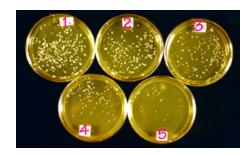
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- Mapping genes and exons
- Catalog transcript complexity
- Transcribed and not translated regions

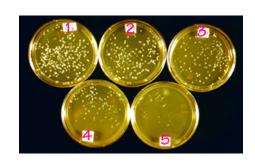
 Steve and Susan wanted to know how food source affects yeast



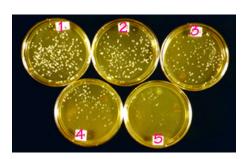
- Steve and Susan wanted to know how food source affects yeast
- They decide to grow the same yeast in 5 different plates in their classroom



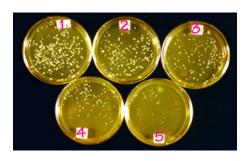
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- What is wrong with this "experiment"?



Dotstorming Check-In

- Did I cover the top questions?
- Dotstorming Board

Learning to Code (and other skills)

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Jennifer, Nayib, Chris

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- Austin, Alan, Raymond

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- Leave with a plan to find data by next Tuesday

The End