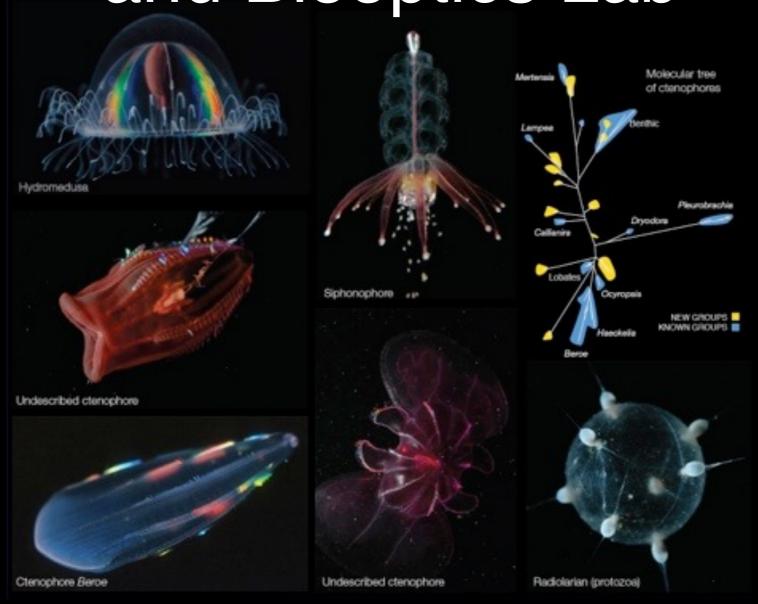
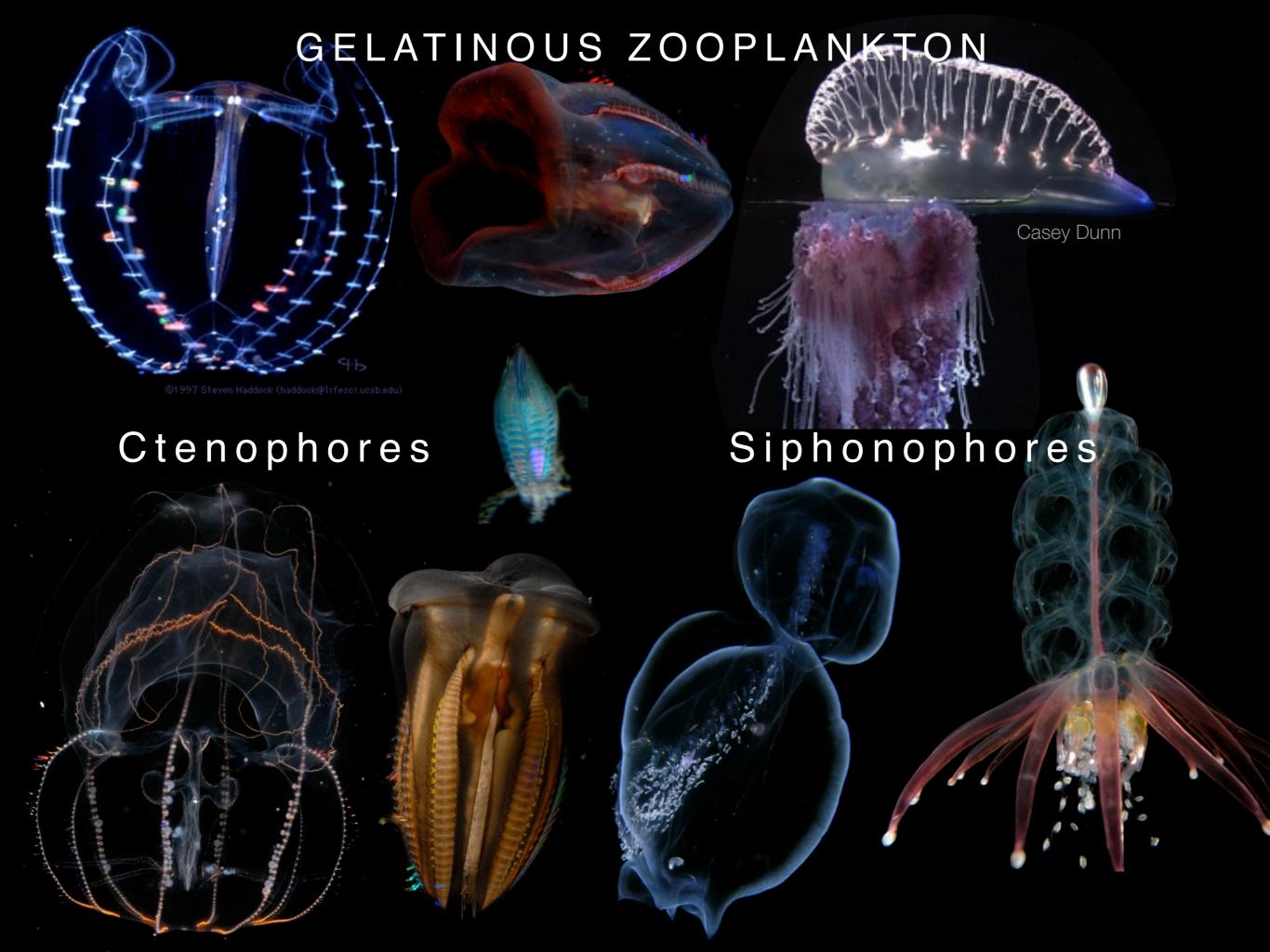
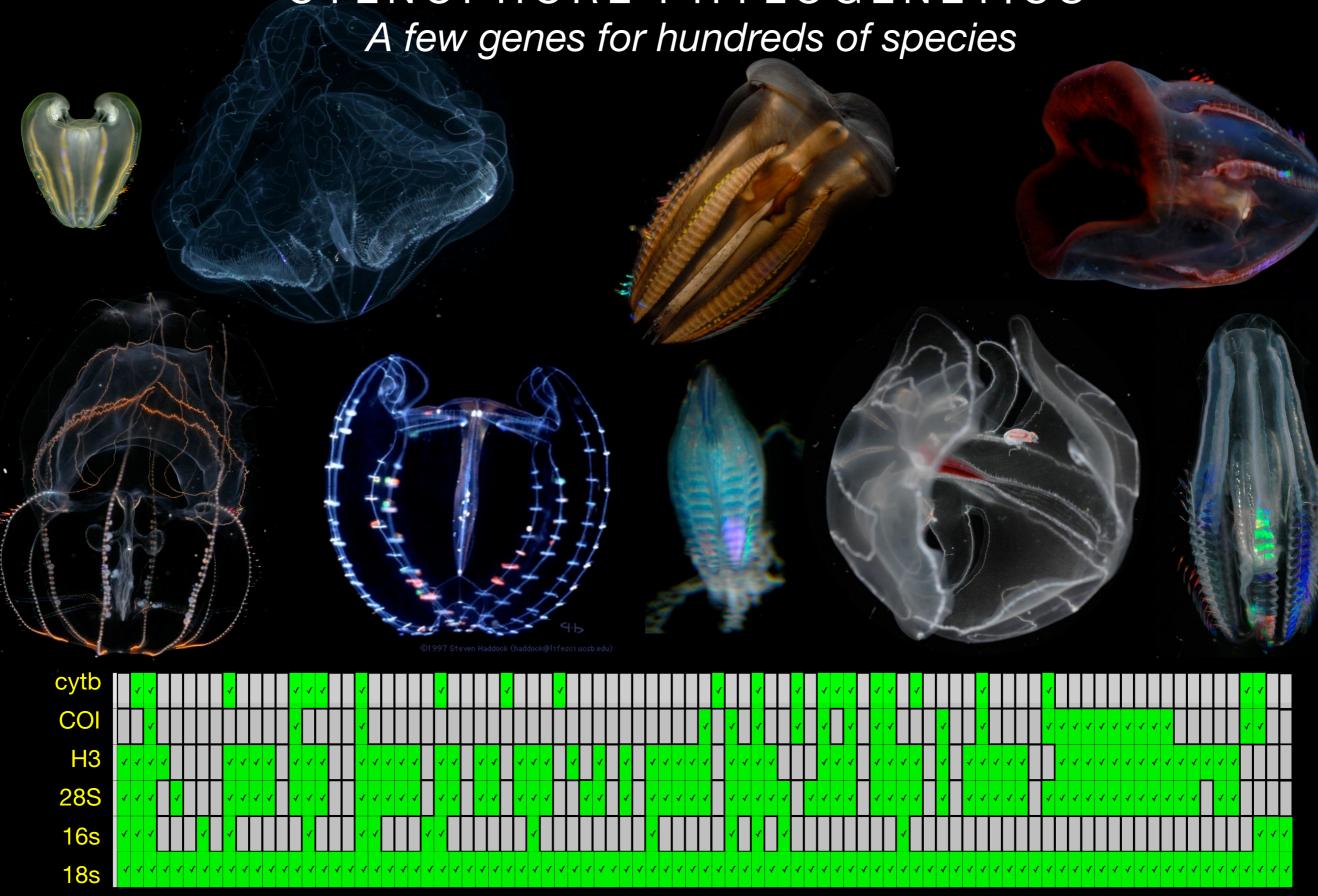
Zooplankton Biodiversity and Biooptics Lab



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# Sanger sequencing for CTENOPHORE PHYLOGENETICS



# Transcriptomes (94) Thousands of genes for dozens species

### **SIPHONOPHORES**

**Abylopsis** 

Apolemia

Chelophyes

Chuniphyes\_moserae

Chuniphyes\_multidentata

Cordagalma

Craseoa

Desmophyes

**Diphyes** 

Frenna

Forskalia

**Hippopodius** 

Lilyopsis

Lions mane

Lychnagalma

Marrus

Nanomia

Resomia

Rhisophysa

Rosacea

Stephalia

### **CRUSTACEANS**

Gaussia Luminous Tail Gaussia Non-Luminous Pleuromamma\_robusta

#### **WORMS**

(Polychaete & Chaetognath)

C.macrocephala

E.fowleri Body

E.fowleri Tail

Harmothoe

**Tomopteris** 

Flota

Swima bombiviridis

### **MOLLUSCS**

Chiroteuthis

**Dosidicus** 

Octopoteuthis

**Phylliroe** 

Pterygioteuthis

Vampyroteuthis

### **CTENOPHORES**

Bathocyroe fosteri

Bathyctena chuni

Benthic ctenophore

Beroe abyssicola

Beroe forskalii

Bolinopsis infundibulum

Charistephane

Ctenoceros red

Dryodora

**Euplokamis** 

Haeckelia rubra

Hormiphora

Lampea

Lampocteis cruentiventer

Nephelo red

Nephelo white

Ocyropsis maculata

Thalassocalyce

Vermillion lobate

Velamen parallelum

Weird cteno

### **OTHER CNIDARIA**

Atolla vanhoeffeni

Halitrephes\_valdiviae

Aegina\_citrea

Solmissus incisa

Tetraplatia volitans

### **PROTISTS** (Radiolaria)

T\_globosa

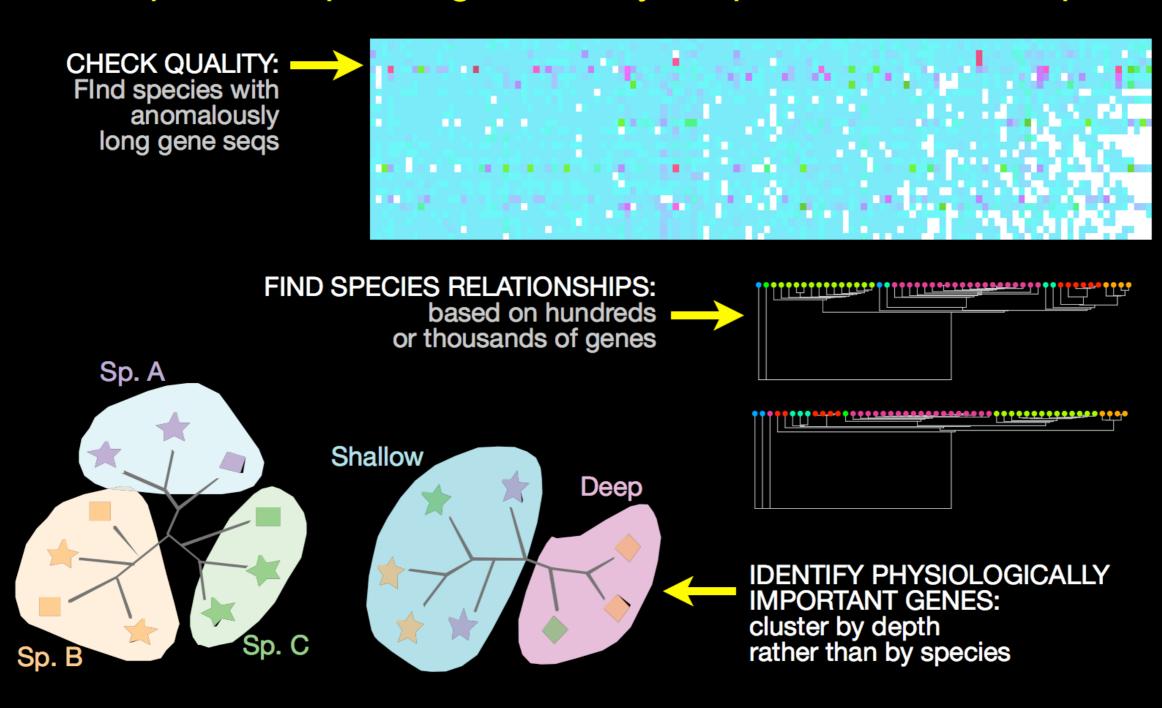
T\_campanella

T. braueri



Transcriptomes -> mtDNA genomic -> primers

### Transcriptome sequencing to identify adaptations to the deep-sea



# KogPlot.R script Transcriptomes give thousands of genes, • bathocyroe • Micromonas these are assigned to clusters Want to then identify outliers in clusters.

# Resources

Internal BLAST database for many hundreds of zooplankton specimens, including undescribed species.

At least one undescribed siphonophore was found in this recent microbial survey

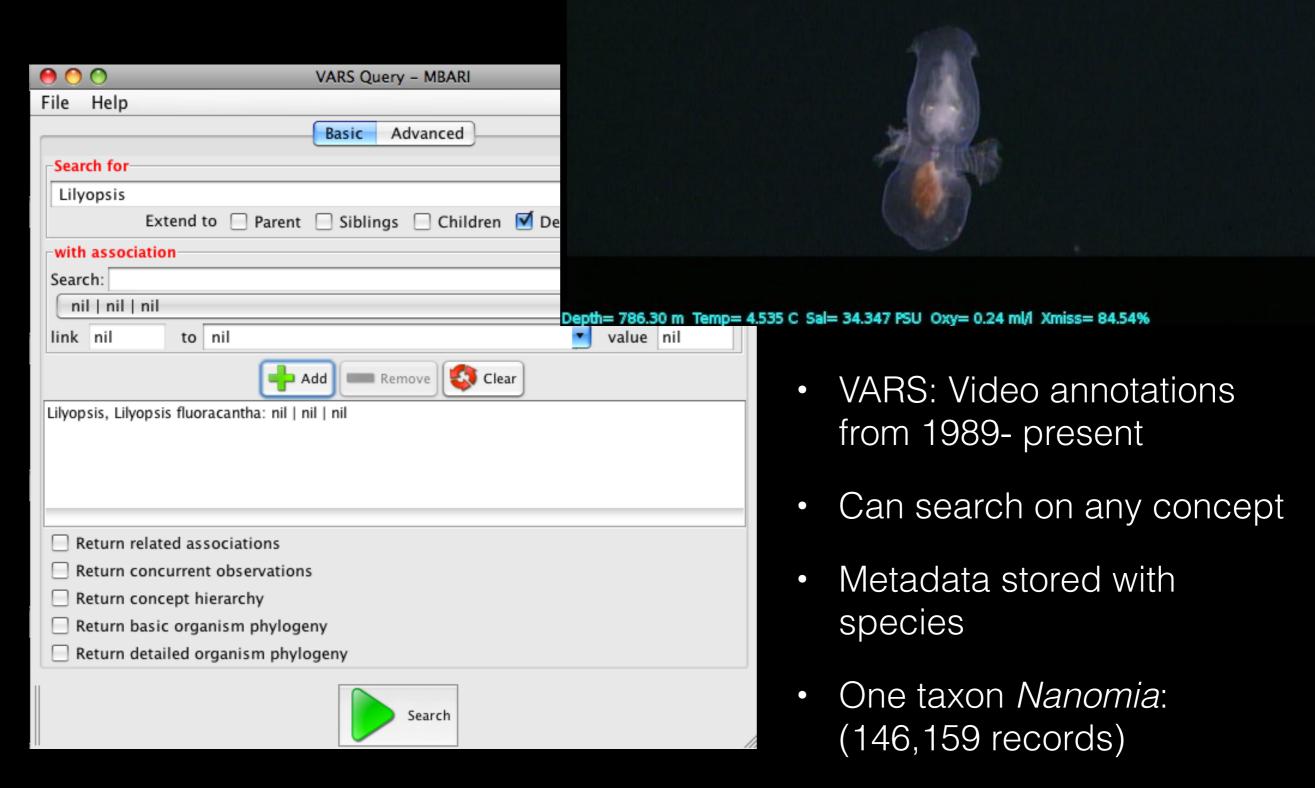


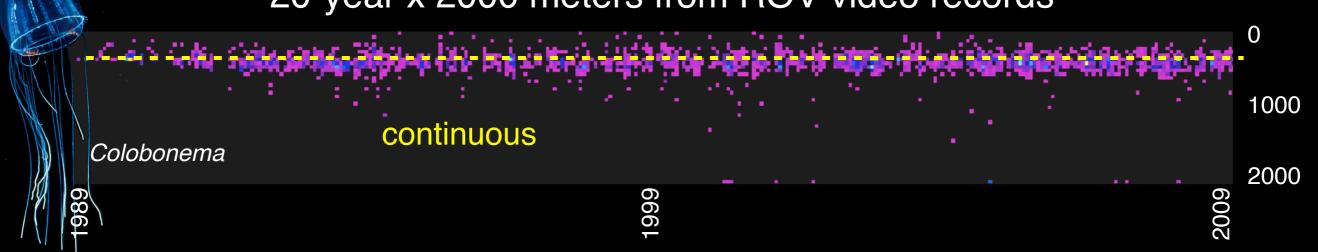
Investigating Microbial Eukaryotic Diversity from a Global Census: Insights from a Comparison of Pyrotag and Full-Length Sequences of 18S rRNA Genes

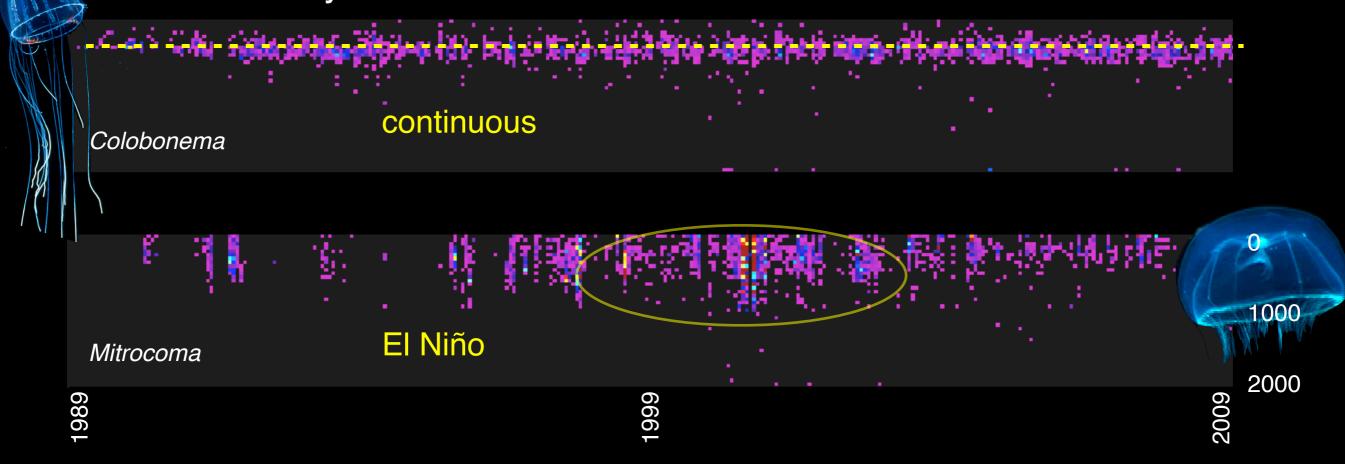
Alle A. Y. Lie,<sup>a</sup> Zhenfeng Liu,<sup>a</sup> Sarah K. Hu,<sup>a</sup> Adriane C. Jones,<sup>a</sup> Diane Y. Kim,<sup>a</sup> Peter D. Countway,<sup>b</sup> Linda A. Amaral-Zettler,<sup>c,d</sup> S. Craig Cary,<sup>e,h</sup> Evelyn B. Sherr,<sup>f</sup> Barry F. Sherr,<sup>f</sup> Rebecca J. Gast,<sup>g</sup> David A. Caron<sup>a</sup>

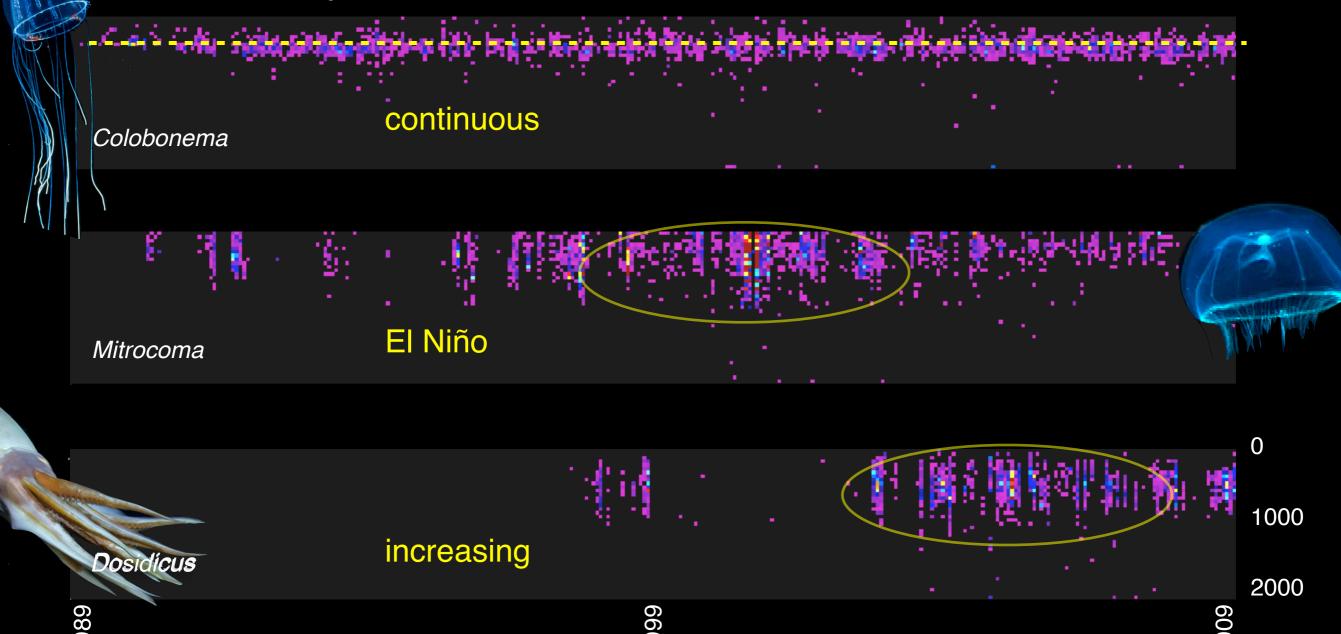
Department of Biological Sciences, University of Southern California, Los Angeles, California, USA<sup>a</sup>; Bigelow Laboratory for Ocean Sciences, East Boothbay, Maine, USA<sup>b</sup>; The Josephine Bay Paul Center for Comparative Molecular Biology and Evolution, Marine Biological Laboratory, Woods Hole, Massachusetts, USA<sup>c</sup>; Department of Geological Sciences, Brown University, Providence, Rhode Island, USA<sup>d</sup>; Environmental Research Institute, School of Science, University of Waikato, Hamilton, New Zealand<sup>e</sup>; College of Oceanic and Atmospheric Sciences, Oregon State University, Corvallis, Oregon, USA<sup>f</sup>; Woods Hole Oceanographic Institution, Woods Hole, Massachusetts, USA<sup>g</sup>; College of Earth, Ocean, and Environment, University of Delaware, Lewes, Delaware, USA<sup>h</sup>

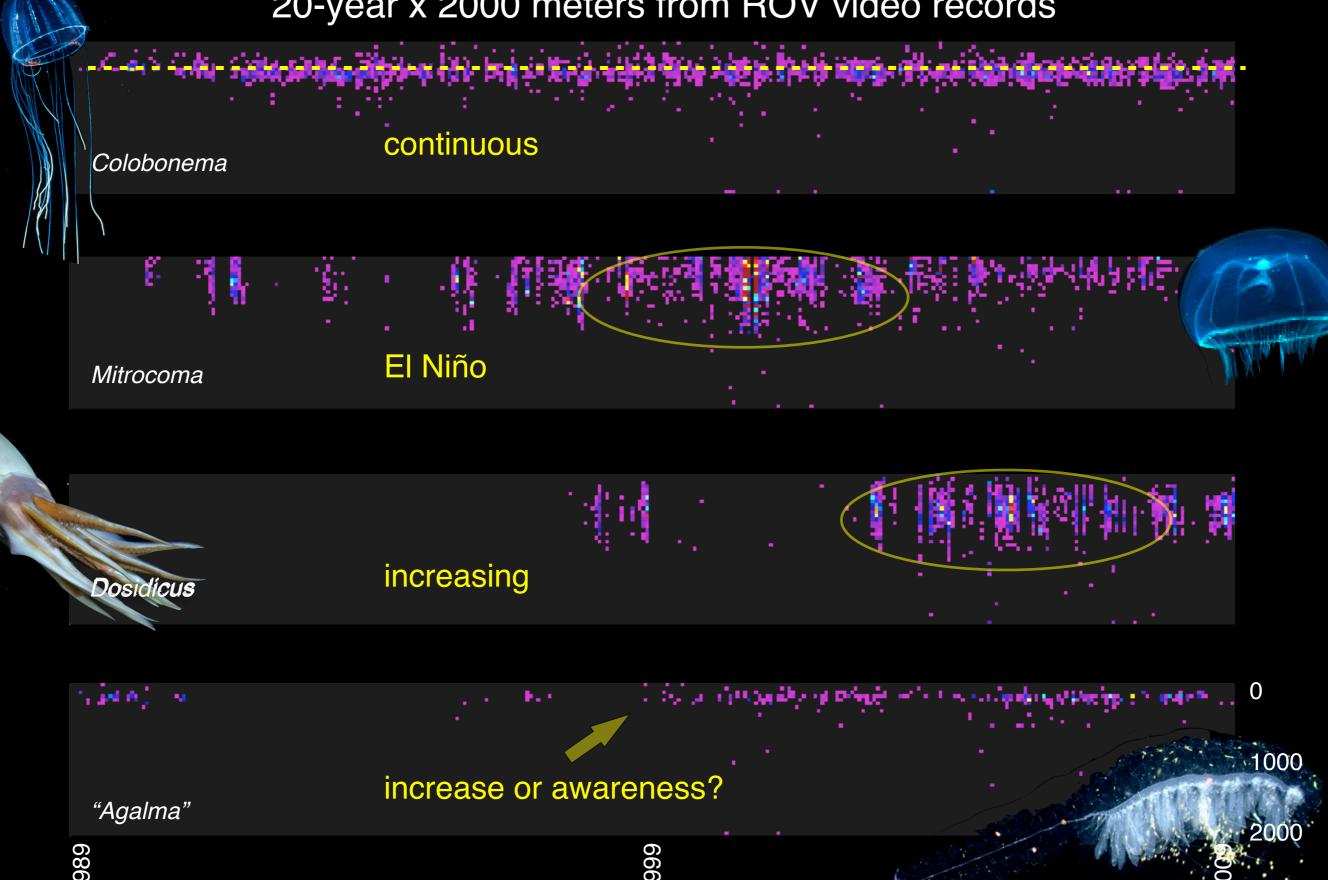
### VIDEO RECORDS of DEEP DIVERSITY



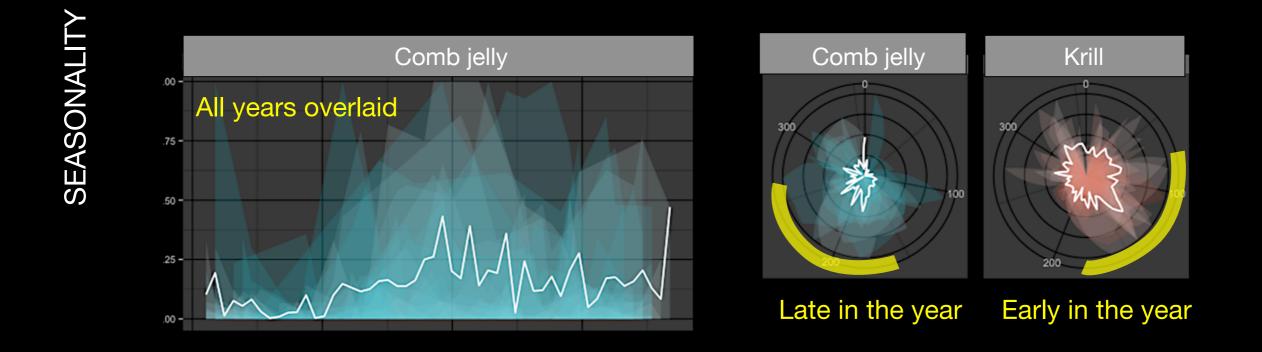


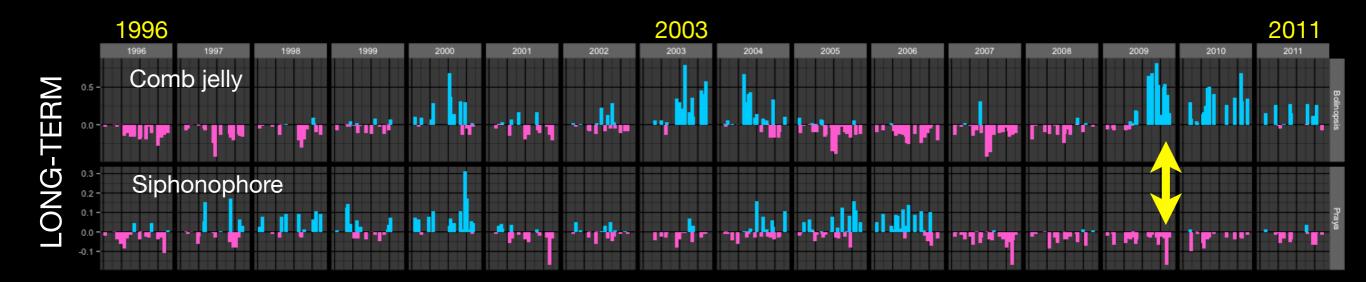




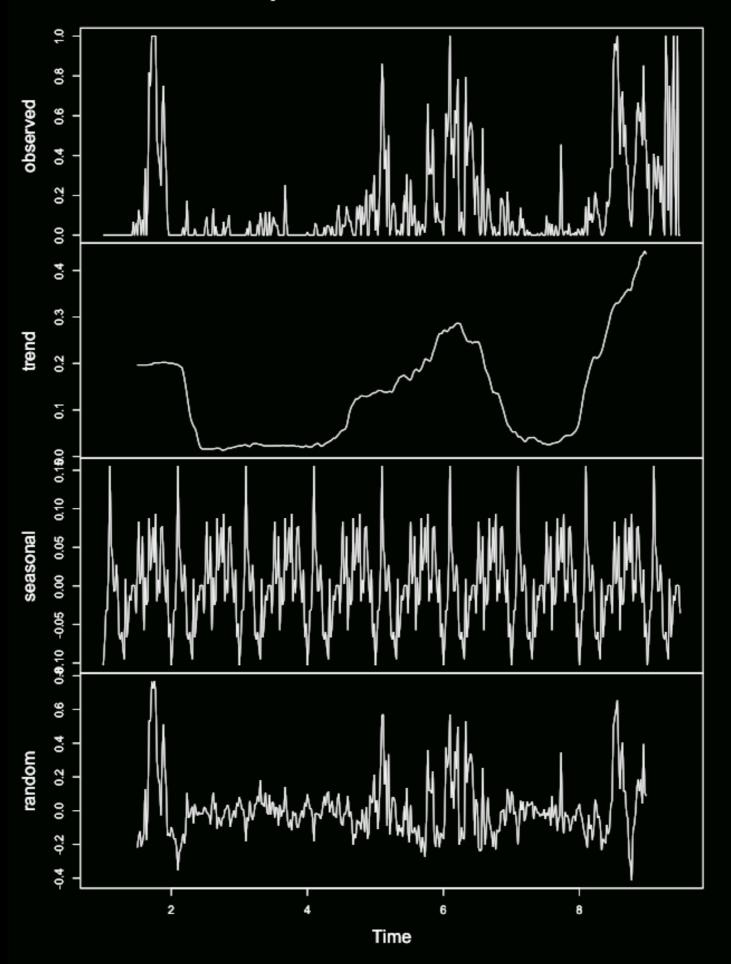


# Tools for analyzing and visualizing data Identifying long-term ecosystem trends





### Decomposition of additive time series



Original data (= sum of below)

Long-term trend

Periodic element

Random element

