compgen final project

Final Project

Hi C! (Get it?!!)

Introduction

This is a final project for the Comparative Genomics seminar in the spring of 2019. This project is meant to examine 'neural' gene loss in sponges and ctenophores.

The goal

Our goal is to classify whether absences for particular 'neural' genes in sponges and ctenophores are ancestral (i.e. gene was never there) or secondary.

The data

- Data source: Published, and unpublished but publically available
  So far:
  -Mnemiopsis genome [1]
  -Pleurobrachia genome [2]
  -Amphimedon genome [3]
  -No paper for Oscarella genome, but deposited in Compgen. See presence/absence of 'neural' gene table in Riesgo et al., 2014 [4]

These genomes were selected because there are presence/absence lists of 'neural' genes readily available for them.

Other genomes to think about: Salpingoeca rosetta, Monosiga brevicollis, Trichoplax (can use as positive control?), Nematostella vectensis, Hydra magnipapillata, Homo sapiens - to put these presence/absences in sponges and ctenophores into perspective.

- Data structure: FASTA files, GFF3 files, contingency table of presence/absence of 'neural' genes. More?

Background

While biologists characterize most animals by what they have, non-bilaterians are sometimes characterized by what they don't have. In sponges, traditionally these absences have been considered ancestral, an assumption contributing to their primitive image.

One timely discussion is whether sponges have lost a nervous system. The flip side of this debate, that ctenophores have a convergent one, also rests on assumptions of absence - because ctenophores lack many fundamental 'neural' genes they must use a very different mechanism. For both animals, it may be productive to first understand whether these absences are ancestral or secondary. This would be valuable for inferring whether the LCA of metazoans may have had a bilaterian-like sensory/coordinating system.

Synteny analysis provides one method of determining loss. In particular, the ghost locus hypothesis suggests that in the case of gene loss, the synteny surrounding the locus of the gene may be preserved even in the absence of the gene itself [5]. I will look for the ghost loci of absent 'neural' genes in sponges and ctenophores using synteny analysis.

That's all I really got at the moment... thoughts welcome. One major *assumption* I make is that that surrounding syntenic block does not exist before the emergence of the gene itself. (How bad is that assumption?).

Methods

Synteny analysis to search for ghost loci of absent 'neural' genes in sponges and ctenophores.

Results

Assessment

Was it successful in achieving the initial goal?

What are the main obstacles encountered?

What would you have done differently?

What are future directions this could go in?

References

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