1 BEAST

I have added these classes:

AlloppSpeciesBindingsApSpInfoParser
AlloppSpeciesBindingsIndividualParser
AlloppSpeciesBindingsParser
AlloppSpeciesNetworkModelParser
AlloppSpeciesBindings
AlloppSpeciesNetworkModel
AlloppSpeciesTreeModel - now AlloppLeggedTree

At the moment, can parse some bits of XML, reading in info about species, individuals and sequences (=taxa) to make an AlloppSpeciesBindings.

Then read in XML for AlloppSpeciesNetworkModel which just contains a parameter for population sizes. This only works for the one tetratree, no diploid tree case, and where there are 2 or 3 species. The node times are just 1.0 and 2.0, and the hybridization times unset.

I have code for translating a network representation into a mullab representation, which is tested by a small case in a test unit AlloppSpeciesNetworkModelTest. That does 3 tetra species, and 2 diploid species, in various arrangements. This isn’t very relevant to the tetra only case, but it will be needed. I have not tested what it does in the tetra only case.

1.1 XML Parsers

AlloppSpeciesBindingsApSpInfoParser, AlloppSpeciesBindingsIndividualParser,
AlloppSpeciesBindingsParser, AlloppSpeciesNetworkModelParser

I have copied and adapted code from other parsers. I don’t have a good understanding of how they work. I have added getSyntaxRules() implementations, but it is hard to tell if I have done as much as I should or could.
1.2 AlloppSpeciesBindings

Subclasses

Individual - for one individual, one or more sequences

ApSpInfo - One (allopolyploid) species, containing one or more individuals

GeneTreeInfo - A gene tree as used by BEAST, plus popfactor, plus indices for each individual to map sequences to indices (0 or 1 for tetraploids) which identify the legs of the tetraploid subtree.

[Aside: in cases where both parental diploid species are extinct, there is only one leg, so what exactly is identified here? It matters whether two genes are assigned the same index, or a different one but not what the indices are.]

GeneTreeInfo.SpeciesSequenceIndices - where the indices just mentioned are stored.

GeneTreeInfo.GeneUnionNode - for GeneUnionTree.

GeneTreeInfo.GeneUnionTree - serves same function as JH's CoalInfo, storing the set (union) of species-sequence pairs belonging to a node in the gene tree. I copy gene tree topology and times into a GeneUnionTree to do calculations.

Methods

A lot of mapping of one kind of index or indices to others, one to get list of species at a given ploidy level, etc.

Also fitsInNetwork() which visits nodes in gene trees (as GeneUnionTree's) and calls CoalescenceIsCompatible() from AlloppSpeciesNetworkModel.

1.3 AlloppSpeciesNetworkModel

This contains an AlloppSpeciesBindings, and two representations of the network:

1. As a 2D array of AlloppSpeciesTreeModel (=AlloppLeggedTree)'s. First index is ploidy level, second is index of (sub)tree within ploidy level

2. As a multiply labelled binary tree.

Subclasses

MulLabNode - for MulLabTree

MulLabTree - the multiply labelled binary tree.

MulLabTree.LegLink - for conversion of network made of various trees joined together into a multiply labelled binary tree.

MulLabTree.FootLinks - for conversion of network made of various trees joined together into a multiply labelled binary tree.

Methods

makeInitialOneTetraTreeNetwork() - called by a constructor.

makesmallexample() - called by test code.
CoalescenceIsCompatible() - not written

The MulLabTree() constructor is complicated and calls simpletree2mullabtree(),
nodeofunion()

MulLabTreeAsNewick() - for testing.

numberOfpopparameters() - calculates the number of points in the network where populations are
estimated.

1.4 AlloppSpeciesTreeModel (=AlloppLeggedTree)

This is almost a subclass of AlloppSpeciesNetworkModel - or MulLabTree almost deserves to be
top level. It implements a tree with legs.

Subclass

Leg - joins root of tree to branch in a lower ploidy tree.

Methods

I have two constructors: for tetraploid-only case; and for small example for testing network to
mullab tree conversion.

There are loads of methods delegating to SimpleTree.

2 XML

I have edited the TrialAlloppApr18.xml file so it contains bits for the parsers to read