

The current state

All of us

Today

1 Dulce's work

1. change the measured value to the bitscore.
2. only take into account the coordinates for gene, and not the combined coordinates.
3. Test on real data could be made on the next week

2 Observability

1. Fitch relation is what can be obtained for HGT

The mexican mafia tried to develop observability axioms considering $\{\odot, \bullet, \triangle, \square\}$. However, defining an observable speciation was a trouble. The question turned into what relations can be drawn between species. We found that Marc did a lot of work regarding this matter, however he doesn't take into consideration the biological constraints of the used methods to detect orthology and HGT's of a given methodology.

After talking about this in Leipzig, the conclusion was to ask what are the relations that can be observed?, the HGT as last common ancestor of two genes or the fitch relations?

Resolving this doubt, we should be able to define observability axioms.

If we define a given a model and techniques, basic observability axioms can be constructed in order to develop any forward mathematical theory.

It was concluded, after the meeting, that the Fitch relations were the ones that can be obtained by methodology.

Now we have to analyze Fitch relations and orthology relations together.

2. Marc has done some work about the scenarios when both orthology and fitch relations are considered.

However, March has already some work about it. A message was sent, and a repository is made, and we are waiting for it.

3. Stop asking this.

Since the meaning of observability is really ambiguous, it creates a lot of problems on communication and axiomatic construction. Therefore, the idea of general observability can not be defined in a congruent matter. This means again "If we define a given a model and techniques, basic observability axioms can be constructed in order to develop any forward mathematical theory".

3 rBMG BMG ... OMG

1. only bidirectional edges give orthology information

Manuela started to work on the n-species rBMG. The main inference is that relations indicate genes related to each other at the same time. However, there seems to not be enough information in order to have a unique inferred tree. Additional constrains can be found in the species tree topology, or extra measurements of distance between genes.

2. There are 3 basic structures in which a tree structure can be inferred

The rBMG has different recurrent structures that can be resolved independently. (imagine nice drawings here)

3. is not clear if the resulting relations can be a cograph

At this point is not clear if a rBMG gives a cograph. in one hand, the basic structures clearly have P4's. The question here is. Is it possible to have a the same inference and a p4 free rBMG? o.o ?

4. additional constrains might come from consistency with species labeling

If we considere that the labeled gene tree has to be mapable to a species tree, then additional constrains can be applied in order to minimize inferred losses. This parsimony approach can cause additional troubles too, adding losses and relabeling inner nodes as duplications have to applied.

5. the directed edges can give more measurement information

Additional information can be acquired from the BMG. directed edges can be used to detect HGT. This causes to change orthology edges. Since a HGT will replace an orthology relation, a new bidirectional relation should appear.

6. Symbolic ultrametrics can give more measurement information

If turns out that rBMG actually gives a cograph, then a direct relation with Symbolic ultrametrics can be done. In this case the measurment is given by the succession of inner labeld edges. The info in the rBMG plus the anlisis of the cograph, can give a new resolved tree. Whether it is unique o even possible in every scenario, are questions that follows.

7. The empirical part of the cographs in rBMG

Of course there is also the possibility to compare how much far apart does a theoretical cotree is apart from a rBMG-tree. Artificial gene stories can be made taking into account duplications and/or gene losses and/or HGT (any possible combination). Then a rBMG can be created from it. And analyze how much the actual orthology relations differ from the rBMG. A gut-feeling says that difference should depend from gene loss and number of duplications. We need to work on this details.