Everything you wanted to know about RNAseq

C. Ryan Campbell

Duke University c.ryan.campbell@duke.edu

12 Sept 2017

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



- Steve and Susan wanted to know how water affects plant growth
- 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



- Each day they give the pots 2 cups of water
- At the end of 3 months they measure the length of the vine



- Each day they give the pots 2 cups of water
- At the end of 3 months they measure the length of the vine
- What is wrong with this "experiment"?



Central Dogma

DNA codes for

Central Dogma

- DNA codes for
- RNA codes for

Central Dogma

- DNA codes for
- RNA codes for
- Protien

Static, non-changing

- Static, non-changing
- You're stuck with the genome you have

- Static, non-changing
- You're stuck with the genome you have
- Good for investigating large scale and inflexible impacts of environment

- Static, non-changing
- You're stuck with the genome you have
- Good for investigating large scale and inflexible impacts of environment
- A written record of selection over time
 - (or population size changes)
 - (or species histories)

RNA

Dynamic, ever-changing

RNA

- Dynamic, ever-changing
- Transcribed "as needed" from DNA

RNA

- Dynamic, ever-changing
- Transcribed "as needed" from DNA
- 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

Sequencing the RNA molecules in a cell

- Sequencing the RNA molecules in a cell
 - Use as a proxy for identifying active proteins

- Sequencing the RNA molecules in a cell
 - Use as a proxy for identifying active proteins
- Why not DNA?

- Sequencing the RNA molecules in a cell
 - Use as a proxy for identifying active proteins
- Why not DNA?
- Why not Proteins?

Measuring RNA

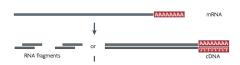
Measuring RNA

- Generate cDNA
- Prepare a sequencing library

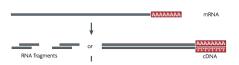
Measuring RNA

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

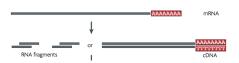
 Isolate RNA from cells and use deoxyribonuclease (DNAse) to remove accidental DNA



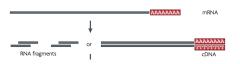
- Isolate RNA from cells and use deoxyribonuclease (DNAse) to remove accidental DNA
- Select for poly-A tails to enrich for mature RNA (often with magnetic beads)



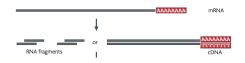
- Isolate RNA from cells and use deoxyribonuclease (DNAse) to remove accidental DNA
- Select for poly-A tails to enrich for mature RNA (often with magnetic beads)
- Reverse transcribe the RNA into cDNA (lasts longer)



- Isolate RNA from cells and use deoxyribonuclease (DNAse) to remove accidental DNA
- Select for poly-A tails to enrich for mature RNA (often with magnetic beads)
- Reverse transcribe the RNA into cDNA (lasts longer)
 - Lose strand info

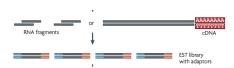


- Isolate RNA from cells and use deoxyribonuclease (DNAse) to remove accidental DNA
- Select for poly-A tails to enrich for mature RNA (often with magnetic beads)
- Reverse transcribe the RNA into cDNA (lasts longer)
 - Lose strand info
 - Can be kept with labeling



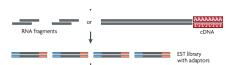
prepare a sequencing library

 Take the now-cDNA into a standard library prep



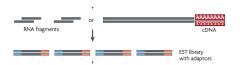
prepare a sequencing library

- Take the now-cDNA into a standard library prep
- Add adapters

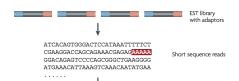


prepare a sequencing library

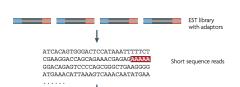
- Take the now-cDNA into a standard library prep
- Add adapters
- Amplify (with PCR) and sequence



Single-end or paired-end



- Single-end or paired-end
 - Because genes are often shorter than the full length of paired-end, data is analyzed one end at a time



- Single-end or paired-end
 - Because genes are often shorter than the full length of paired-end, data is analyzed one end at a time
- Generate billions of reads



- Single-end or paired-end
 - Because genes are often shorter than the full length of paired-end, data is analyzed one end at a time
- Generate billions of reads
- "fastq" format



 Sequence header information regarding the machine

@HWI-EAS209_0006_FC706VJ:5:58:5894:21141#ATCACG/1
TTAATTGGTAAATAAATCACCTAATAGCTTAGATHTTACCTTNINNINNINNTAGTTTC
+HWI-EAS209_0006_FC706VJ:5:58:5894:21141#ATCACG/1
efffffffddfffeddfffeddfffagdffaedfl_Ba___[YBBBBBBBBBRTT]][[

- Sequence header information regarding the machine
- 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\]]][

- Sequence header information regarding the machine
- Sequence content bases
- Sequence header repeat of above (+ instead of @)

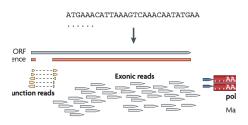
@HMI-EAS209_0006_FC706VJ:5:58:5894:21141#ATCACG/1
TTAATTGGTAAATAAATCACTTACATTTTTTGGTAATAAGTTTC:
+HMI-EAS209_0006_FC706VJ:5:58:5894:21141#ATCACG/1
efcfffffcfeefffcffffffddf^feed]^]_Ba_^__[YBBBBBBBBBTT\]][

- Sequence header information regarding the machine
- Sequence content bases
- Sequence header repeat of above (+ instead of @)
- Sequence quality -ASCII coded

@HHT-EAS209_0006_FC706V1:5:58:5894:21141#ATCACG/1
TTAATTGGTAATAAATCTCCTAATAGCTTAGATNTTACCTTNNNNNNNNTAGTTTC:
+HHT-EAS209_0006_FC706V1:5:58:5894:21141#ATCACG/1
efcfffffcfeefffcffffffddf^feed]^]_Ba_^__(YBBBBBBBBBTT\]]][

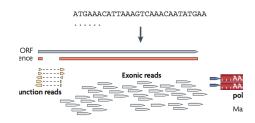
Now what do we do?

- Map reads to a genome/annotation
 - (or not! de novo)



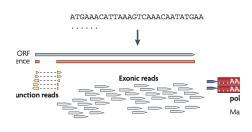
Now what do we do?

- Map reads to a genome/annotation
 - (or not! de novo)
- Count depth of reads at each gene



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



- Map to genes? or exons?
 - Exon mapping can help determine splice variants

- Map to genes? or exons?
 - Exon mapping can help determine splice variants
- Standardize by amount of data

- Map to genes? or exons?
 - Exon mapping can help determine splice variants
- Standardize by amount of data
 - FPM Fragments (mapped) Per Million bases (of NGS data)

- Map to genes? or exons?
 - Exon mapping can help determine splice variants
- Standardize by amount of data
 - FPM Fragments (mapped) Per Million bases (of NGS data)
- Standardize by length of gene as well

- Map to genes? or exons?
 - Exon mapping can help determine splice variants
- Standardize by amount of data
 - FPM Fragments (mapped) Per Million bases (of NGS data)
- Standardize by length of gene as well
 - FPKM Fragments Per Kilobase of transcript per Million mapped reads

- Map to genes? or exons?
 - Exon mapping can help determine splice variants
- Standardize by amount of data
 - FPM Fragments (mapped) Per Million bases (of NGS data)
- Standardize by length of gene as well
 - FPKM Fragments Per Kilobase of transcript per Million mapped reads
- Sampling error at low numbers

- Map to genes? or exons?
 - Exon mapping can help determine splice variants
- Standardize by amount of data
 - FPM Fragments (mapped) Per Million bases (of NGS data)
- Standardize by length of gene as well
 - FPKM Fragments Per Kilobase of transcript per Million mapped reads
- Sampling error at low numbers
 - Not always normal variance (can't sample below 0)

- Map to genes? or exons?
 - Exon mapping can help determine splice variants
- Standardize by amount of data
 - FPM Fragments (mapped) Per Million bases (of NGS data)
- Standardize by length of gene as well
 - FPKM Fragments Per Kilobase of transcript per Million mapped reads
- Sampling error at low numbers
 - Not always normal variance (can't sample below 0)
 - Poisson distribution

Different analyses software packages

- Different analyses software packages
- Different choices (laid out on prior slide)

- Different analyses software packages
- Different choices (laid out on prior slide)
- Expectation is noisy results

- Different analyses software packages
- Different choices (laid out on prior slide)
- Expectation is noisy results
- Recent feud between kallisto and salmon authors

Which genes are being transcribed

- Which genes are being transcribed
 - What genes/proteins are involved in specific functions

- Which genes are being transcribed
 - What genes/proteins are involved in specific functions
 - How those genes change with conditions

- Which genes are being transcribed
 - What genes/proteins are involved in specific functions
 - How those genes change with conditions
- Allele-Specific Expression (ASE)

- 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

- 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
 - How smaller changes in a gene alter expression

- 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
 - How smaller changes in a gene alter expression
- Where the genes are in a genome?

- 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
 - How smaller changes in a gene alter expression
- Where the genes are in a genome?
 - Help annotation (listing exons and introns) of new genomes

- 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
 - How smaller changes in a gene alter expression
- 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

Strengths of RNAseq

No a priori info needed

Strengths of RNAseq

- No a priori info needed
- No limit to discrimination

Strengths of RNAseq

- No a priori info needed
- No limit to discrimination
- Systematically reproducible

Strengths of RNAseq

- No a priori info needed
- No limit to discrimination
- Systematically reproducible
 - qPCR to verify results

Strengths of RNAseq

- No a priori info needed
- No limit to discrimination
- Systematically reproducible
 - qPCR to verify results
 - Controls of known concentration

Library generation has biases

- Library generation has biases
 - Fragmentation of long RNA depletes the ends of gene transcripts

- Library generation has biases
 - Fragmentation of long RNA depletes the ends of gene transcripts
 - cDNA based towards 3-prime end

- Library generation has biases
 - Fragmentation of long RNA depletes the ends of gene transcripts
 - cDNA based towards 3-prime end
- Abundant RNA read or PCR-duplicate artifact?

- Library generation has biases
 - Fragmentation of long RNA depletes the ends of gene transcripts
 - cDNA based towards 3-prime end
- Abundant RNA read or PCR-duplicate artifact?
 - Compare across biological replicates

- Library generation has biases
 - Fragmentation of long RNA depletes the ends of gene transcripts
 - cDNA based towards 3-prime end
- Abundant RNA read or PCR-duplicate artifact?
 - Compare across biological replicates
- Messy results

- Library generation has biases
 - Fragmentation of long RNA depletes the ends of gene transcripts
 - cDNA based towards 3-prime end
- Abundant RNA read or PCR-duplicate artifact?
 - Compare across biological replicates
- Messy results
- Bioinformatic methods (largely improved)

- Library generation has biases
 - Fragmentation of long RNA depletes the ends of gene transcripts
 - cDNA based towards 3-prime end
- Abundant RNA read or PCR-duplicate artifact?
 - Compare across biological replicates
- Messy results
- Bioinformatic methods (largely improved)
- Strand specificity (also fixable)

"New" Insights

(from the 2009 paper)

Mapping genes and exons

"New" Insights

(from the 2009 paper)

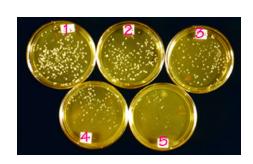
- Mapping genes and exons
- Catalog transcript complexity

"New" Insights

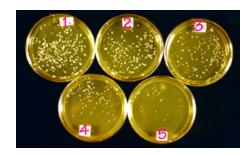
(from the 2009 paper)

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

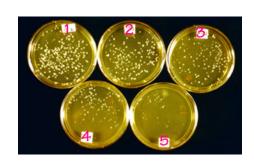
 Steve and Susan wanted to know how food source affects yeast



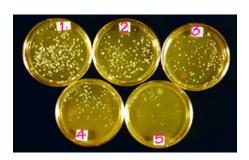
- Steve and Susan wanted to know how food source affects yeast
- They decide to grow the same yeast in 5 different plates in their classroom



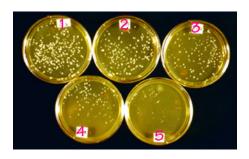
Each plate contains .8% lactose agar



- Each plate contains .8% lactose agar
- At the end of a week the measure the gene expression of each



- Each plate contains .8% lactose agar
- At the end of a week the measure the gene expression of each
- What is wrong with this "experiment"?



Dotstorming Check-In

- Did I cover the top questions?
- Dotstorming Board

Learning to Code (and other skills)

Learning to Code (and other skills)



Today's Tasks:

- Today's Tasks:
- Meet with your group

- Today's Tasks:
- Meet with your group
- Discuss common interests

- Today's Tasks:
- Meet with your group
- Discuss common interests
- Exchange and ideas or datasets you had hoped to use

- Today's Tasks:
- Meet with your group
- Discuss common interests
- Exchange and ideas or datasets you had hoped to use
- Leave with a plan to find data by next Tuesday

The End