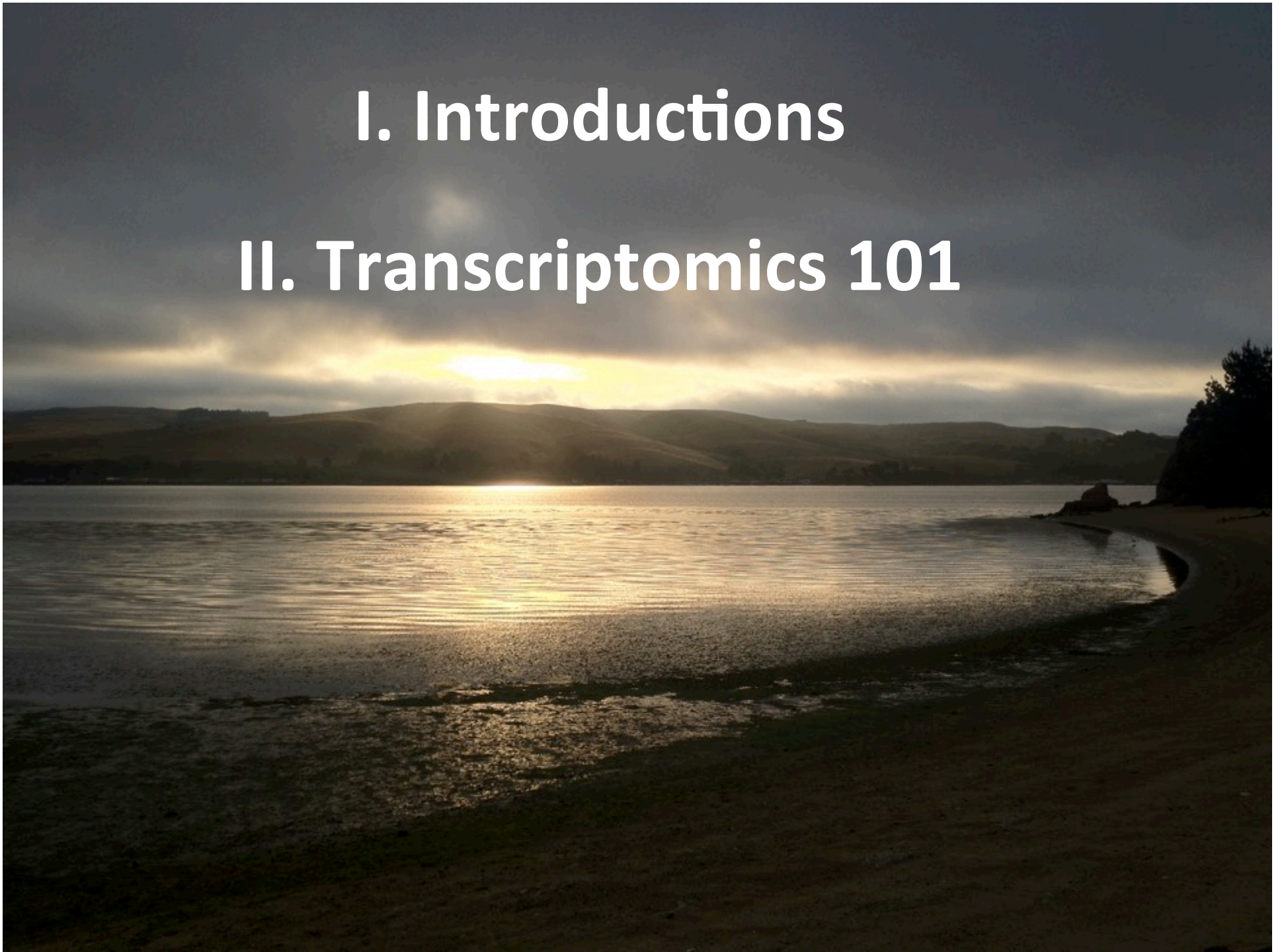


I. Introductions

II. Transcriptomics 101



Workshop Learning Objectives

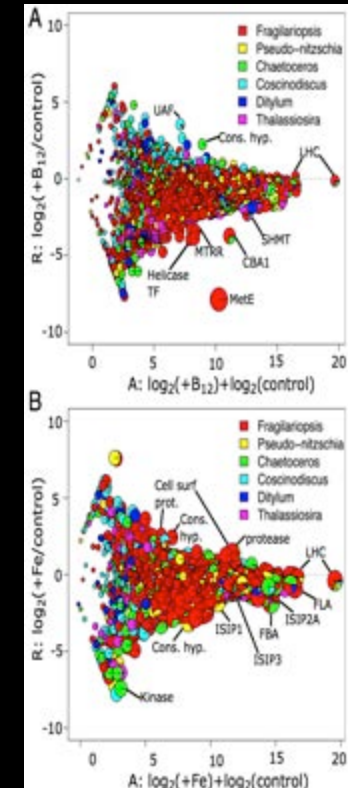
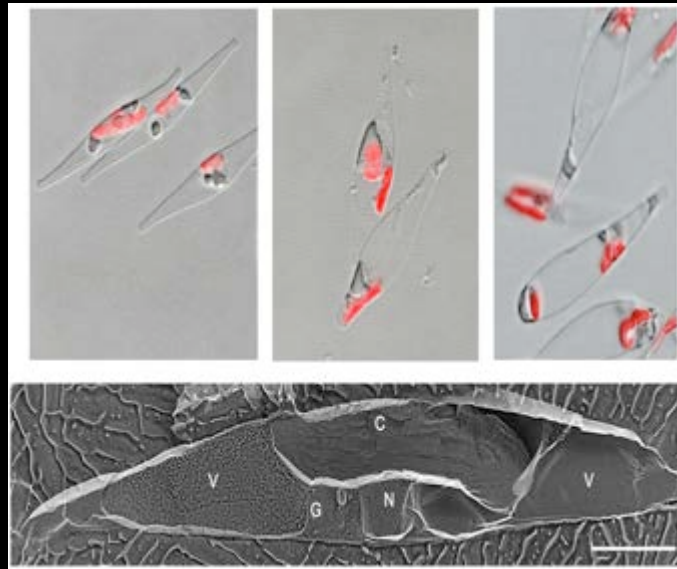
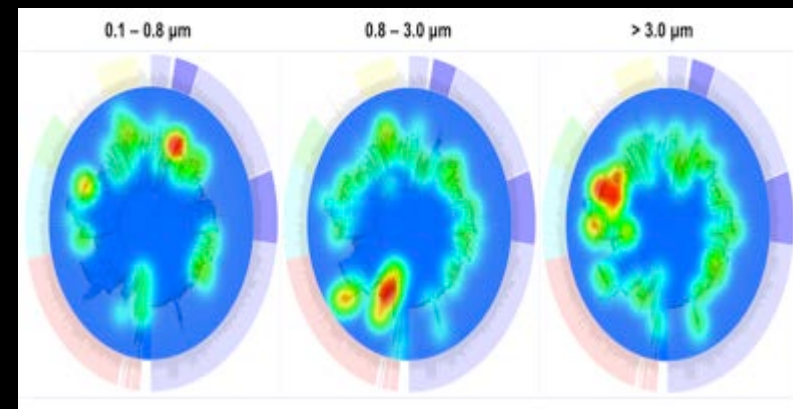
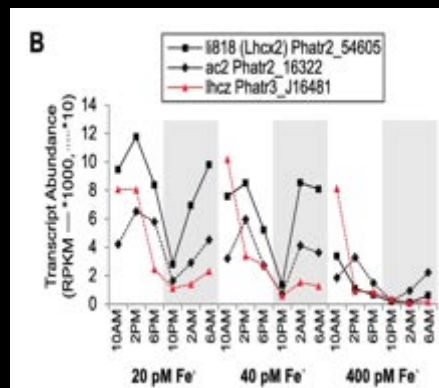
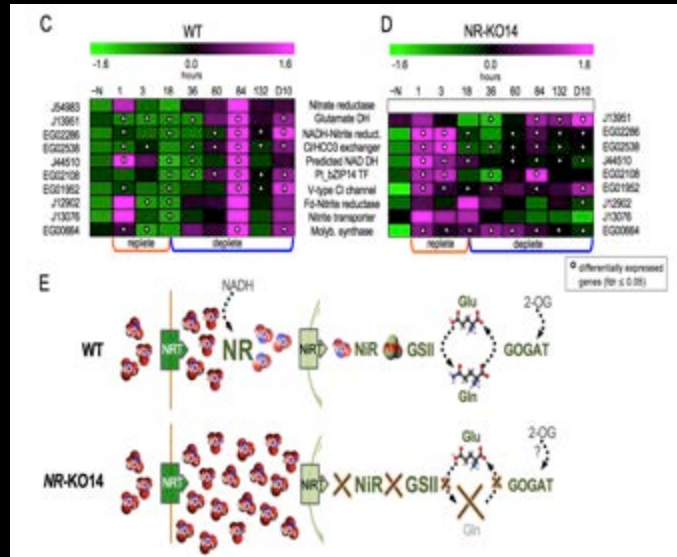
1. What types of research questions that transcriptomics can be used to address
2. Key things to consider in experimental design & analysis approaches
3. Conceptual understanding of steps and decisions involved in RNA-Seq data analysis
4. Become comfortable working with RNA-Seq data in key workflow steps
5. Know about resources and where to go for help/future learning
(including building contacts community here with other participants!)

Schedule & Code of Conduct



Logistics

- Sticky Notes
- Etherpad
- Personal note taking suggestions
- Interactive Environment



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Transcriptomics

Genomics

Amplicon sequencing

Metagenomics

Ecosystem assessment

Data science

Bioinformatics

Fisheries biology

Environmental sequencing



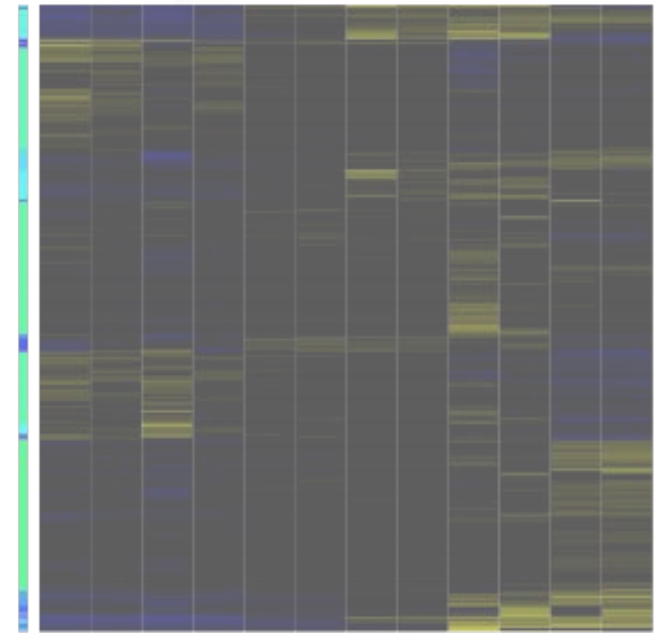


Tessa Pierce

ntpierce@ucdavis.edu

Nonmodel Transcriptomics

- Environmental Stressors
- Time Series Analysis



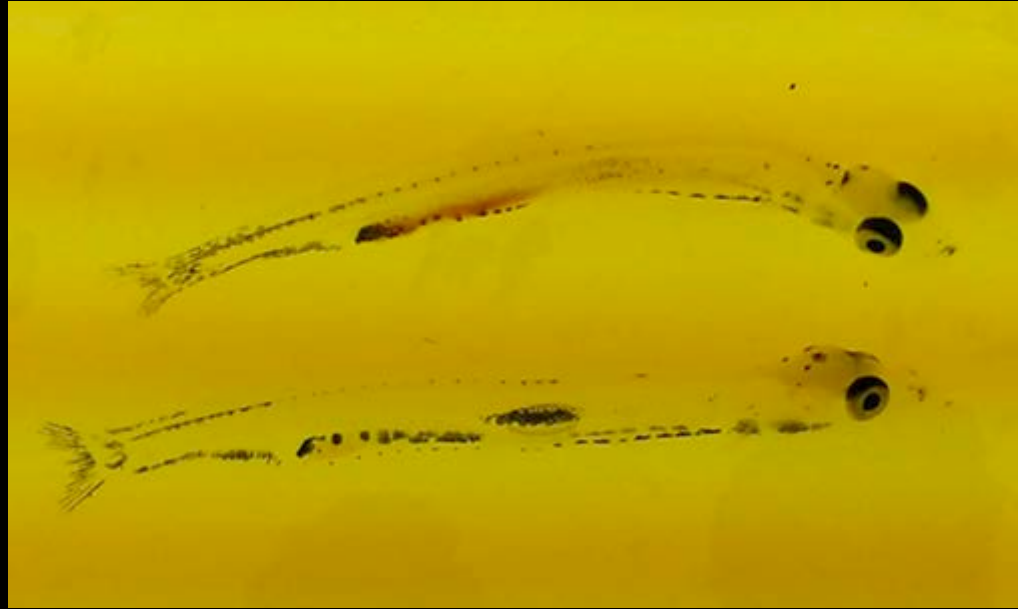
TIME



bluegenes



@saltyscientist



Lisa Komoroske

Dept. of Environmental Conservation
SWFSC Marine Mammal & Turtle Division

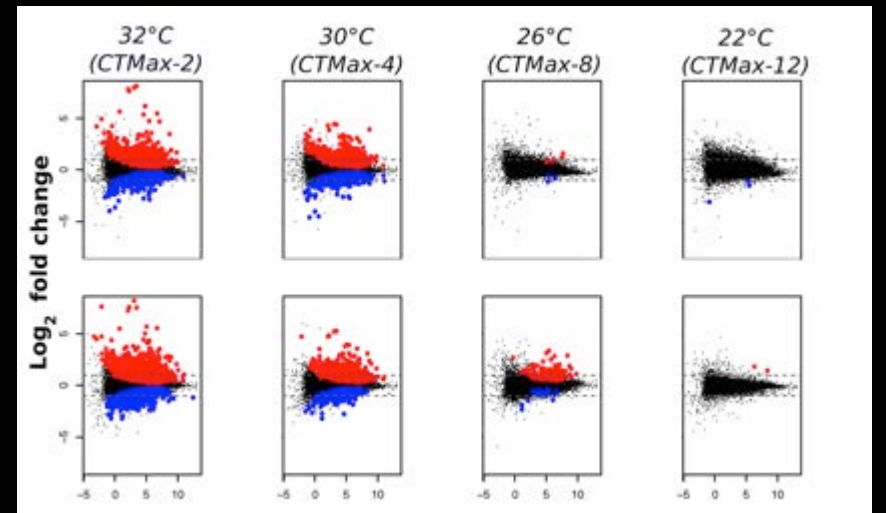
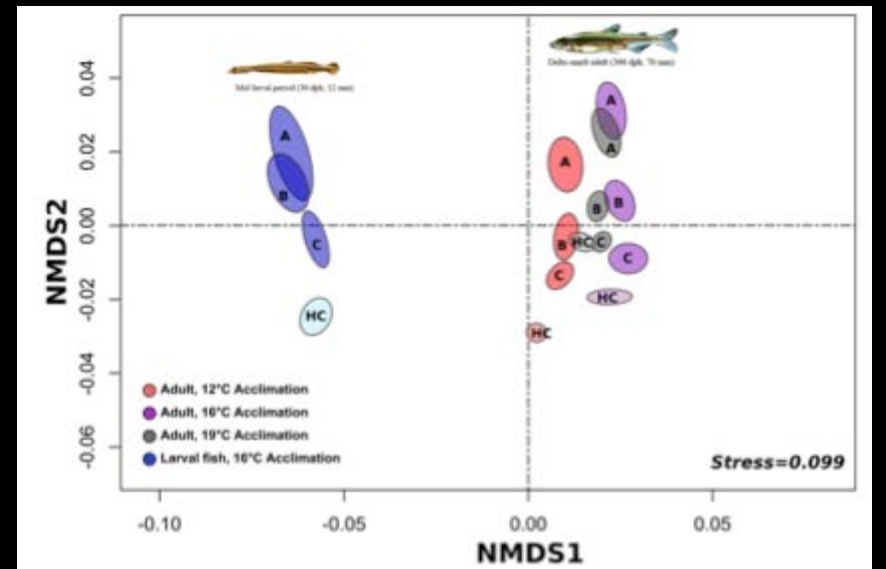
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NOAA FISHERIES
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Southwest Fisheries Science Center





Lisa Komoroske



NOAA FISHERIES
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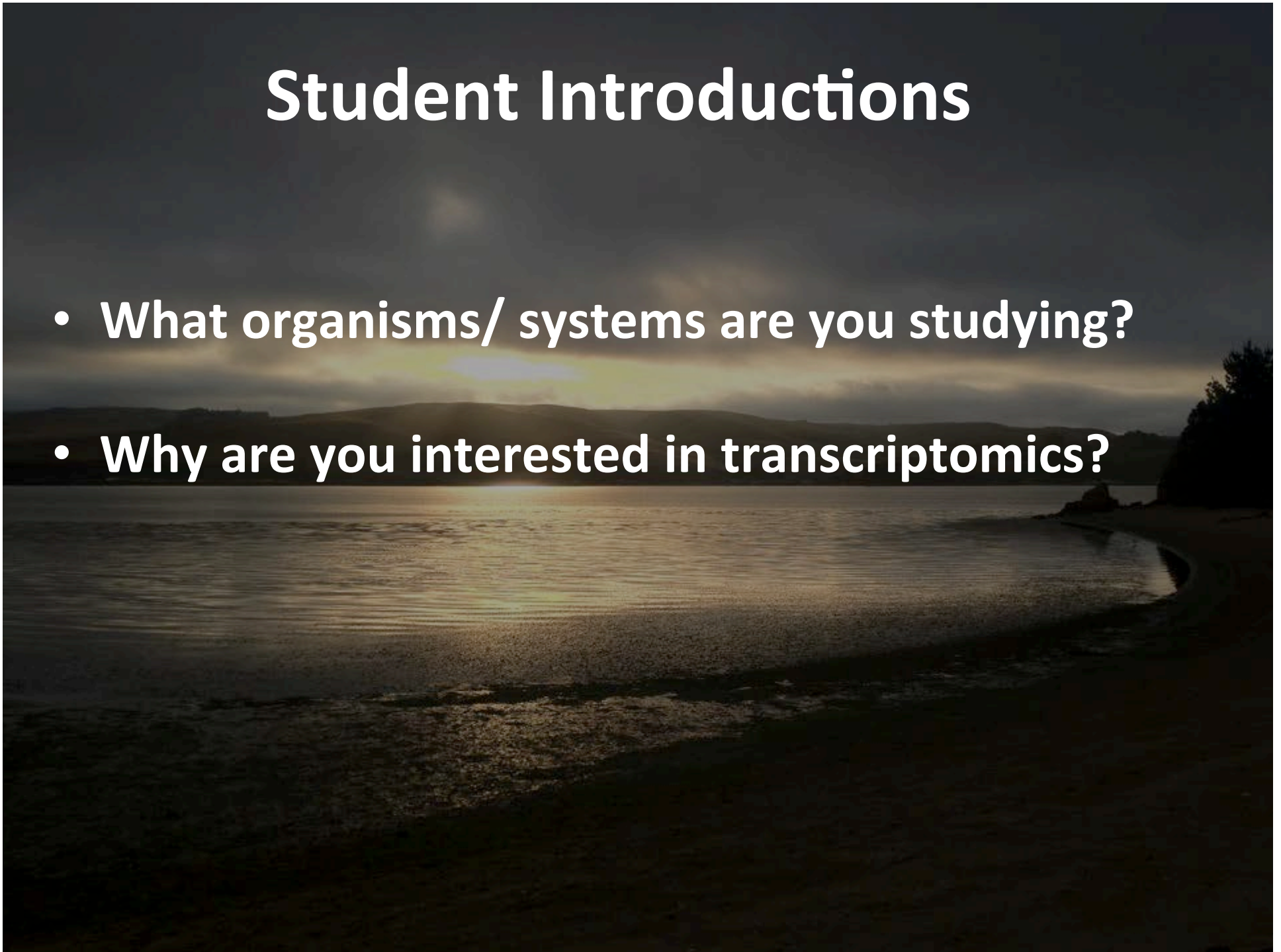
**UMASS
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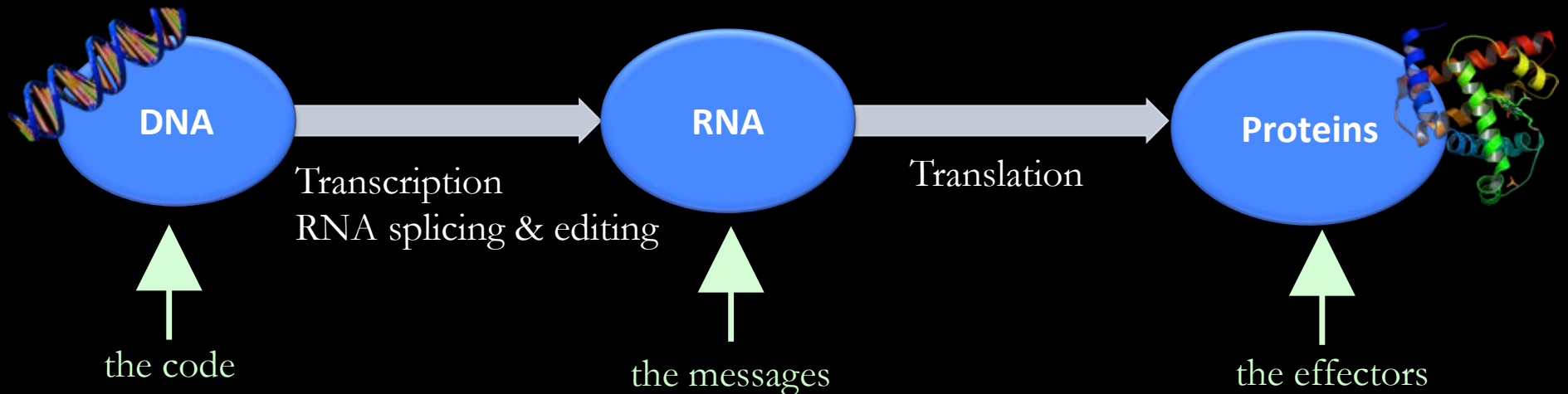
Student Introductions

- What organisms/ systems are you studying?
- Why are you interested in transcriptomics?

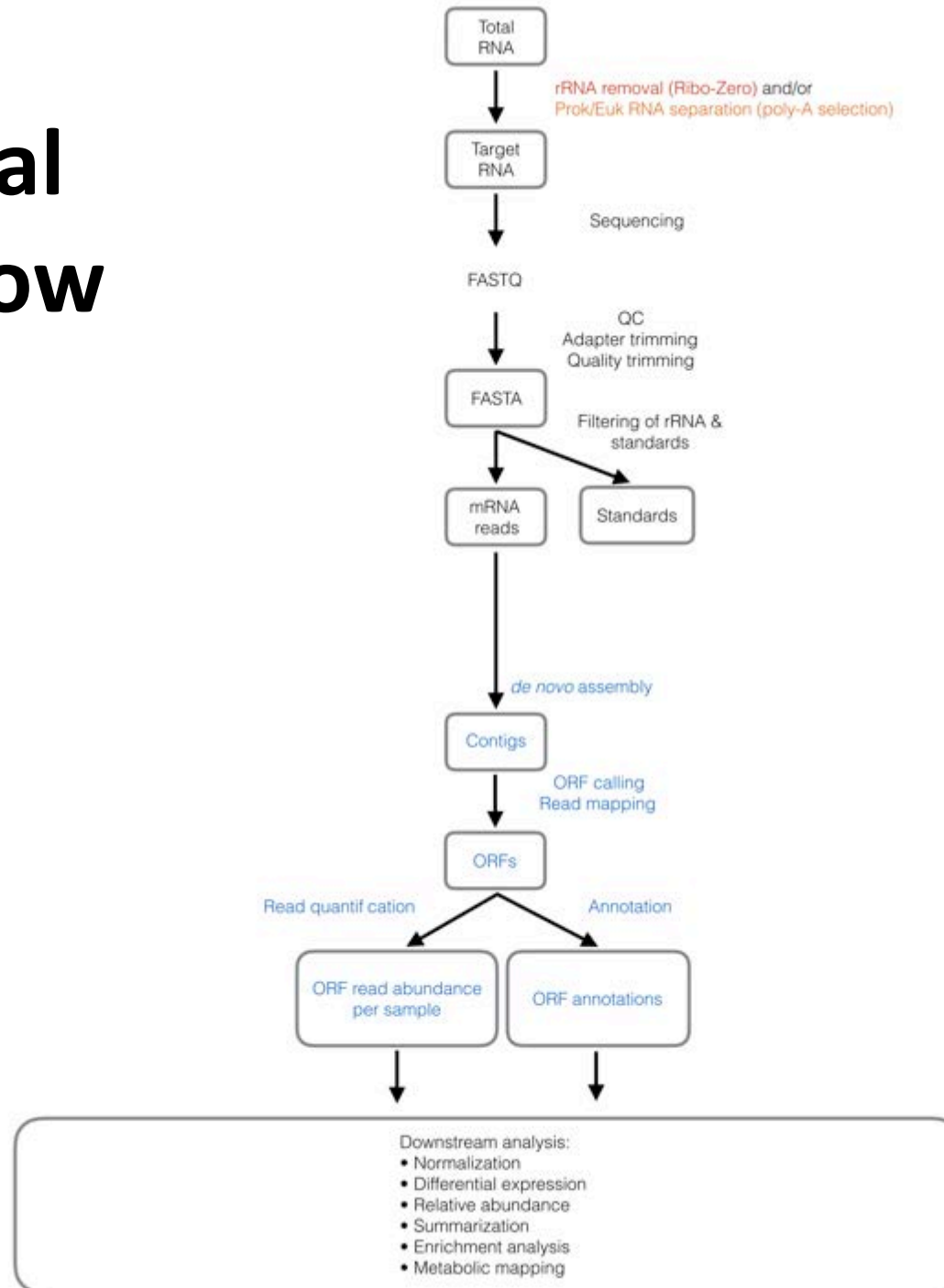


Transcriptomics 101

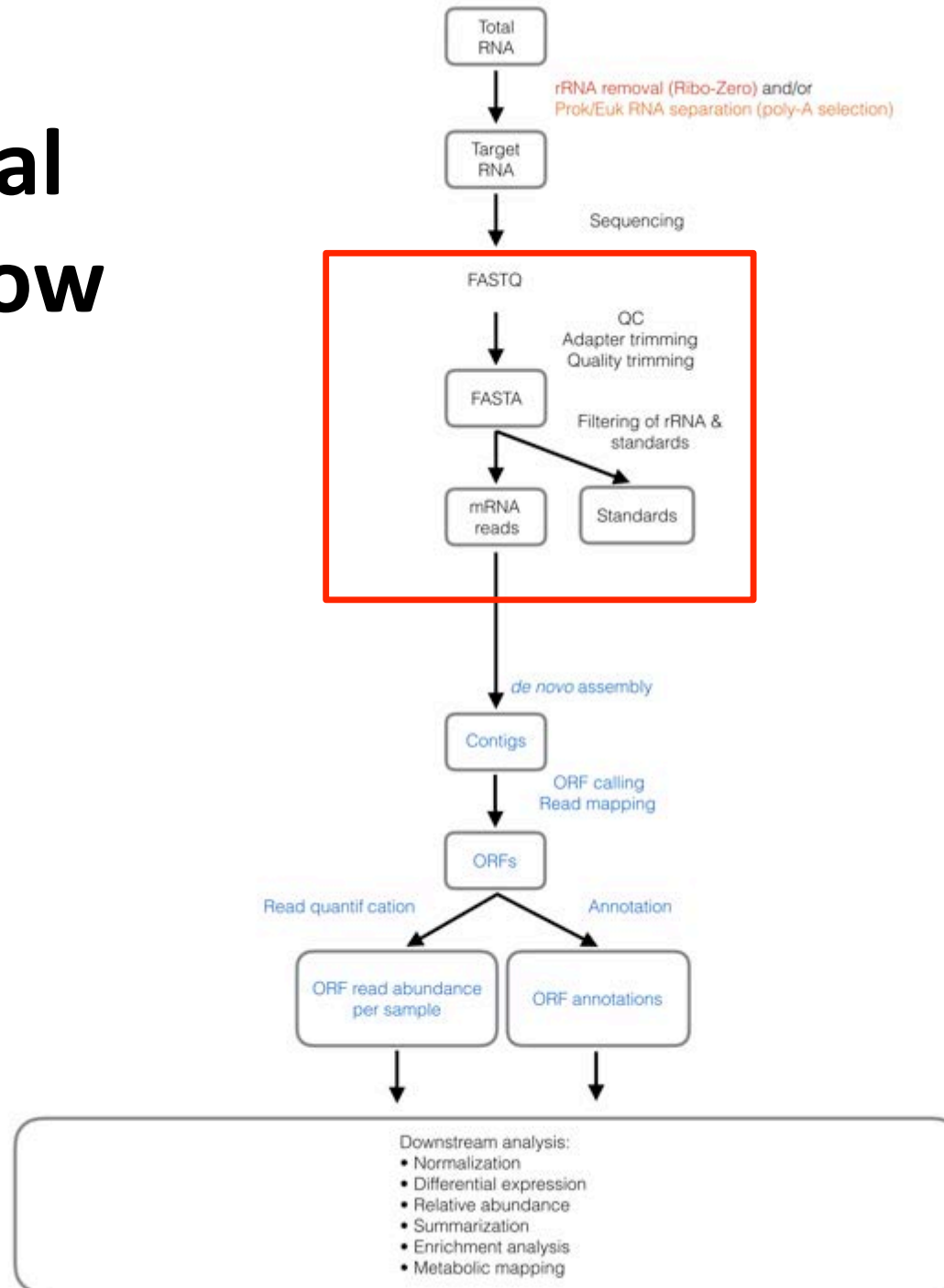
- What is Transcriptomics?
- When would it be a good tool?
- What type of data is generated?



General Workflow



General Workflow



FASTQ format

Illumina format includes read pair and index

```
@K00180:331:HHVHJBBXX:1:1101:32471:1033 1:N:0:GTGGCC  
NCAAGGCGGTGGACGTCCCCAAAACCAACCGAGGAAGCTTTGGGATAGCA  
+  
#<-A-FJFA7FAJFJA<JJAJJJJFJJJJFFA7FFJF<FA<FFJFFJJJJ
```

Header

Sequence

Quality scores
(same length as sequence)

FASTA format

```
>K00180:331:HHVHJBBXX:1:1101:32471:1033 1:N:0:GTGGCC  
CAAGGCGGTGGACGTCCCCAAAACCAACCGAGGAAGCTTTGGGATAGCA
```

Header

Sequence

No quality scores

Trimmed for high-quality bases only (Q30)

What is Transcriptomics?

- Sequencing of cellular mRNA transcripts (or depleted total RNA-prokaryotes)
- Powerful measure of functional response to changing environmental conditions, cell types, or populations, etc.
- Small tissue requirements & multiplexing capacity
- Non-omics approaches: RT-qPCR, RNase protection assay, Northern blot
- Other applications (e.g., variant calling)

Why use Transcriptomics?

- Want to know about many genes, don't know which genes are present or are interesting
- Want to know about overall biological processes and/or pathways affected
- Genomes are not comprised of just single-copy single-function proteins, especially in more complex eukaryotes
- Even when measurement of a short list of genes is desired, value in knowing the context of other genes.