

Genomics of Cultured Species: From Discovery to Mechanism

Plant and Animal Genome

January 13 2012

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Where We Are Going Today

- Impacts of Development on Oysters in Tidal Creeks
- Impacts of Environmental Conditions (physical and chemical) on Oysters
- Impacts of Environmental Conditions and Disease on Oysters

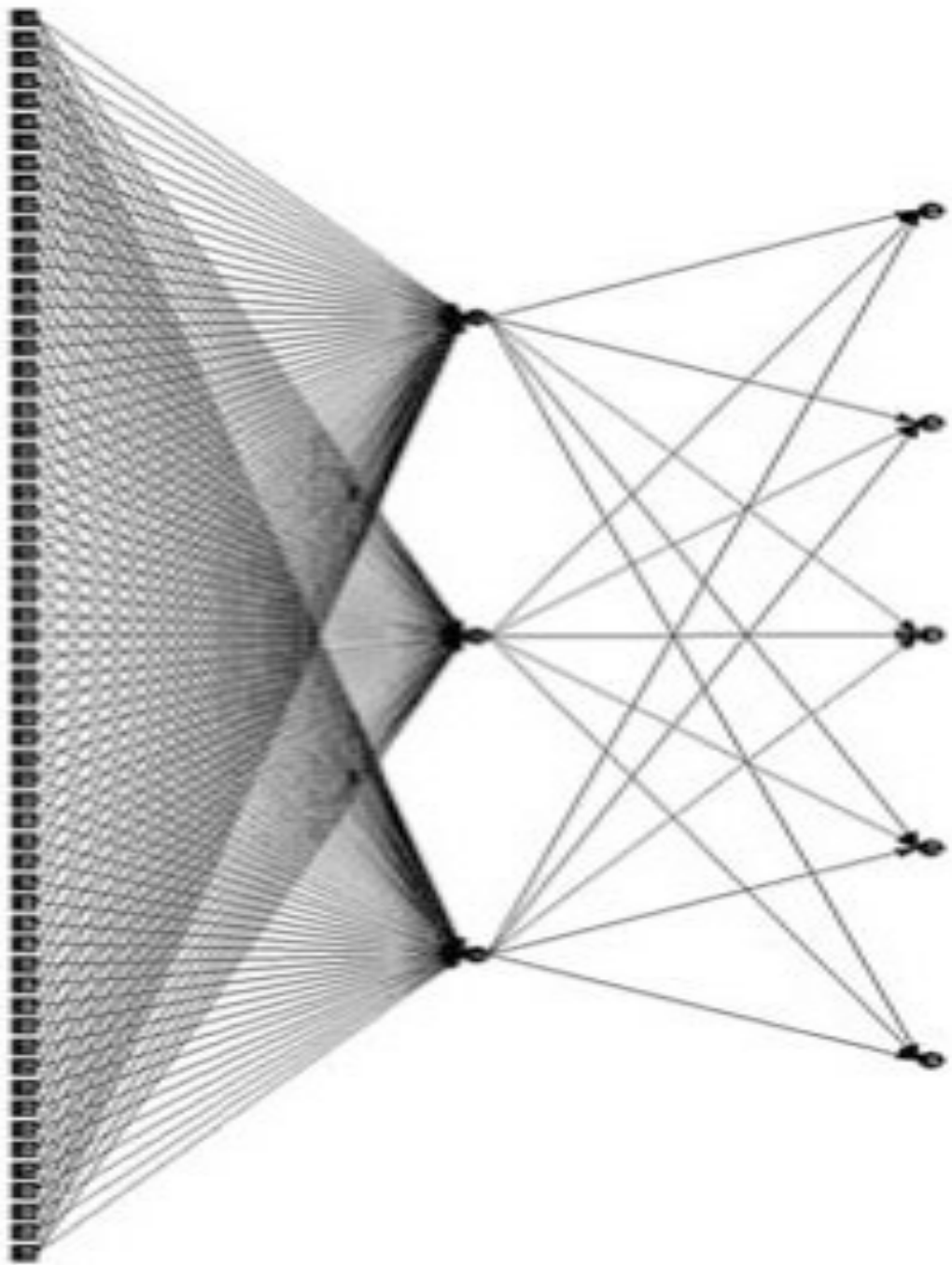
The Problem

- Given 15,000 genes on a microarray, find a set (size unknown) that is an optimal solution (maps to) for an output state.
- Verifying that a given set “fits” the output is easy
- Finding the optimal set(s) is impractical-

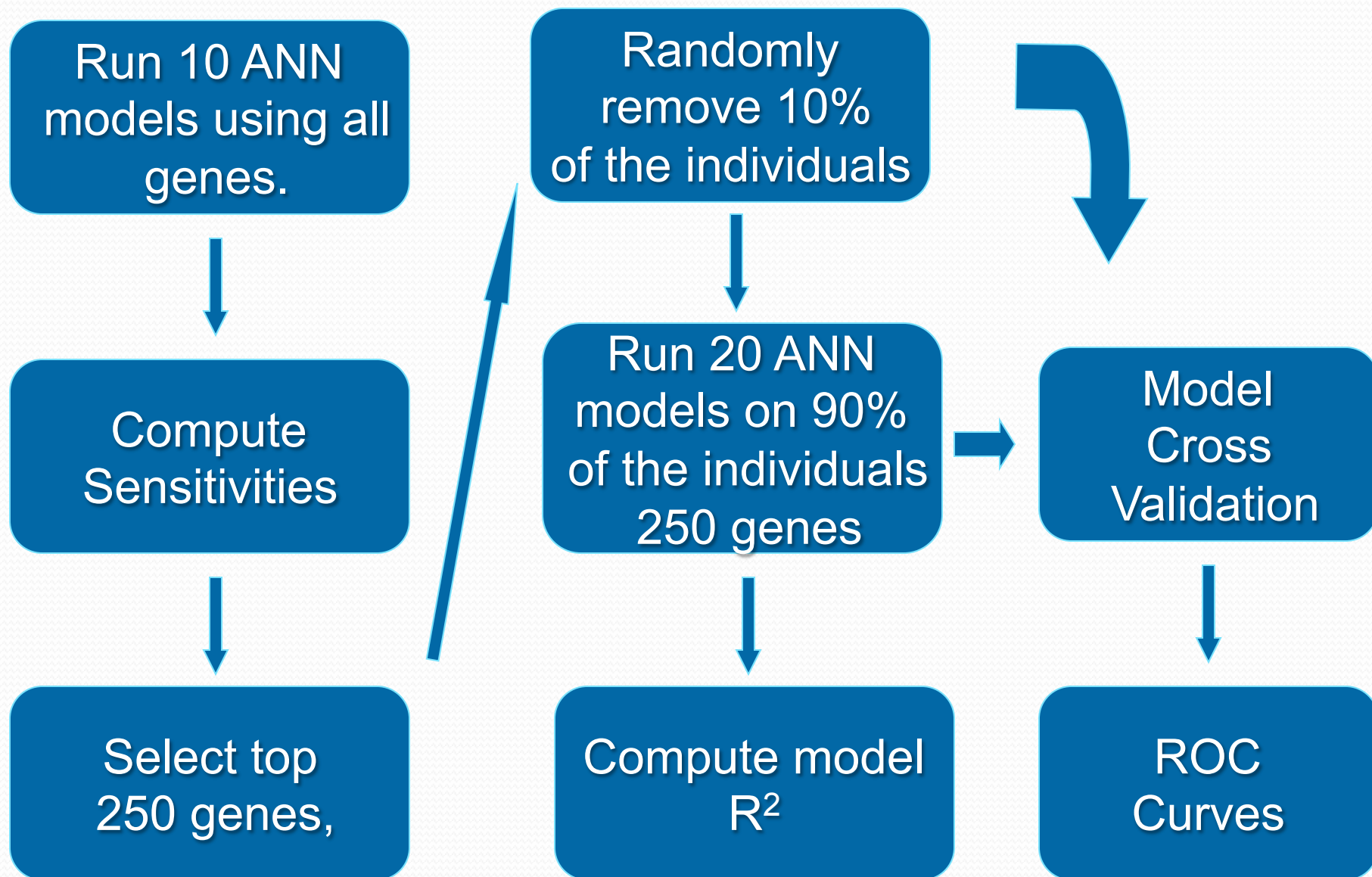
My Bias

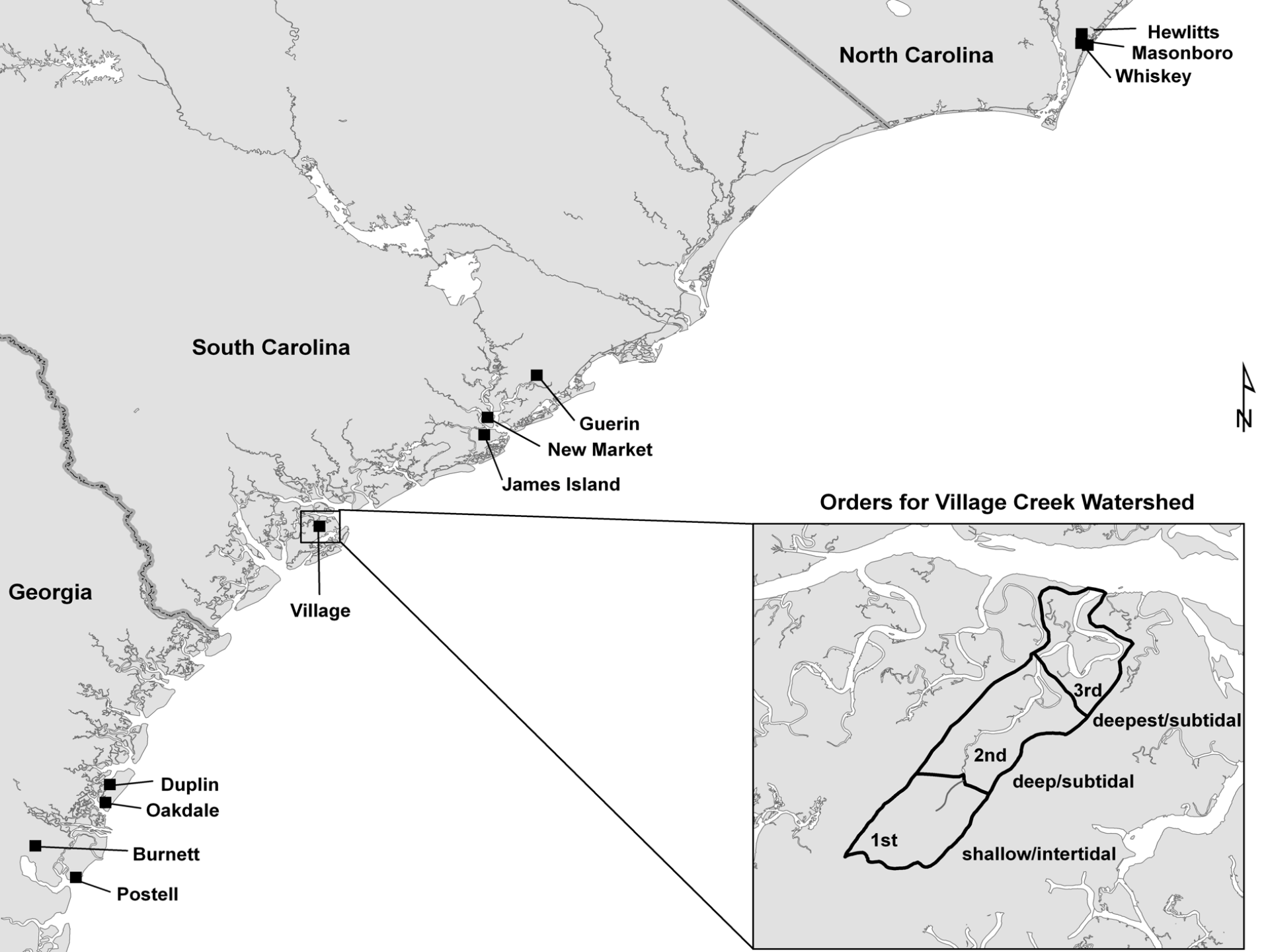
- The transcriptome is a dynamically interacting network and nothing is 'independent'
- Hence linear analysis tools such as ANOVA's are not appropriate

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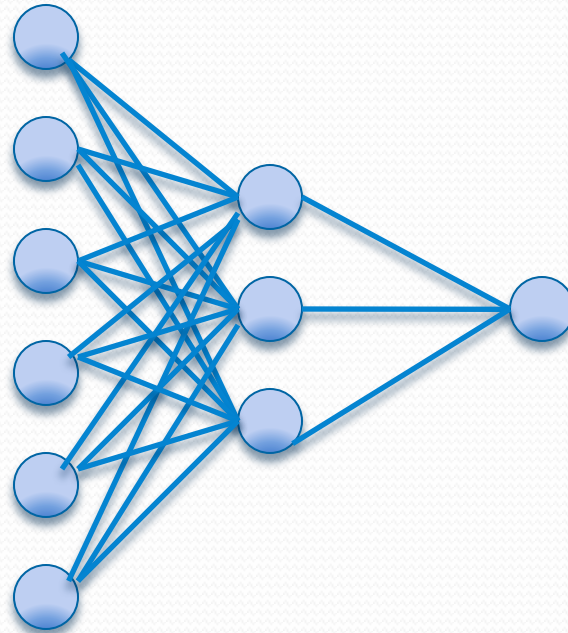


The Environmental Parameters that Affect Oyster Gene Expression

Chapman *et al.* 2011 Molecular
Ecology

- ✧ Let's map Gene Expression to Individual Environmental Conditions (physical and chemical)
- ✧ Then Reverse the Logic and Map Environmental Conditions to Individual Genes

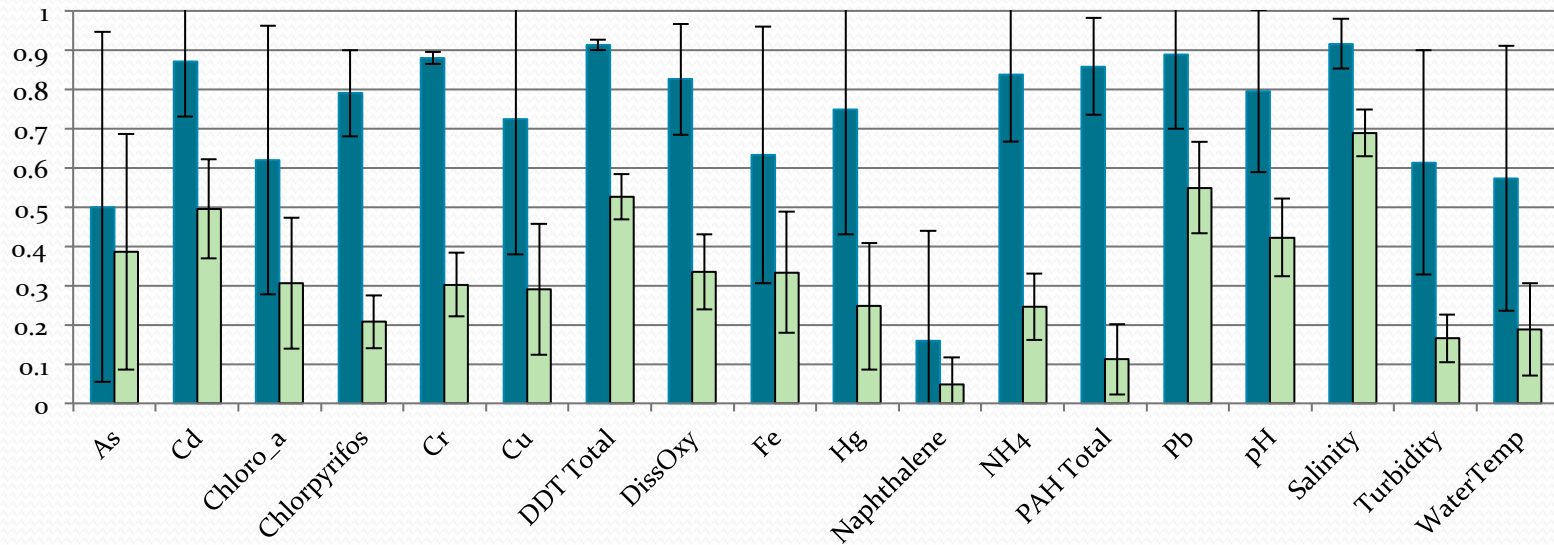
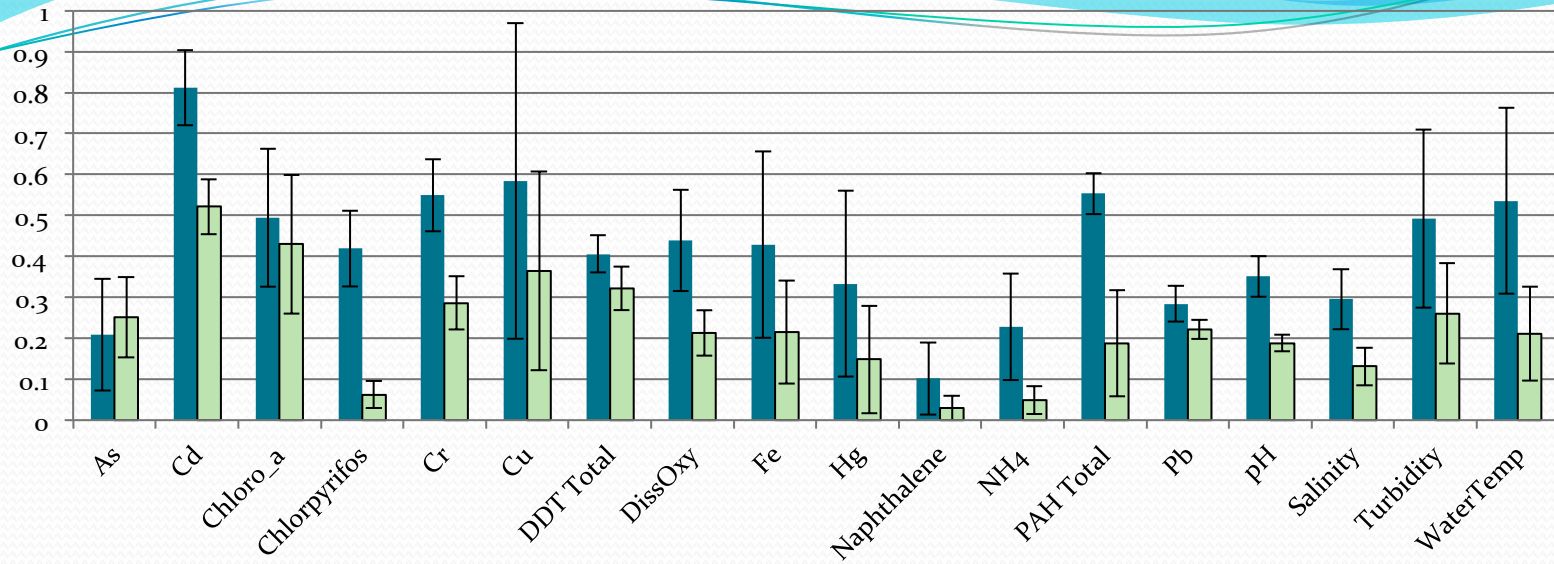
Genes



Environmental
parameters

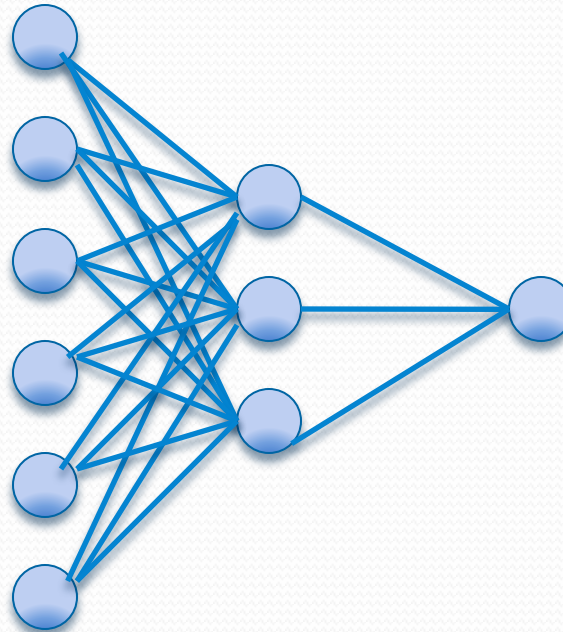
R-squares

Gill

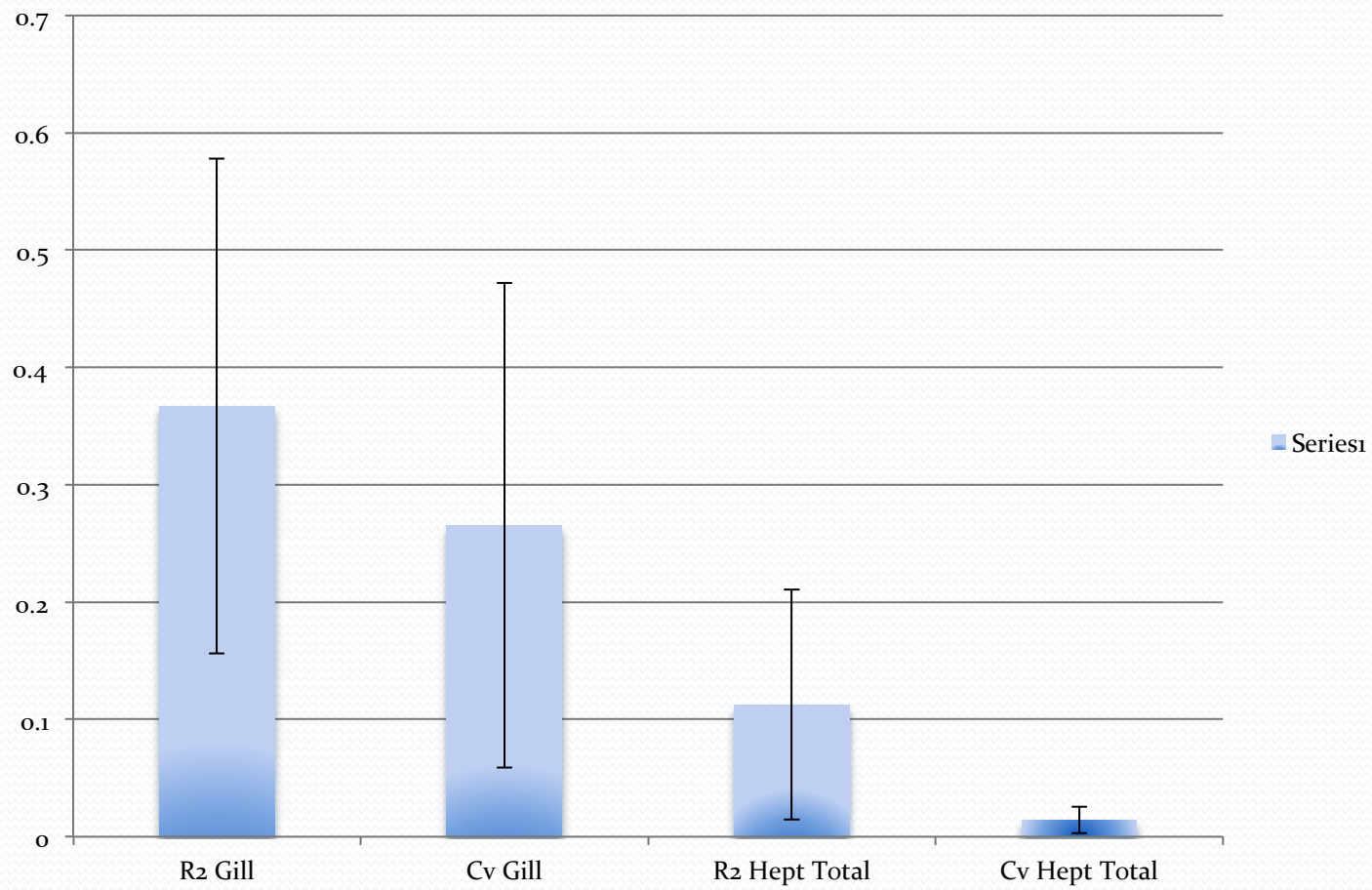


Hepatopancreas

Environmental
parameters

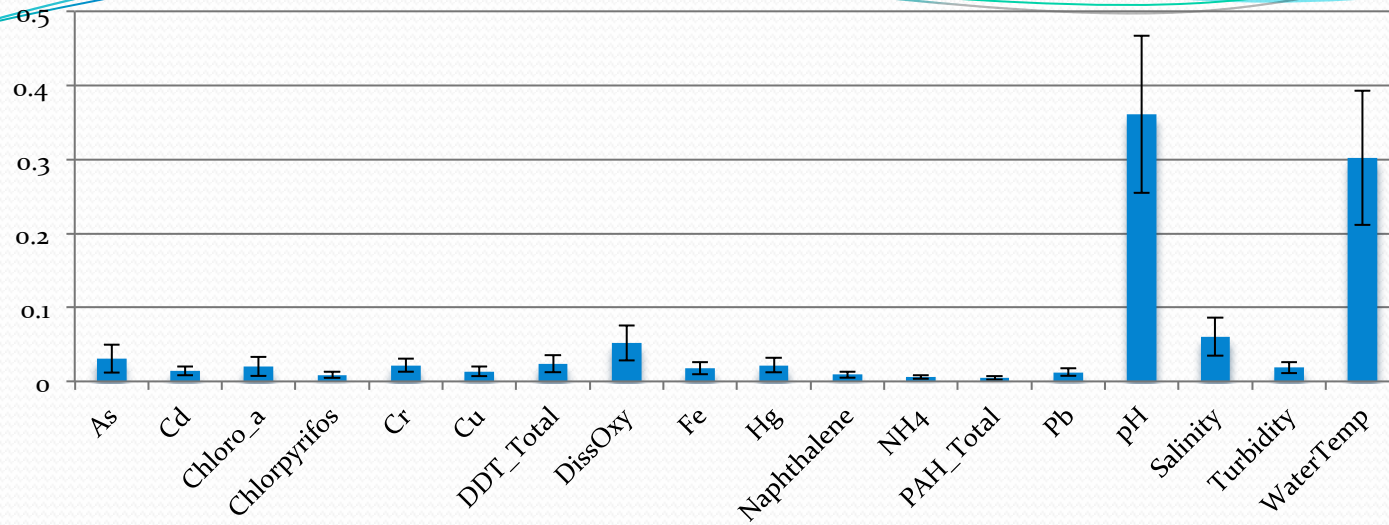


Genes

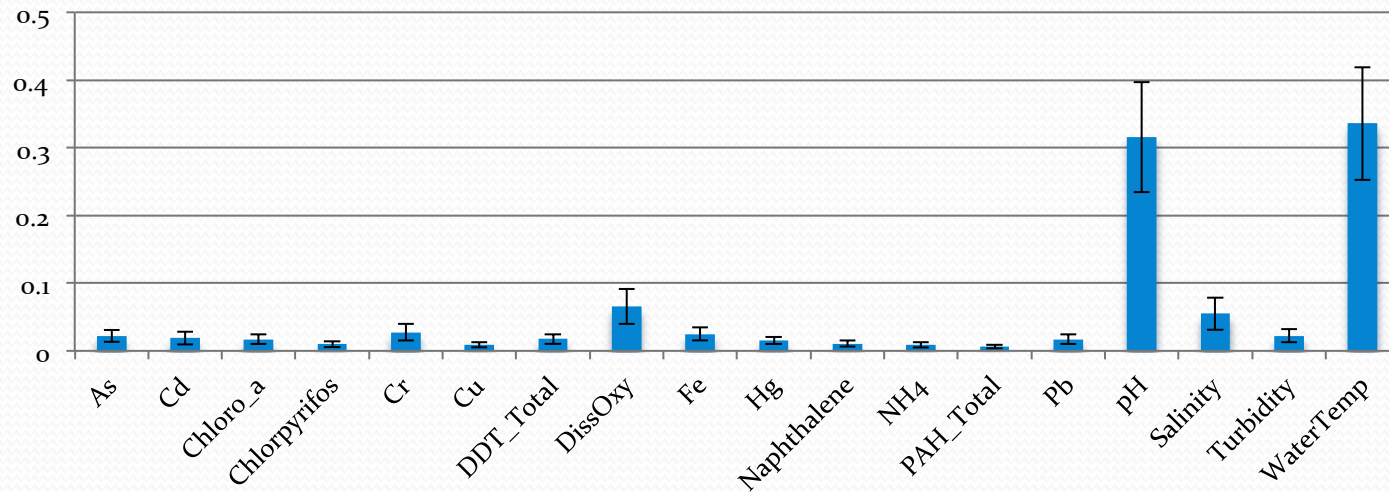


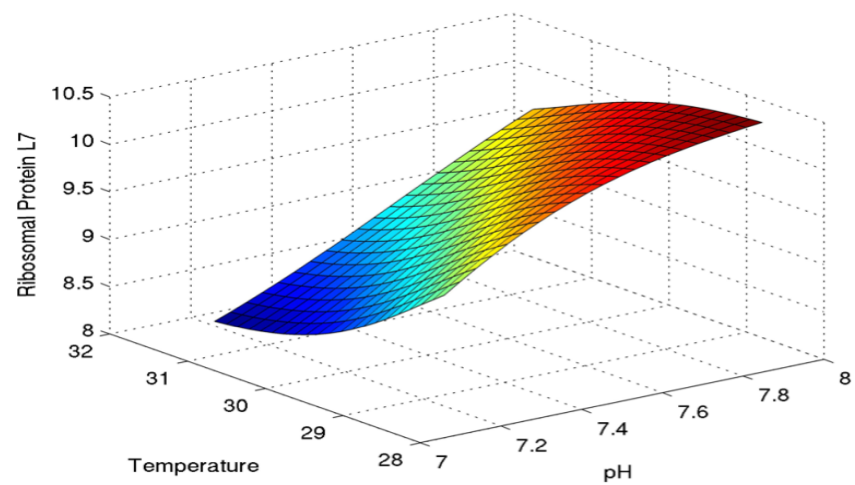
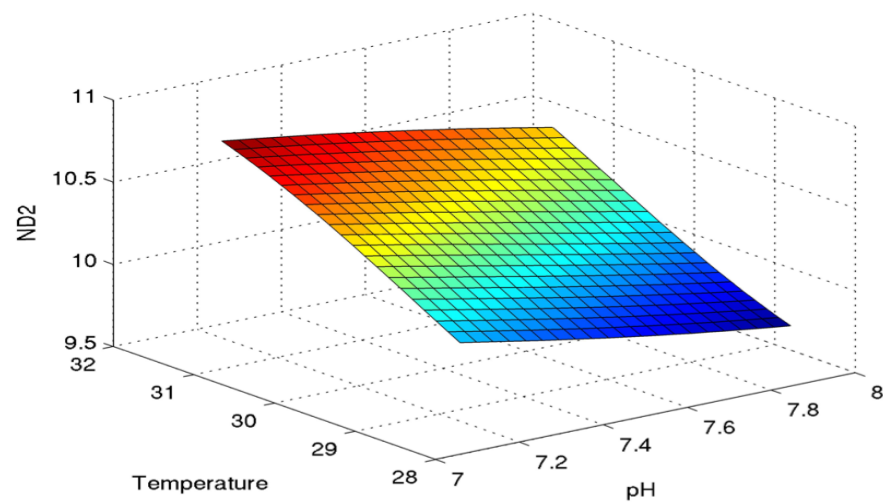
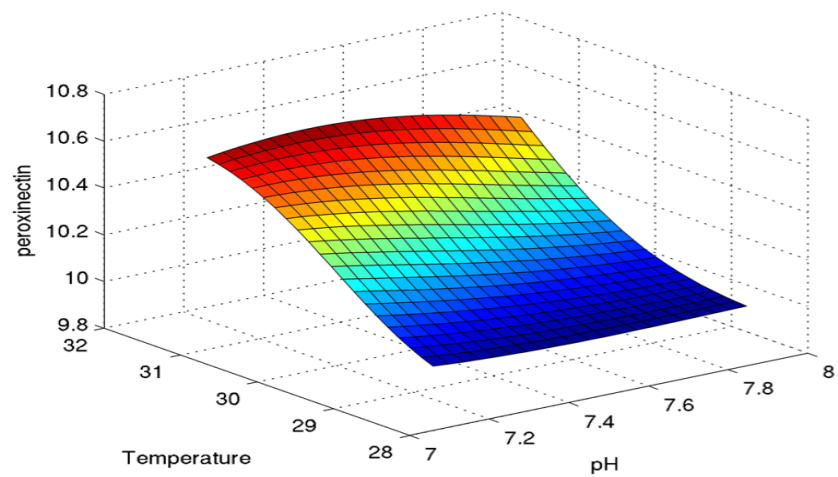
Sensitivities

Gill

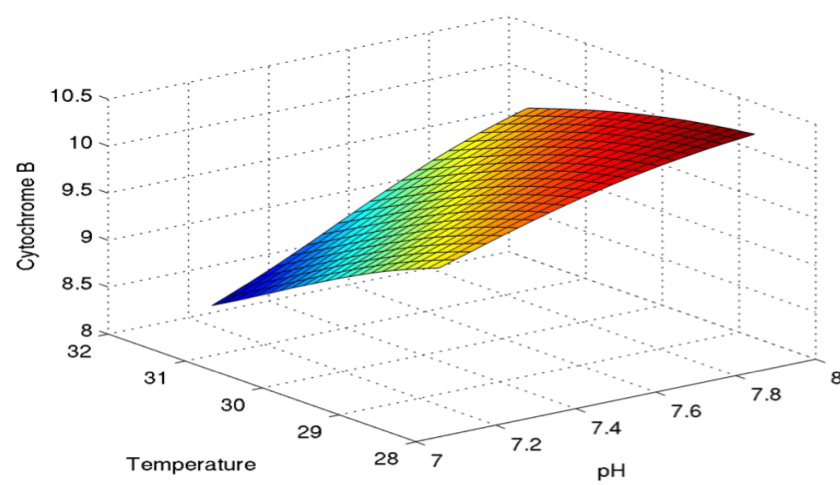


Hepatopancreas





C



D

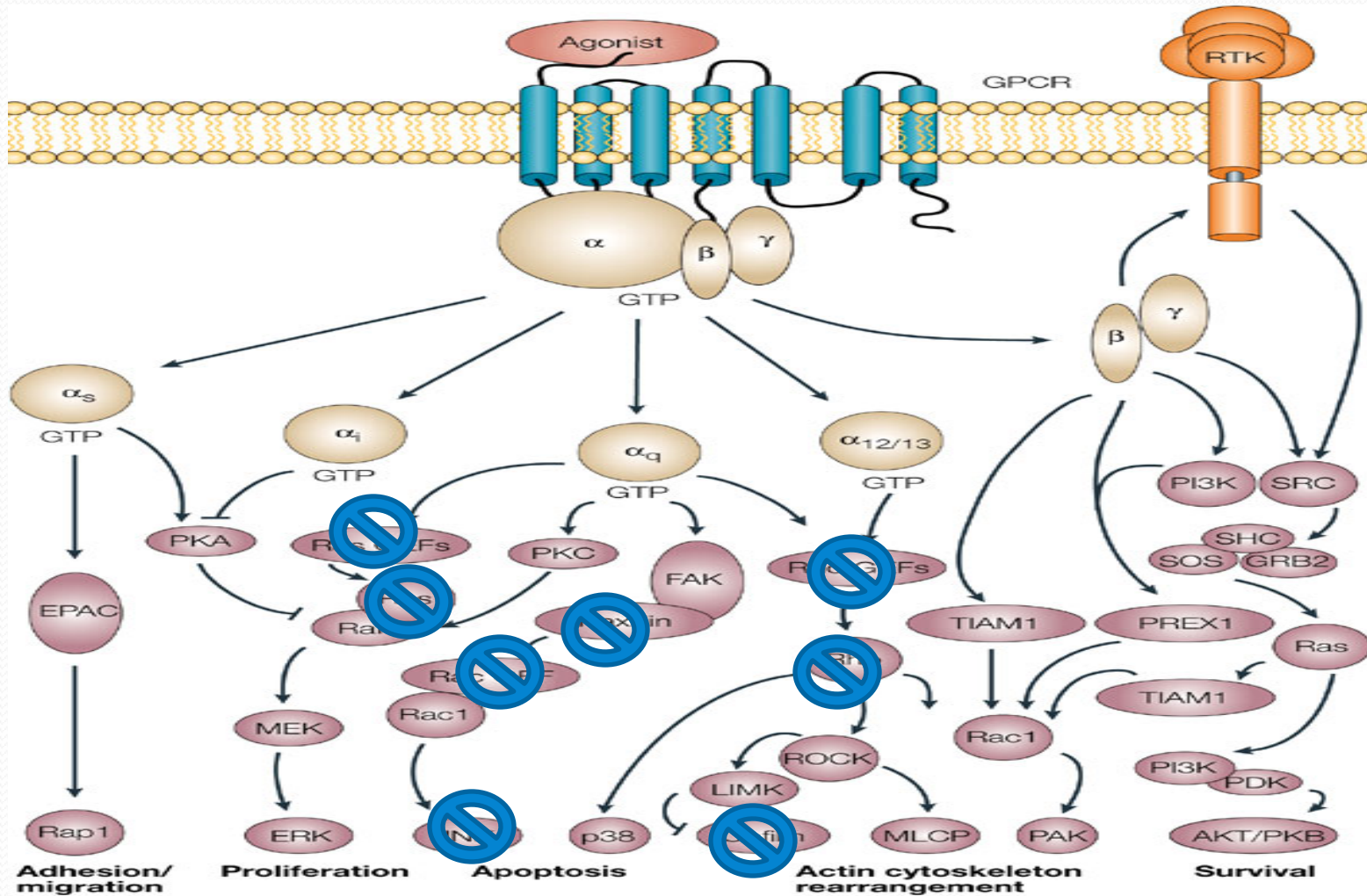
Data to this point

Collective behavior of genes can predict water quality in both gill and hepatopancreas with some precision

Collective behavior of water quality parameters are much less successful in predicting expression levels of individual genes

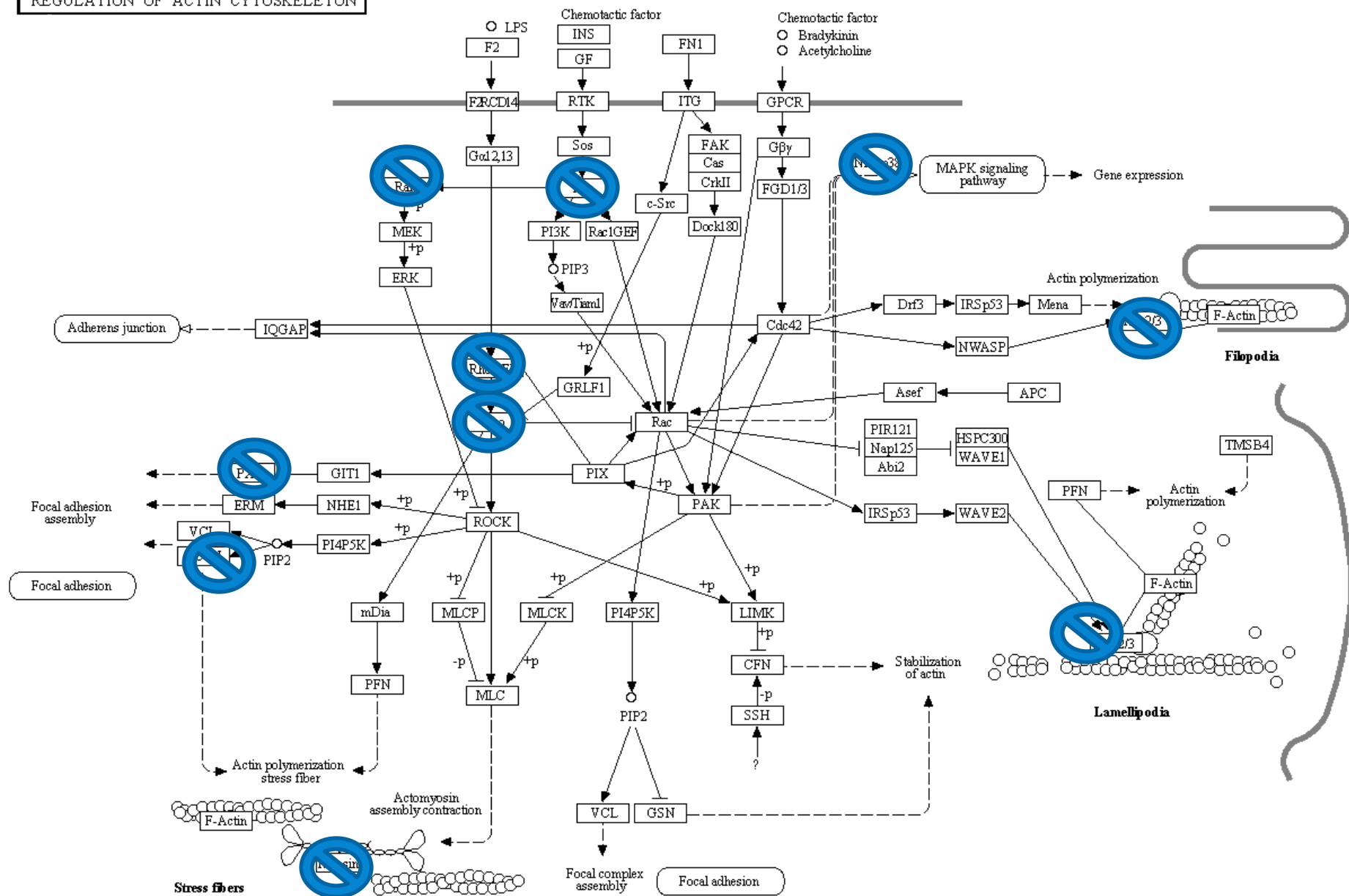
This implies that the value of transcriptomic data is not in expression of individual genes, but rather their collective behavior-THIS BEHAVIOR CANNOT BE EXTRACTED FROM ANOVA

Focal Adhesion Complex

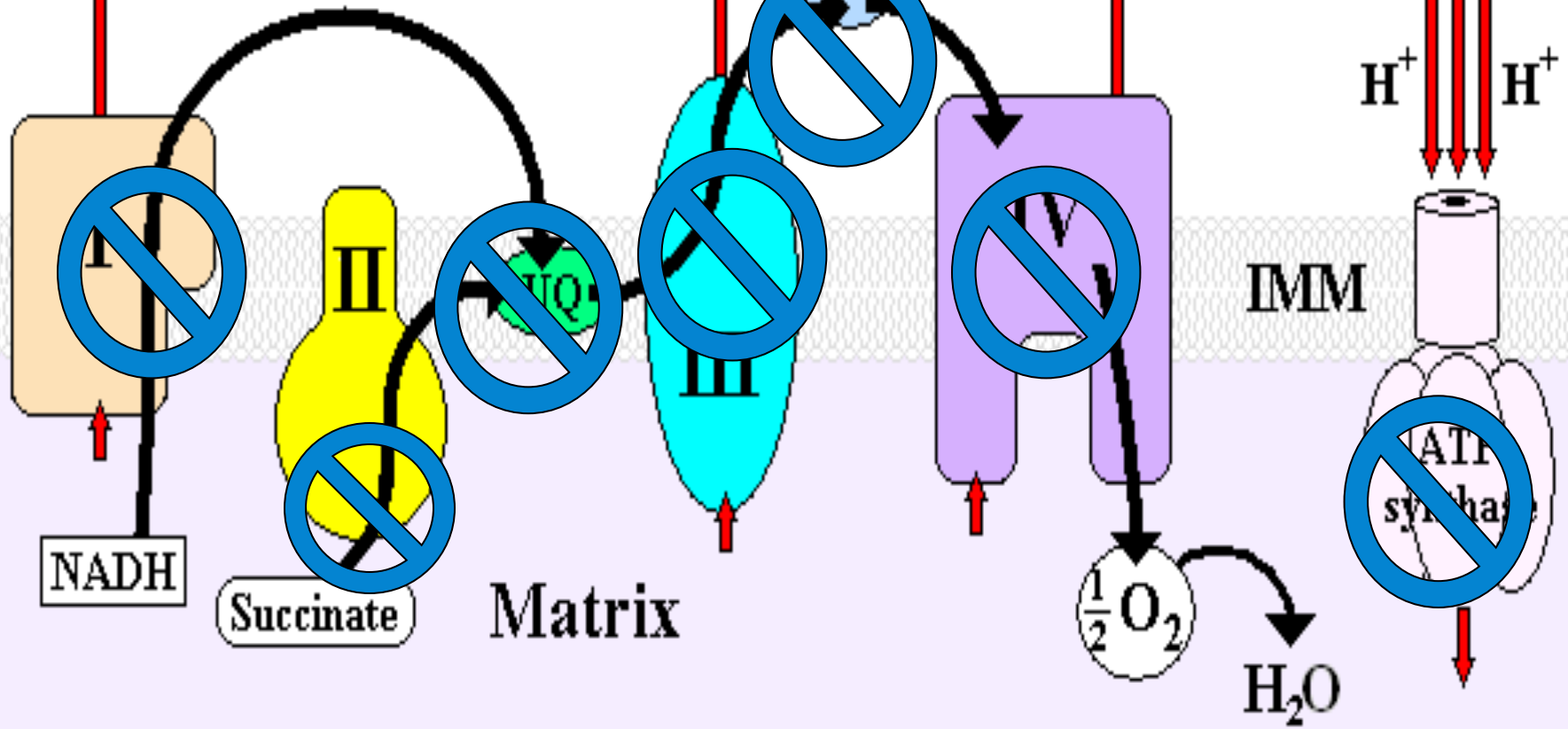


Nature Reviews | Molecular Cell Biology

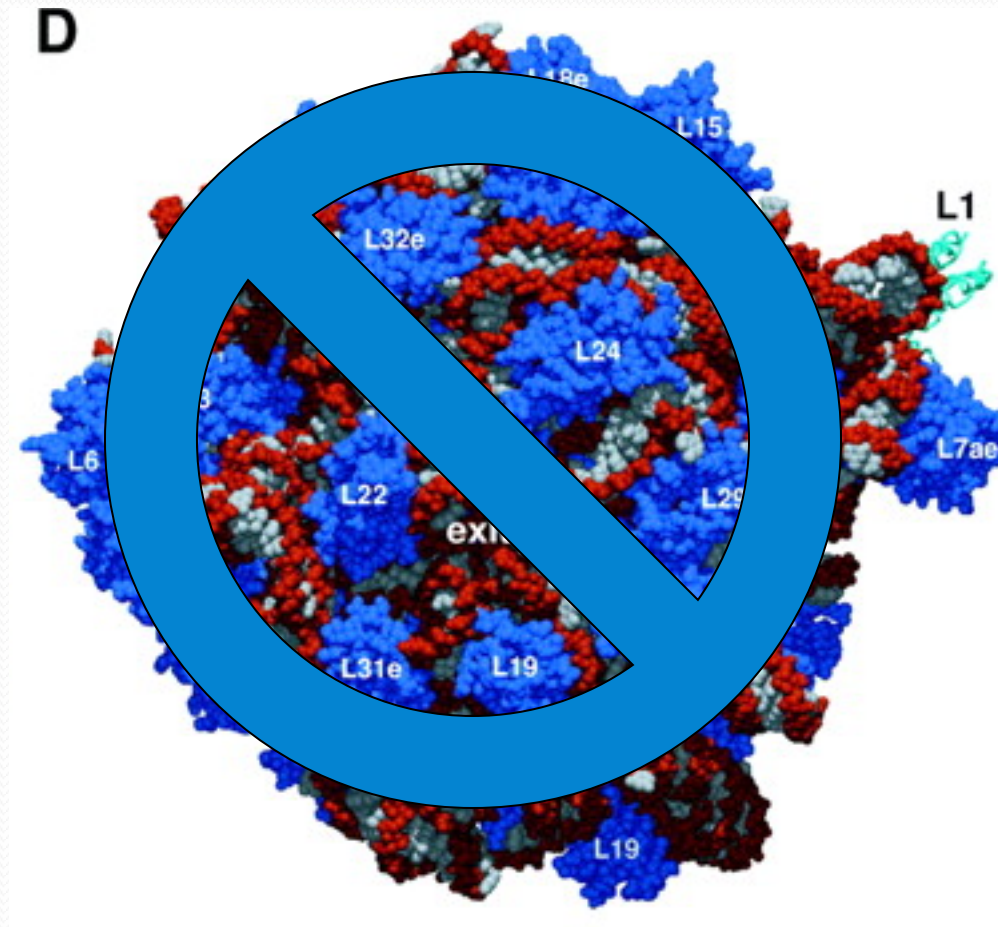
REGULATION OF ACTIN CYTOSKELETON

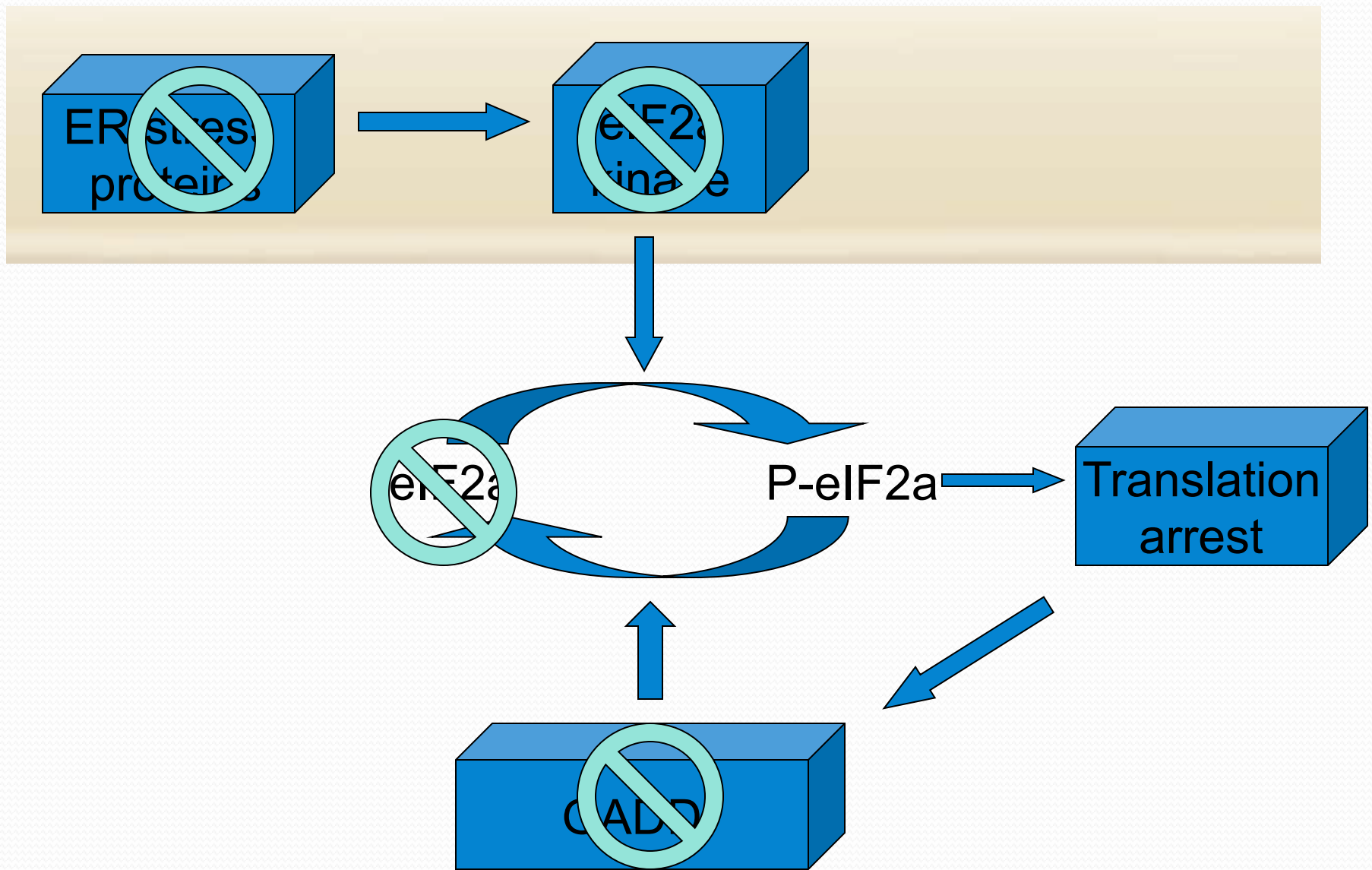


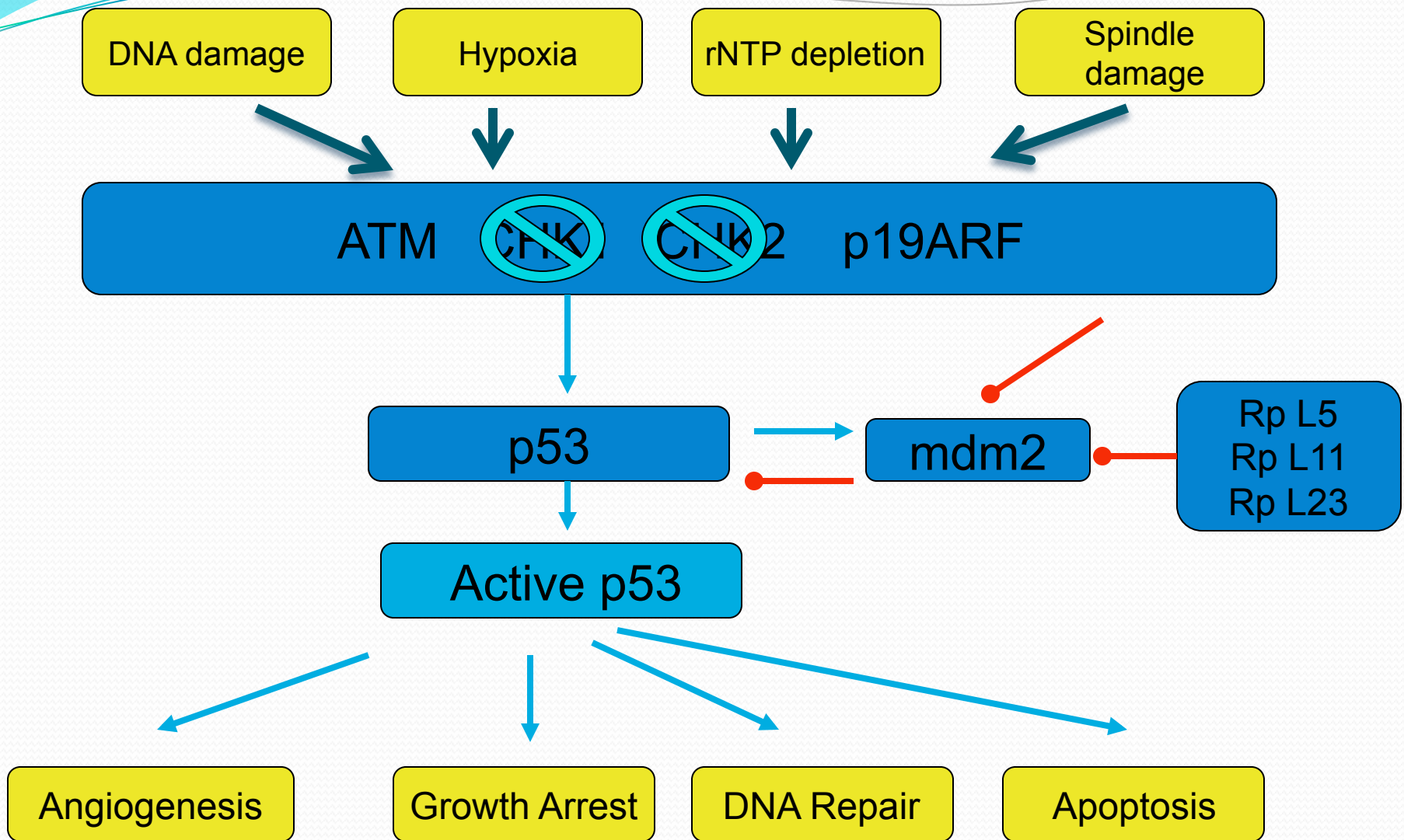
Intermembrane
space



Ribosomal Proteins







Maintenance

Growth

Differentiated tissues

+O₂ -O₂

Glucose

Glucose

Pyruvate

Pyruvate

Alanine, Succinate Octopine

Anaerobic Glycolysis
2 moles ATP

Proliferative tissues

+O₂

Glucose

Pyruvate

85%

Alanine, Succinate
Octopine

Aerobic Glycolysis
4 moles ATP

+O₂



CO₂

Oxidative Phosphorylation
36 moles ATP

+O₂



CO₂

The transcriptome is saying that
development and climate change should
impact

Metabolic processes

The generation of lipids, amino acids etc needed
for growth

Growth rates

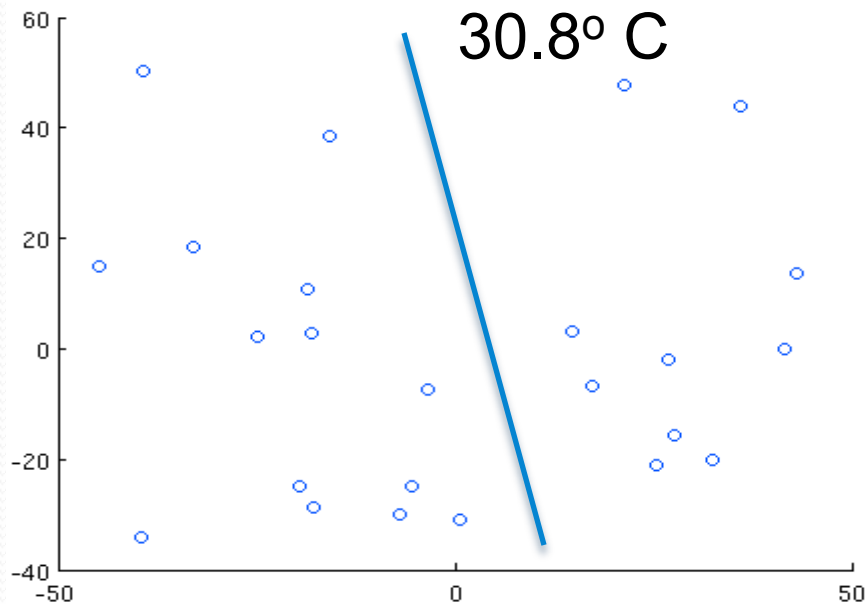
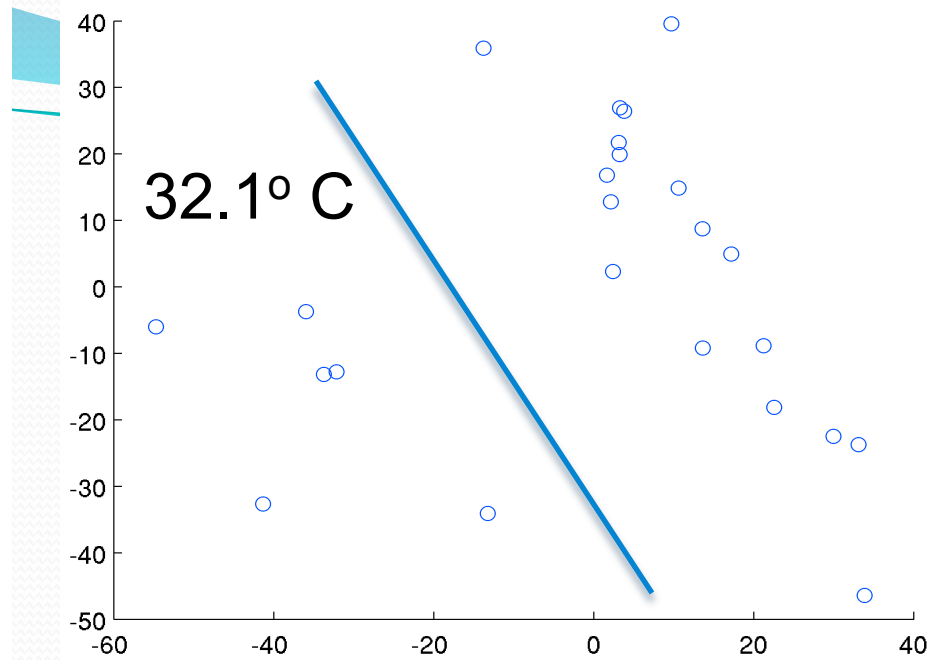
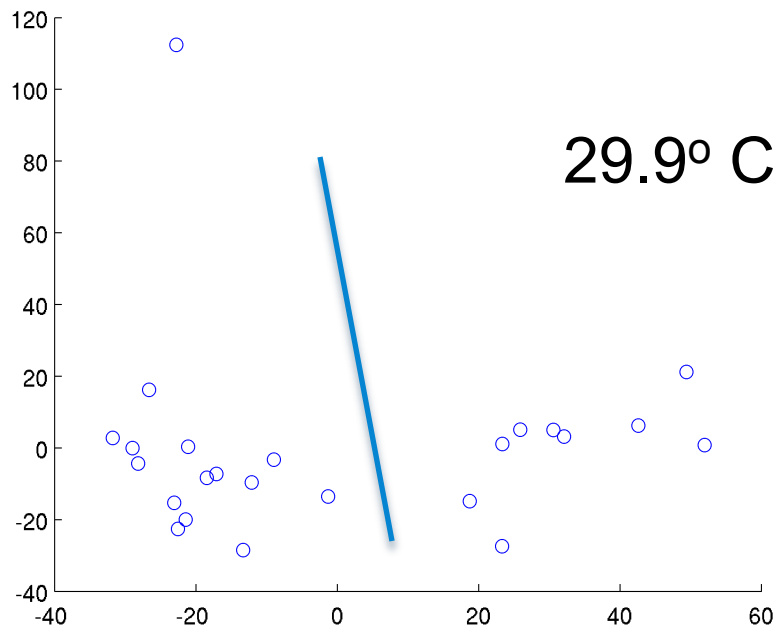
Reproduction

Biom mineralization

Does it???



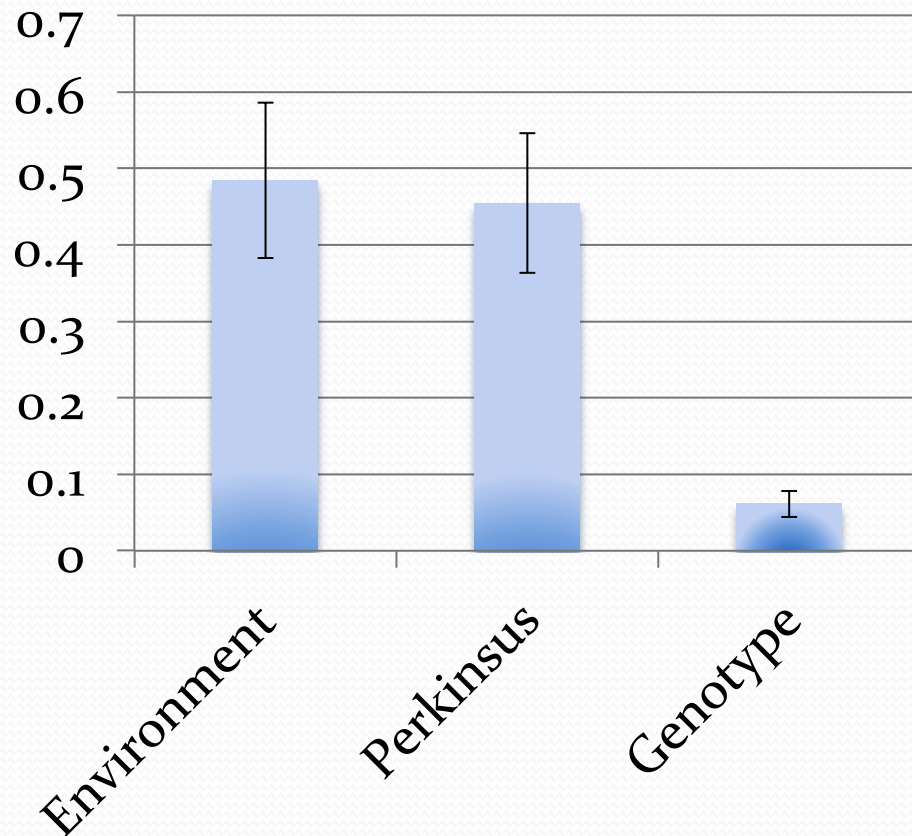
The Impact of *Perkinsus* and Environmental Conditions in the Gulf of Mexico



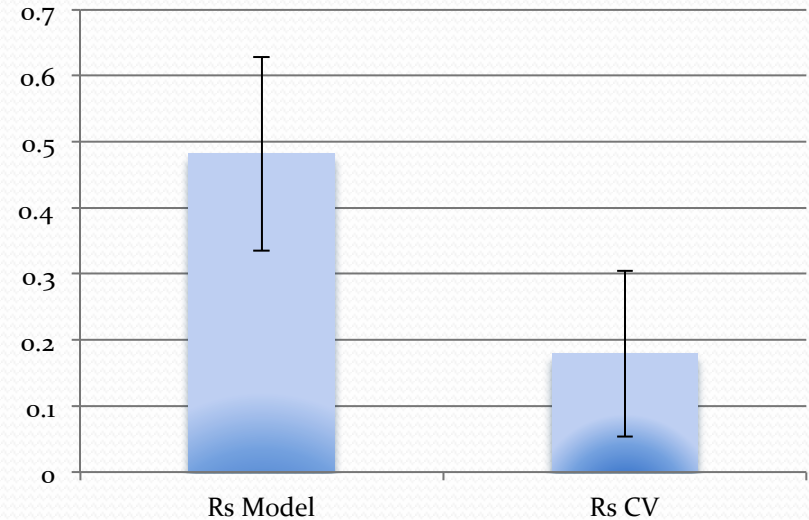
An attempt to find more
in the data using PCA.
Are the two groups in all
locales surveyed. Boys
and girls?-OOPS

Average R-squares and sensitivity of individual genes, N=558

Sensitivities

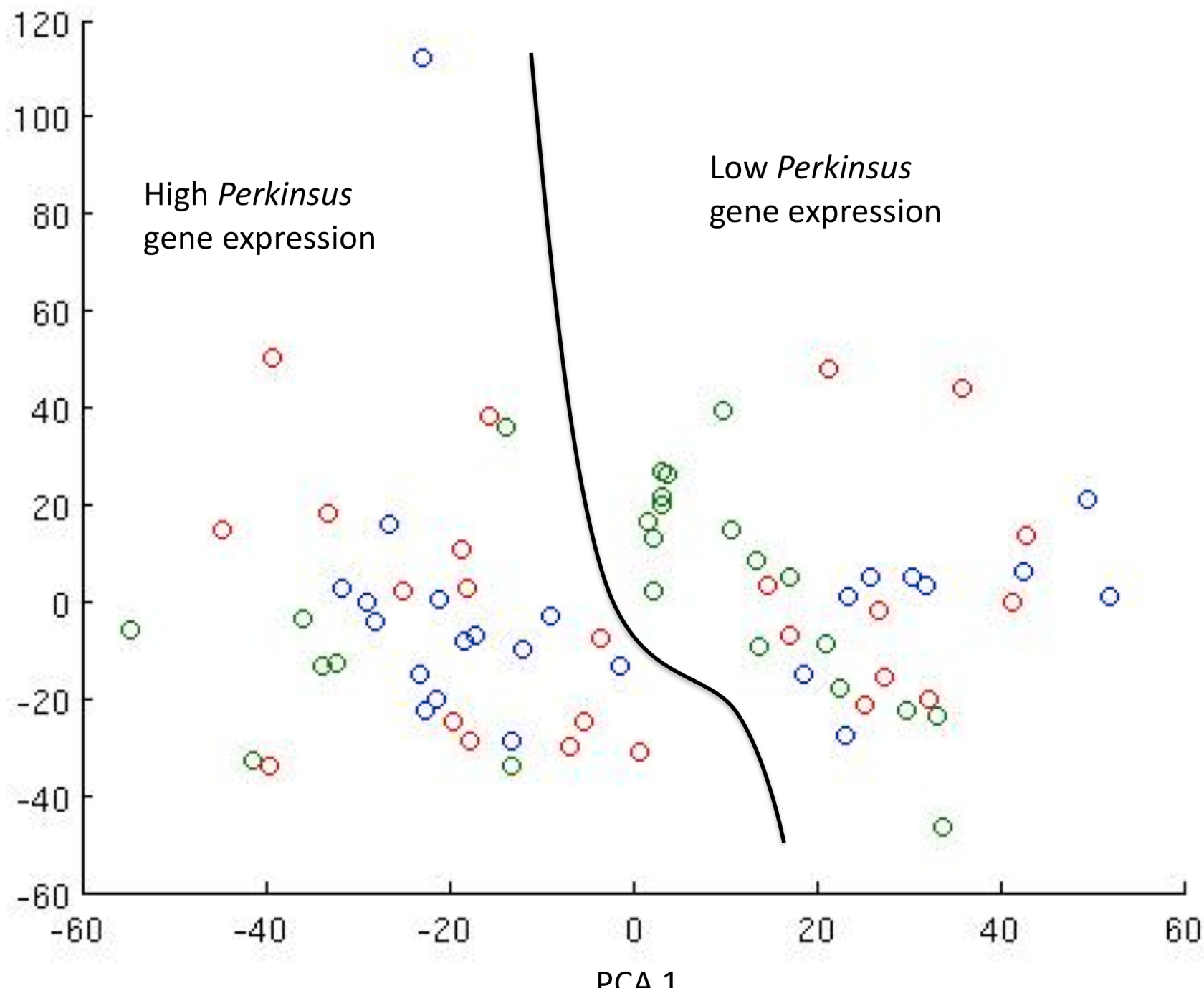


R-square



Mapping Environmental variables, Perkinsus Gene Expression and Oyster Genotypes to Individual Oyster Gene Expression

PCA 2

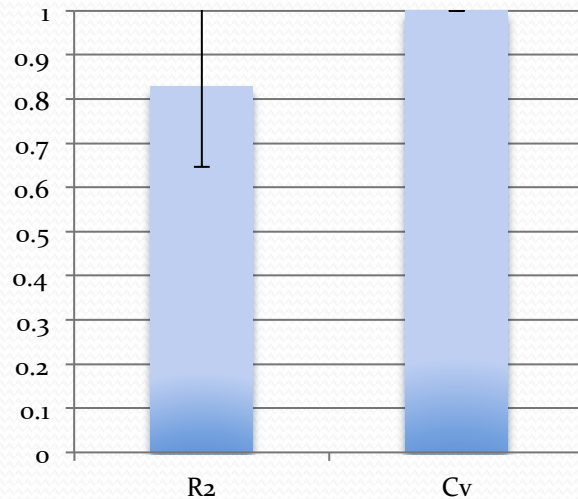


How do you know Perkinsus gene expression is related to infection?

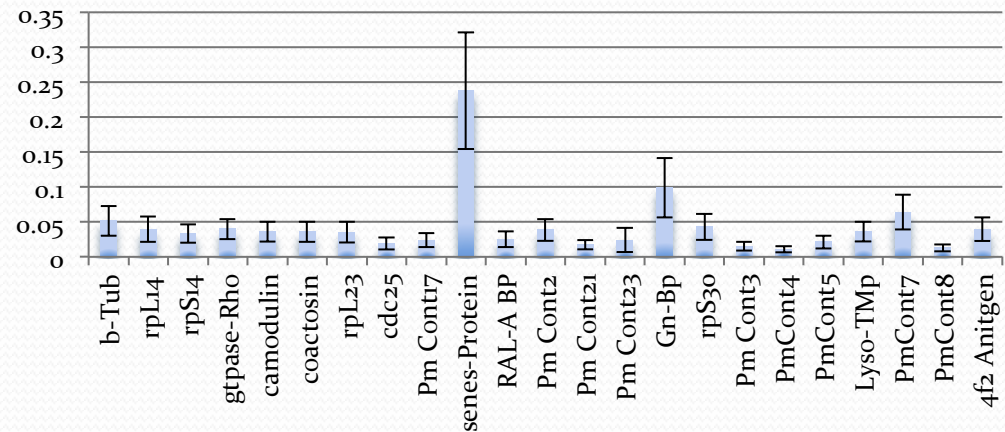
I got data from Shaolin Wang which has 23 Perkinsus genes and RFTM scores from Ximing Guo.

Mapping Perkinsus gene expression to RFTM data generates an Model $R^2 = 1.0$, Cv $R^2 = 1.0$

Shaolin's data : Mapping Perkinsus gene expression to 1462 Oyster genes



Average Sensitivities



Senescence Protein is a deacetylase for p53 promoting its up regulation

We cannot ignore the disease status when working with oysters

I wonder how much misleading or incomplete information is out there with the title

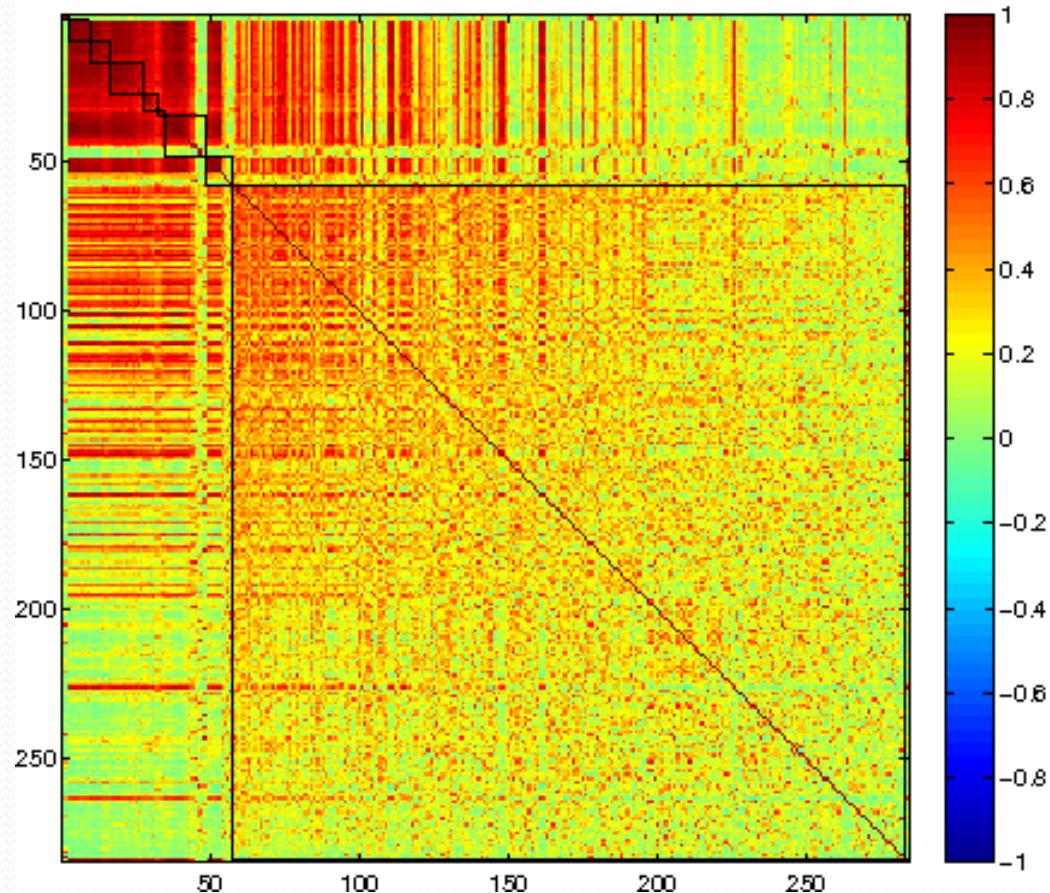
‘Response of Oysters to Environmental.....’

‘Temperature and Salinity Effects on Oyster’

Modified Modularity Clustering

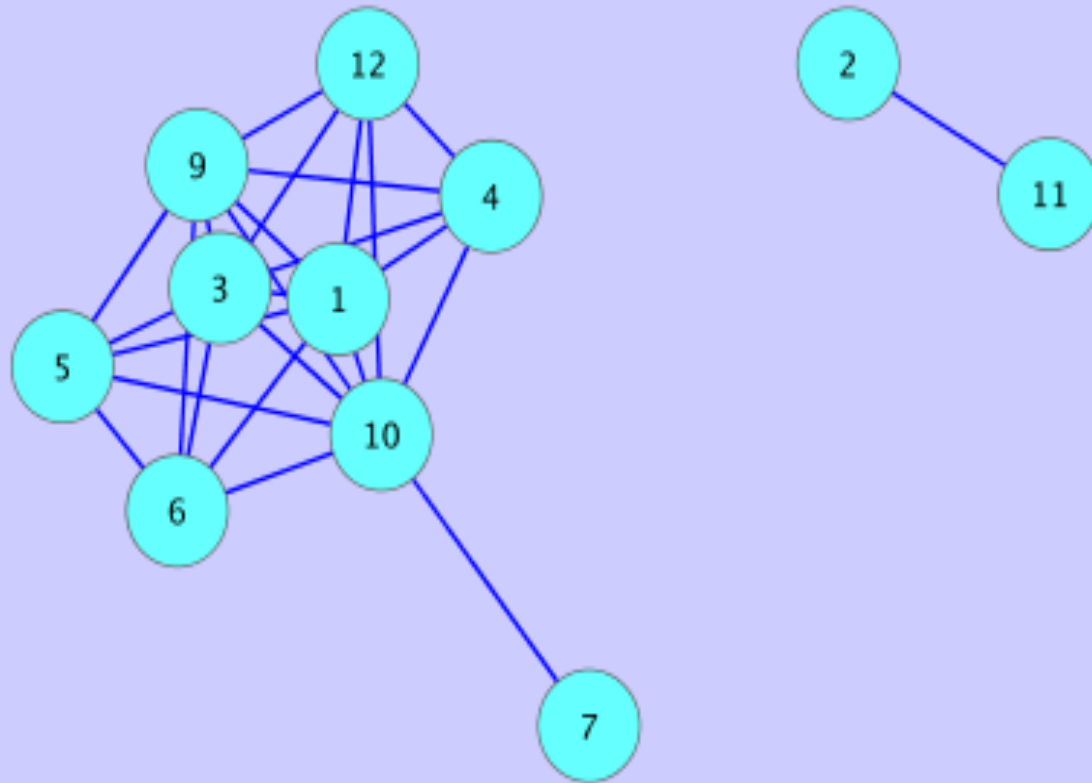
Finding Genes that Co-Vary in GOM study

<http://mmc.gnets.ncsu.edu/>



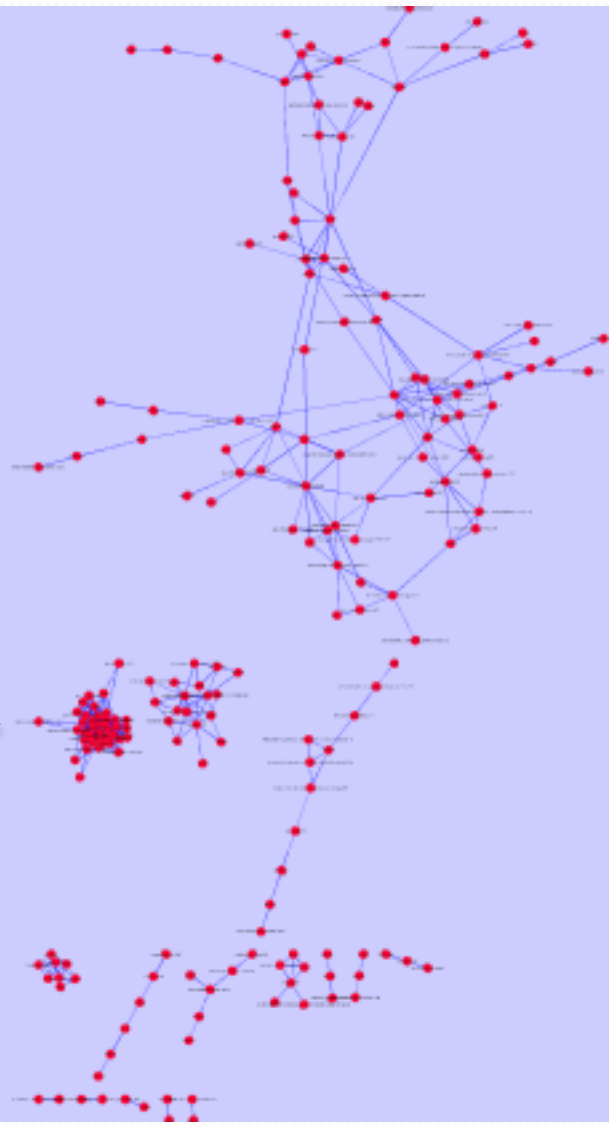
Stone EA, Ayroles JF, 2009 Modulated Modularity Clustering as an Exploratory Tool for Functional Genomic Inference. PLoS Genet 5(5): e1000479. doi:10.1371/journal.pgen.1000479
Ayroles JF, Carbone MA, Stone EA, Jordan KW, Lyman RF, et al. (2009) Systems genetics of complex traits in *Drosophila melanogaster*. Nat Genet 41:299-307.

Cytoscape connections of the modules



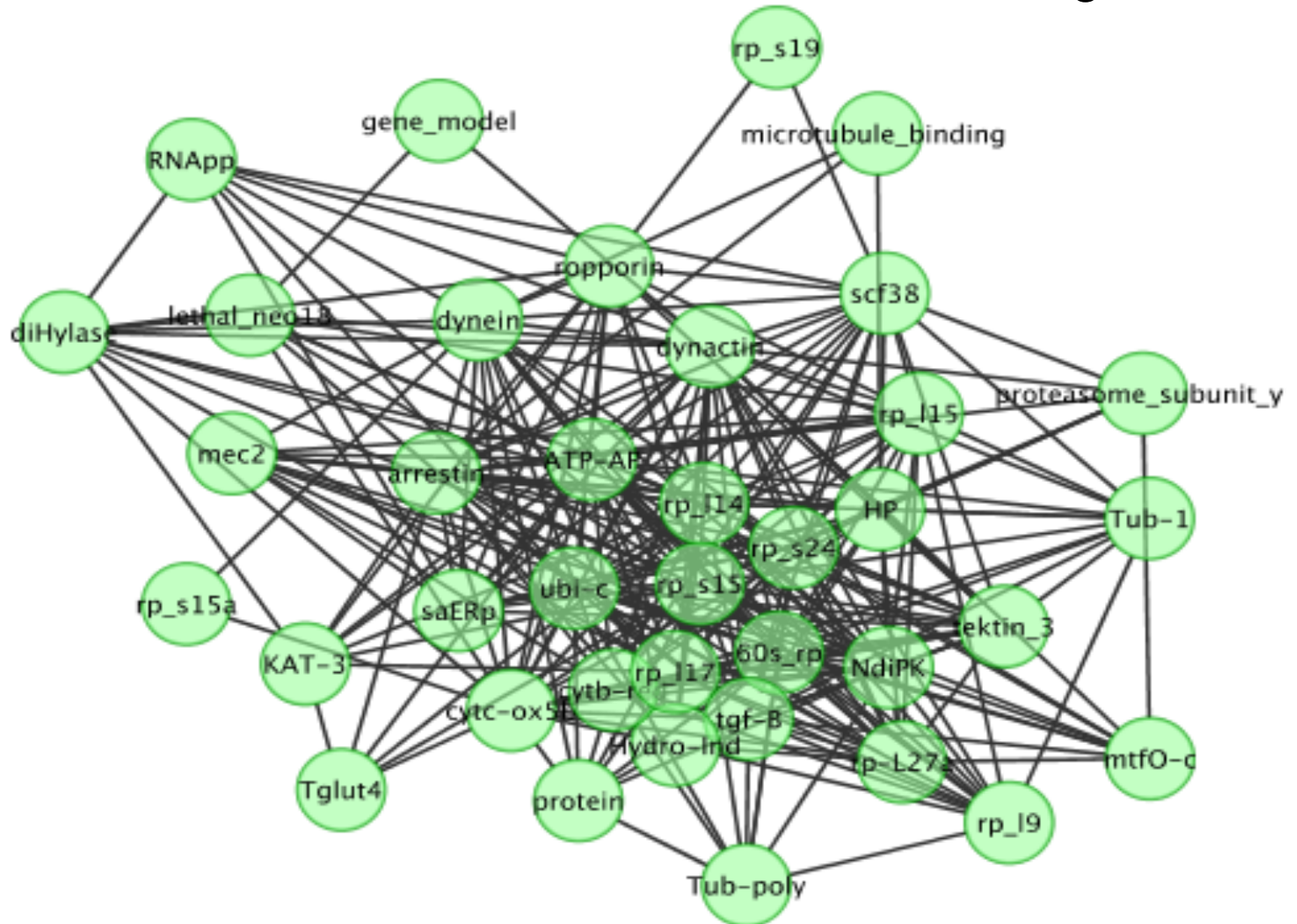
Cytoscape
connection of
individual
genes within all
modules,
 $r^2 \geq 0.5$

Module 3 →

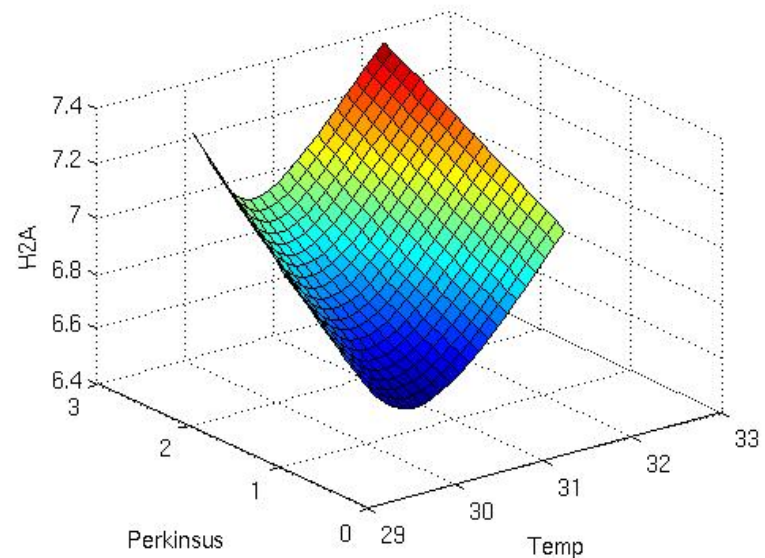
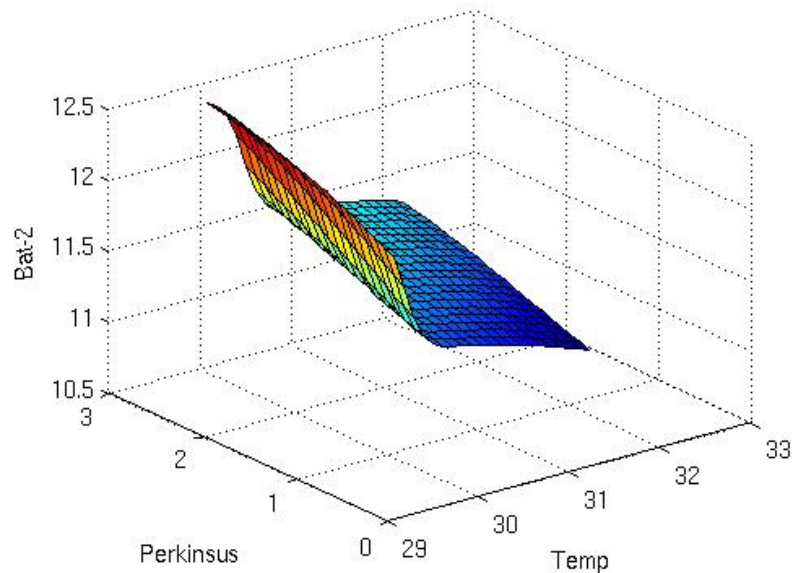
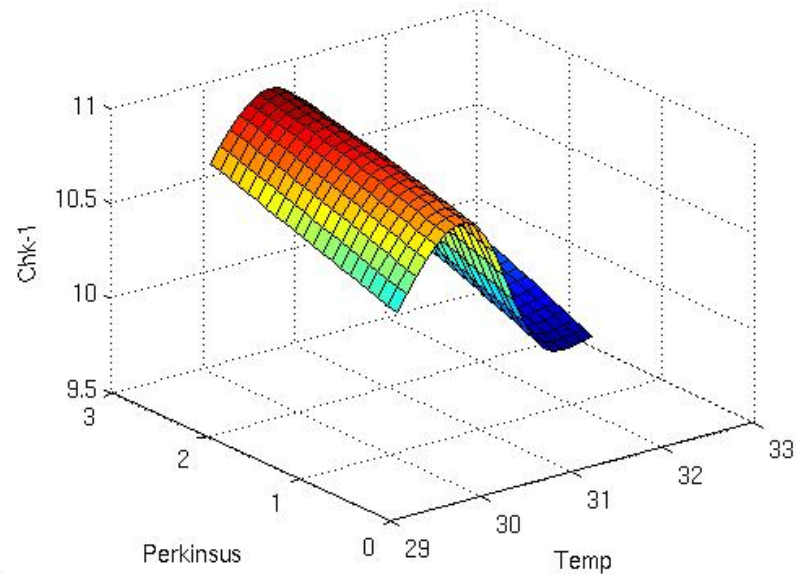
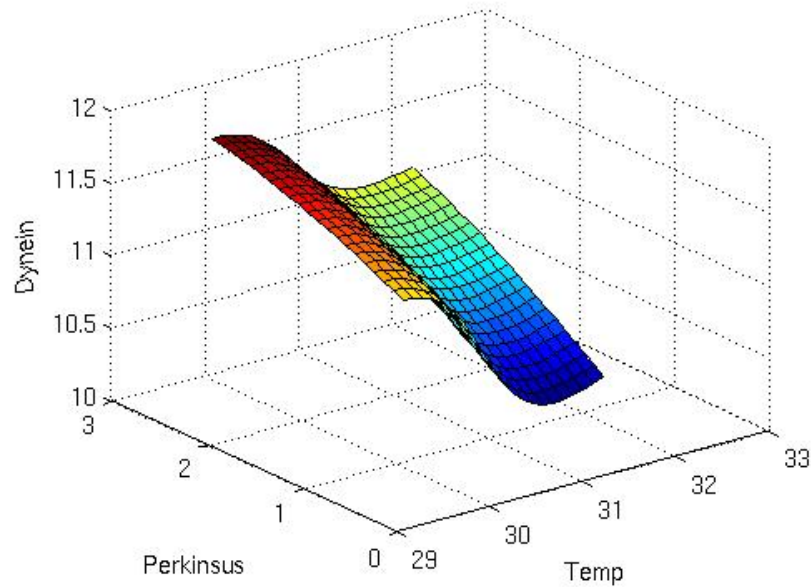


Module 3

Mainly microtubule associated and cellular trafficking

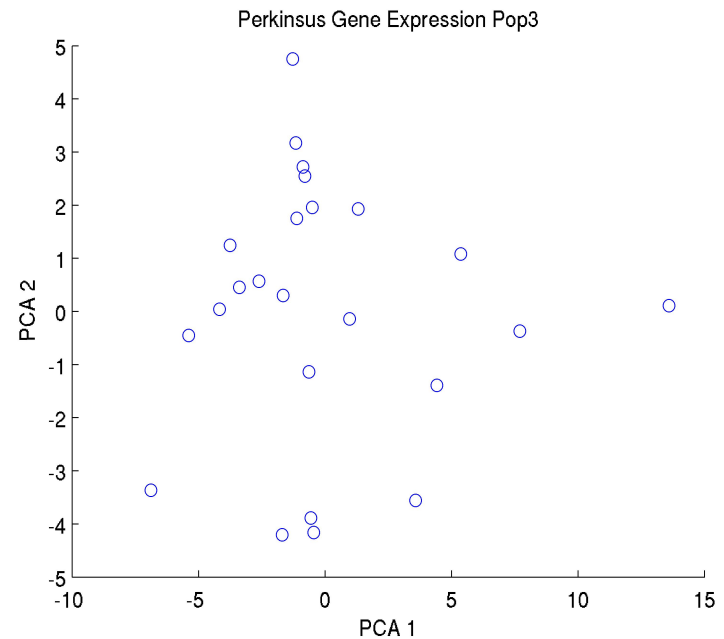
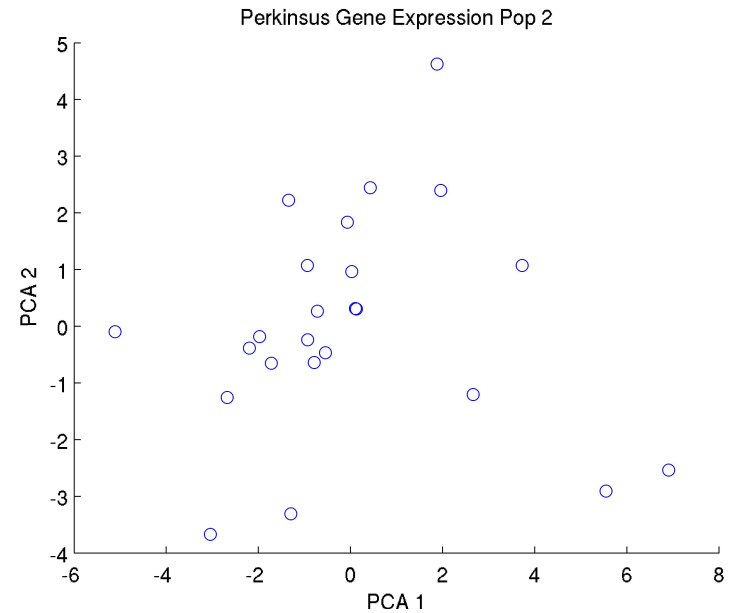
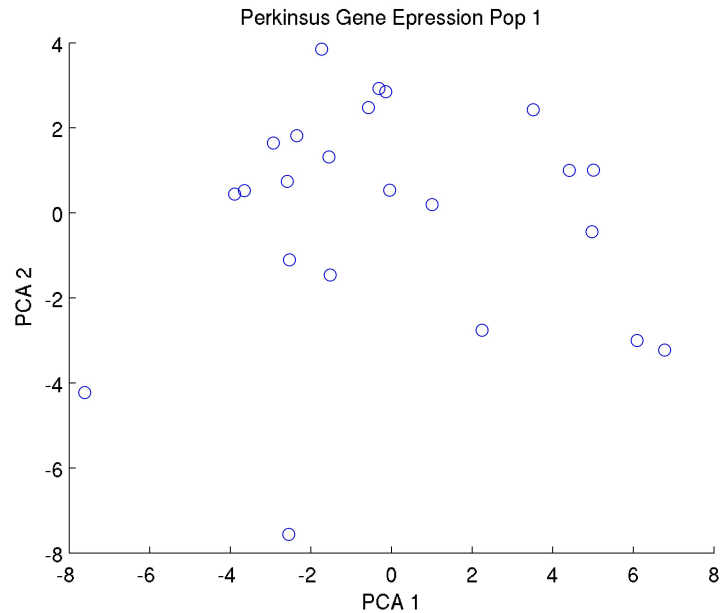


Predictive behavior from Ann models-All models are wrong, some models are useful

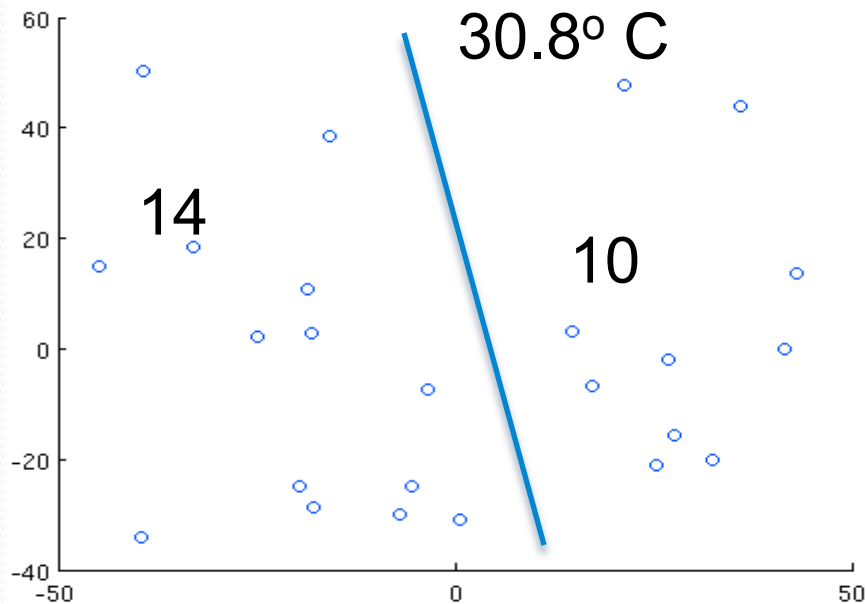
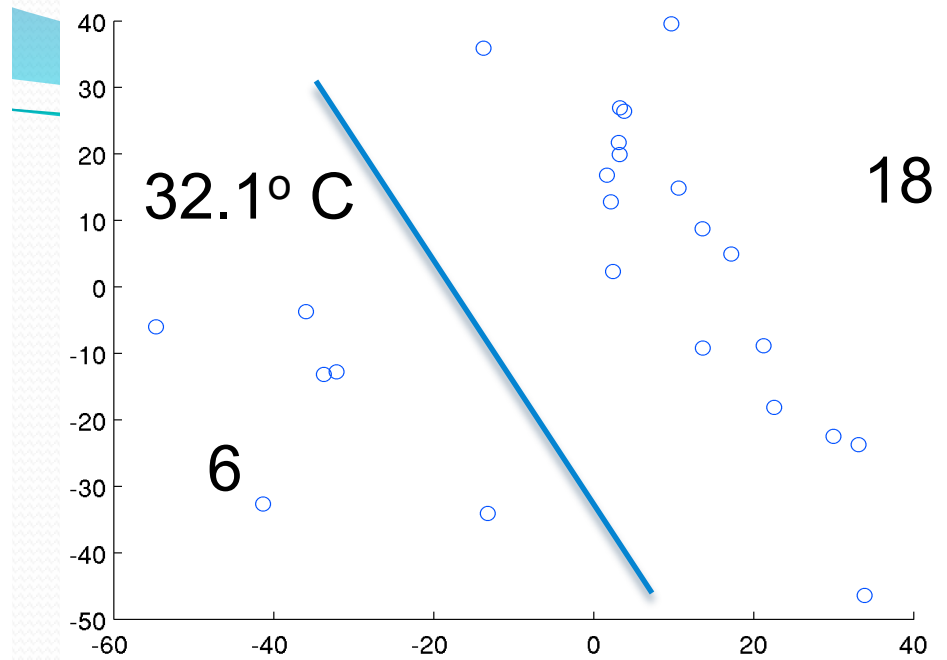
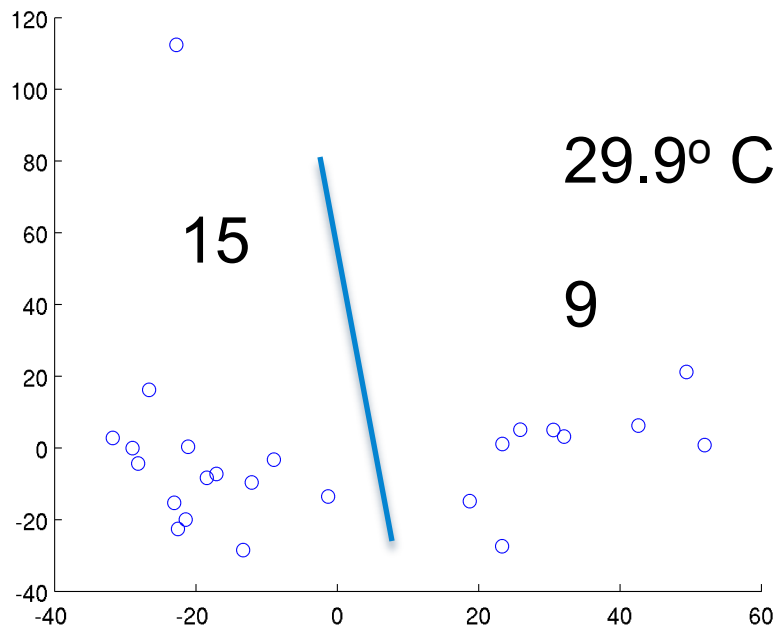




How do you know the
transition to an alternative
Transcriptomic state is due
to Oyster genes and not
Perkinsus genes?



No obvious separation within populations and certainly nothing that correlates with the oyster PCA-hence the transition is not due to levels of Perkinsus gene expression



Why I made a point of the rapid transition. If the transcriptomic transitions were not steep and concerted, then we would not see clusters in PCA

Speculation

Southern oyster populations do not suffer declines as a result of Perkinsus infection even though 100% are infected

These oysters are intertidal and routinely experience temperatures above 40C during low tides in the summer

If the GOM data can be taken at face value, it implies that somewhere around 32 C Perkinsus becomes inactive

It isn't that southern oysters are immune to Perkinsus, but rather the environment provides a high temperature thermal refuge