



Rooting the Tree of Life

Ivana Premasinghe

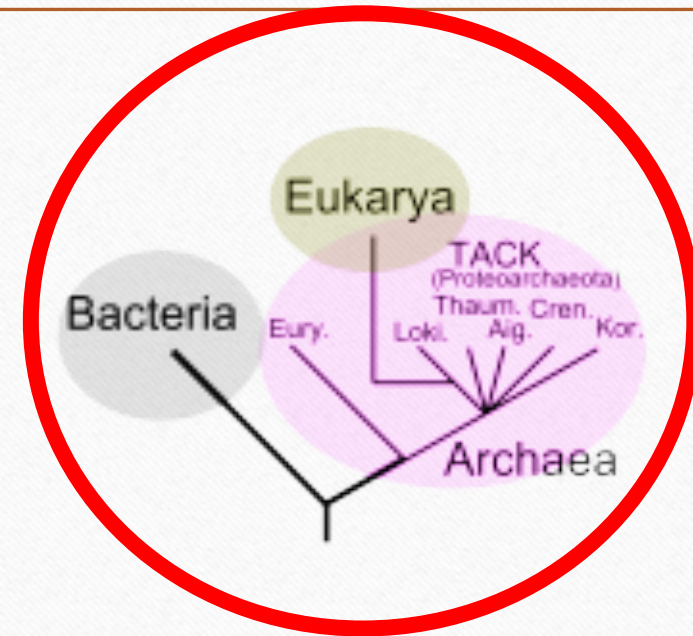
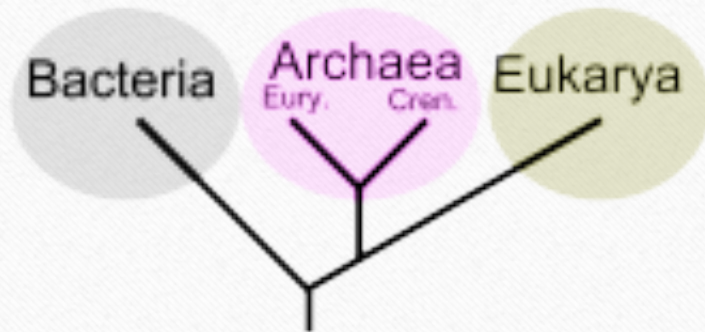
Schedule

- 3:05-3:35 → Skype with Dr. Gribaldo
- 3:35-3:55 → Introduction: Two Domain Hypothesis
- 3:55- 4:30 → Research: Three Domain Hypothesis
- 4:30-5:00 → Three Domain Hypothesis Discussion
- 5:00-5:15 → Follow Up Discussion: Two or Three Domains?
- 5:15-5:30 → Looking to the Future

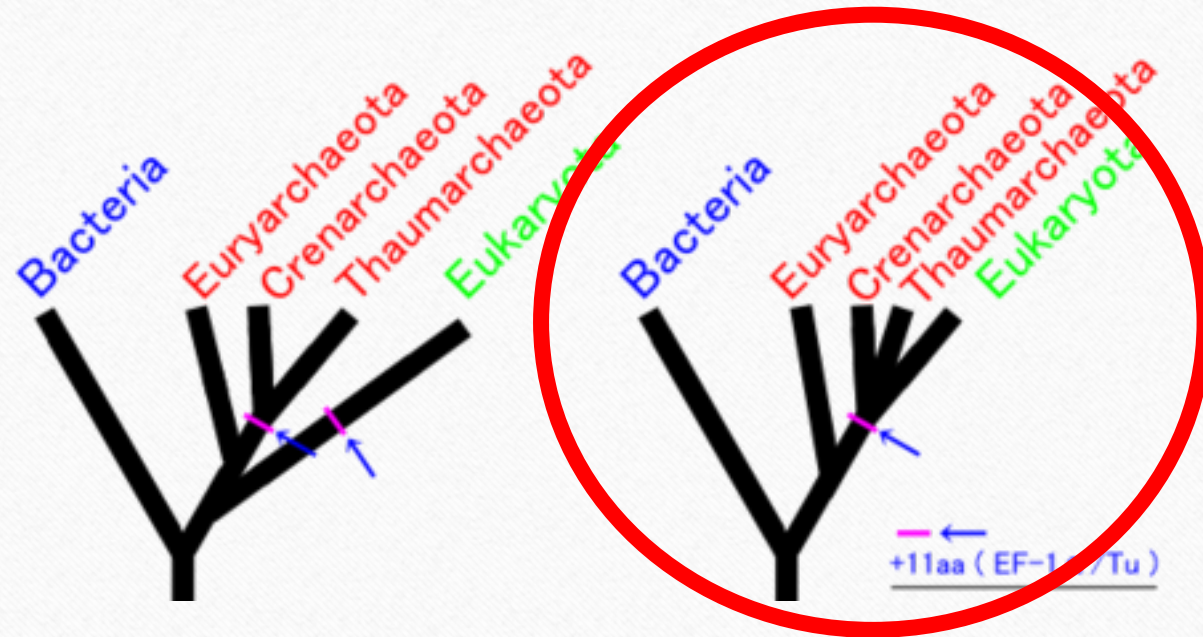


Introduction: Two Domain Hypothesis

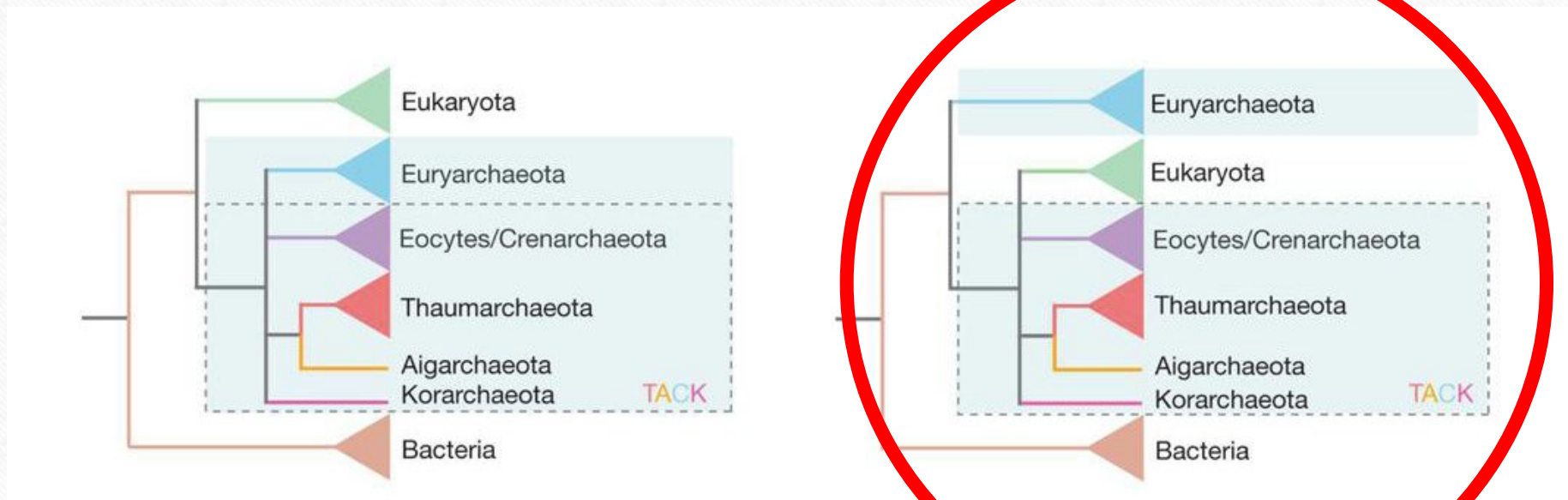
Which tree shows the two domain hypothesis?



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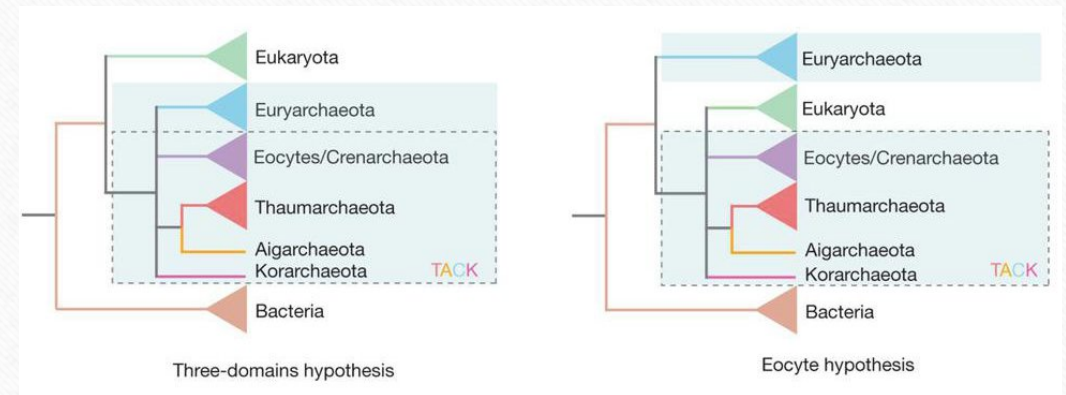
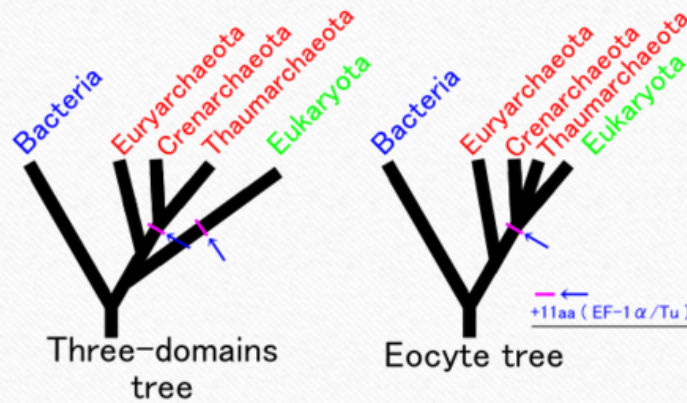
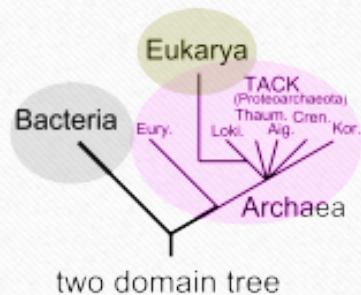
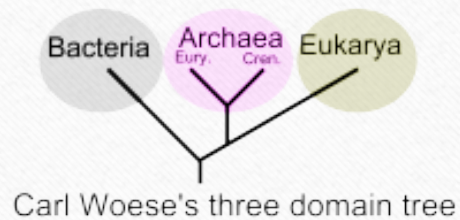


Which tree shows the two domain hypothesis?



Williams et. al. 2013, Nature

Two vs. three domain hypothesis

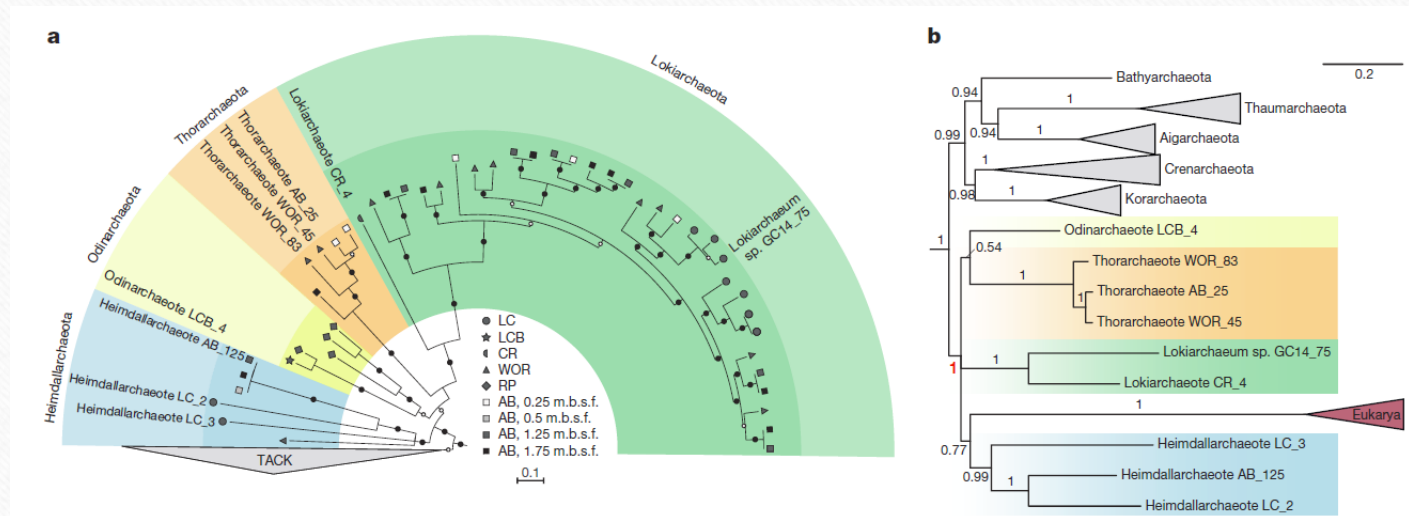


Topics:

- New discoveries
- Genes with eukaryotic complexity
- Improvements in phylogenetic analysis
- Room for improvement

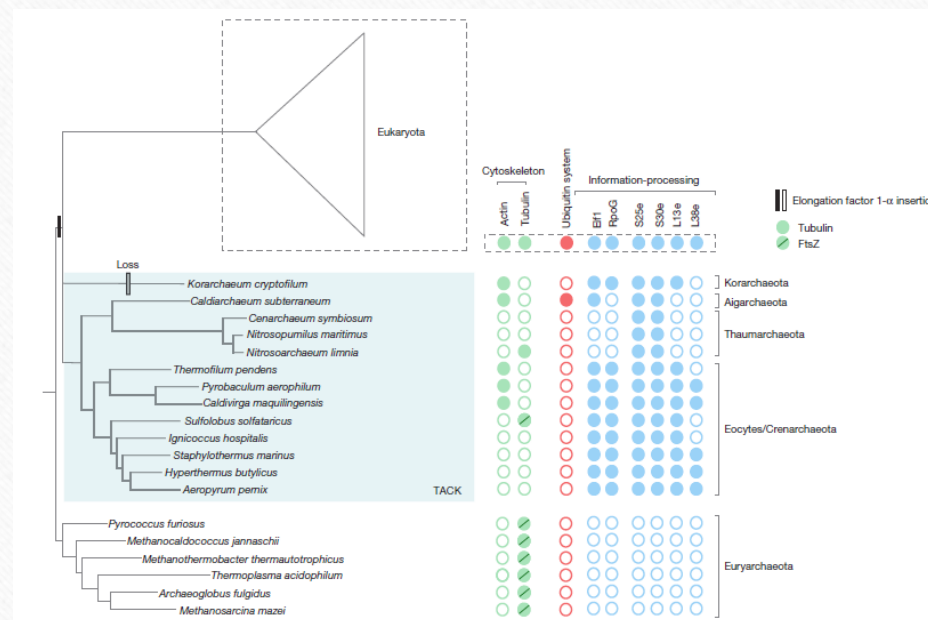
New discoveries

- Lokiarchaeota, Asgard superphylum, and TACK superphylum



Zaremba-Niedzwiedzka et. al, 2017, Nature

Genes with eukaryotic complexity

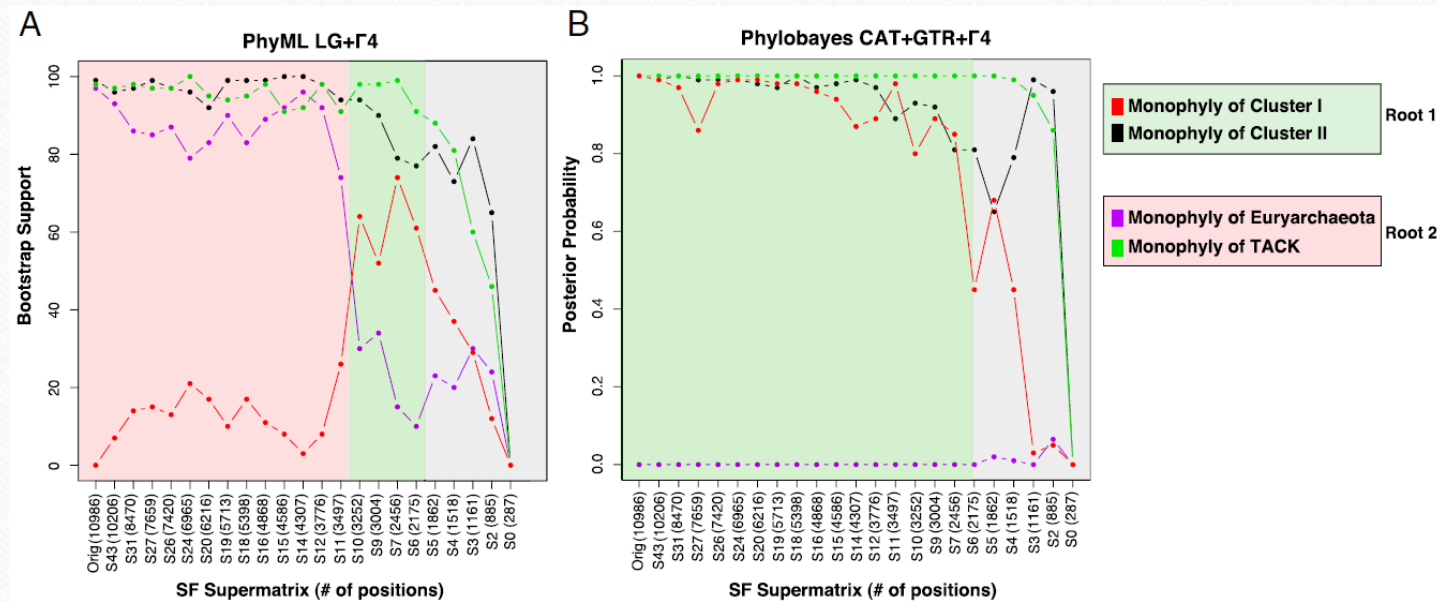


What does this mean about the complexity of the eukaryotic archaeal common ancestor?

Williams et. al. 2013, Nature

Improvements in phylogenetic analysis

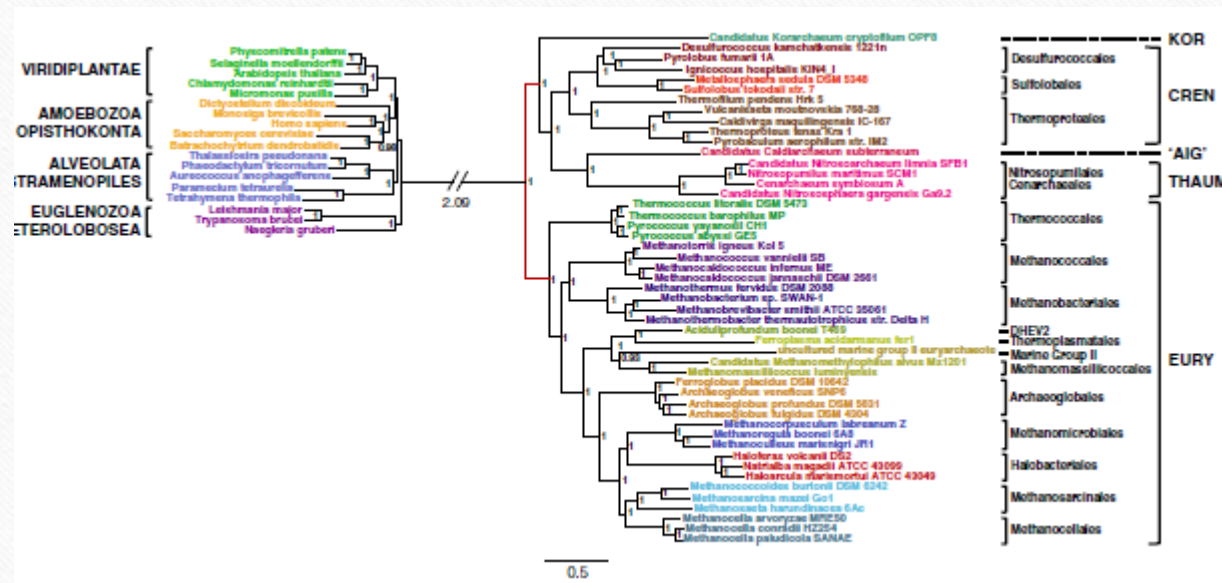
- Fast vs. slow evolving lineages and Long Branch Attraction



Raymann et. al, 2015, PNAS

Improvements in phylogenetic analysis

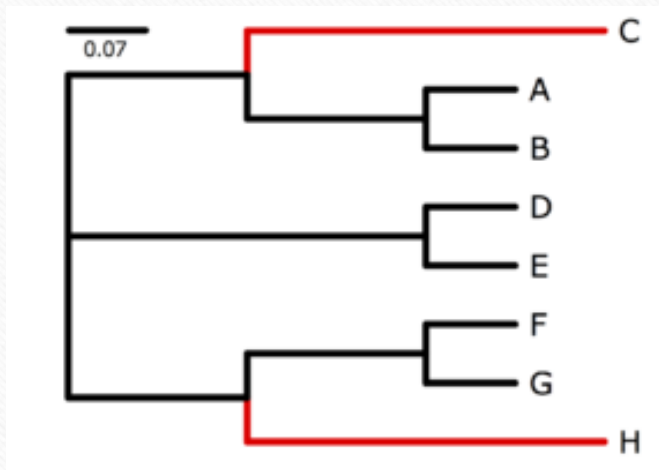
- Separately analyzing the markers



Raymann et. al, 2015, PNAS

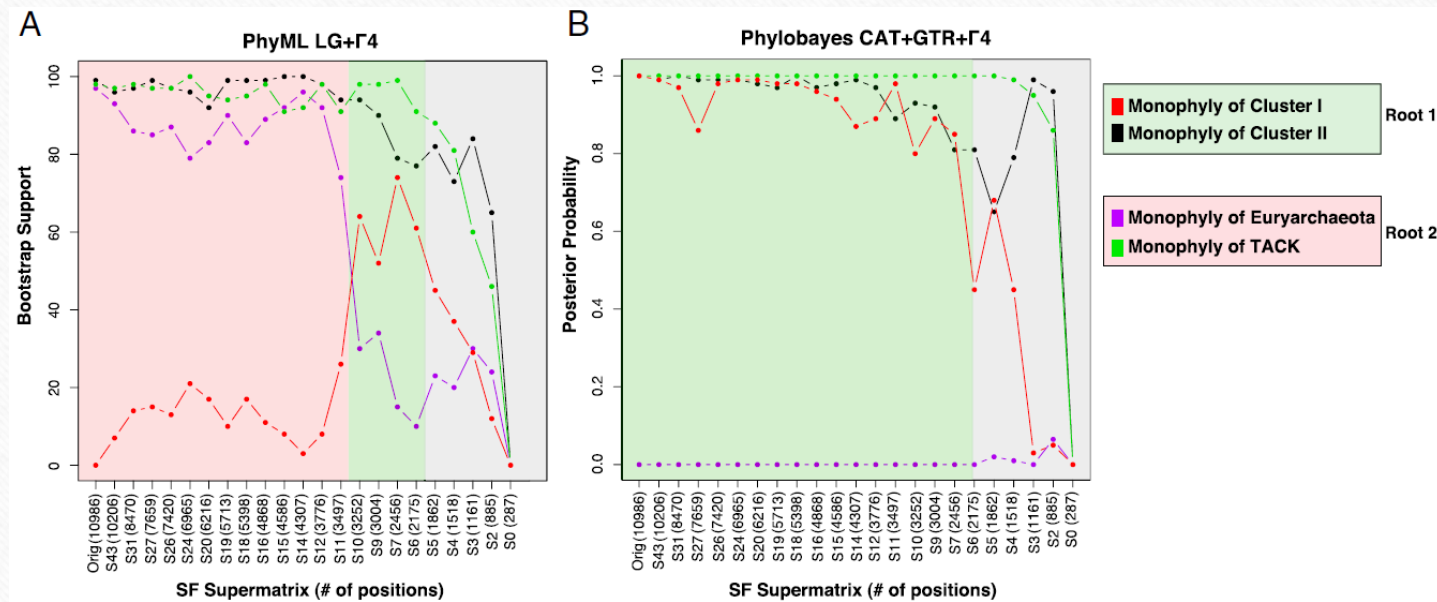
Improvements in phylogenetic analysis

- Compositional heterogeneity

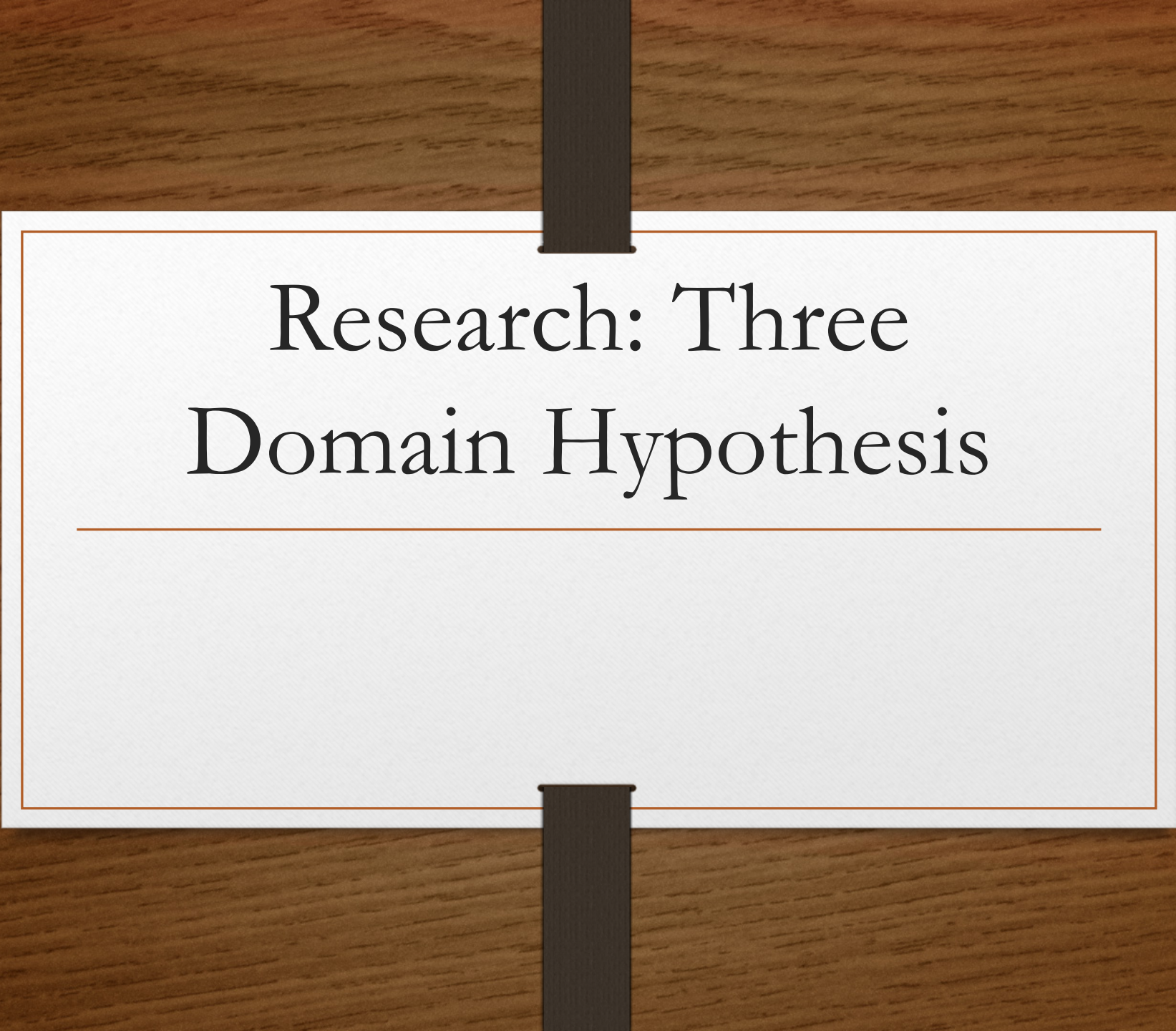


Given the limited manpower, machine power, and time, how do we optimize discovery of new analysis methods? With the limitations mentioned, is it in our best interest to redo old analyses from previous experiments or to use these new methods on new discoveries?

Room for improvement



Raymann et. al, 2015, PNAS



Research: Three Domain Hypothesis

Pointers while searching for information

- New discoveries
- Genes with eukaryotic complexity
- Improvements in phylogenetic analysis
- Room for improvement

New discoveries

- New discoveries
 - Have there been any new discoveries that support the three domain hypothesis as opposed to the two domain hypothesis?

Genes with eukaryotic complexity

- Genes with eukaryotic complexity
 - Have any genes been discovered that contradict the theory that the eukaryotic archaeal common ancestor had eukaryotic complexity?
 - Also, think about counterarguments to the information presented earlier, such as the membrane argument in the Williams paper

Improvements in phylogenetic analysis

- Improvements in phylogenetic analysis
 - Have analyses using the new phylogenetic analysis improvements resulted in the three domain tree instead of the two domain tree?
 - Also think about times when the two domain tree was generated but without statistical significance, as listed in the Williams paper

Room for improvement

- Room for improvement
 - Are there any gaps or unresolved questions within the three domain hypothesis? What sort of data do we need to fill these gaps?

Follow up Discussion:
Two or Three Domains?

Follow-up discussion: Two or three domains?

- Keeping in mind the four categories- new discoveries, eukaryotic gene complexity, improvement in phylogenetic analysis, and room for improvement- which hypothesis are you more convinced by?



Looking to the Future

Looking to the Future

1. The three domain hypothesis is the one that is still used in textbook. If you to teach it, how would you teach it?
2. Will we ever be able to look at the fossil record without having to worry about contamination? Similarly, how could we continue to get rid of tree reconstruction issues caused by horizontal gene transfer?
3. How does the idea of endosymbiosis challenge our definition of “life”? How should it be incorporated into the tree of life?

Bibliography

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