Names of Reviewers: Yucheng Yang, Steven Kauwe

Comments:

- Usefulness/possibility to download source data or link to the node/genetic part's SynBioHub page (in the thorough info box?)
- Indication for genetic part's "level" of tree, or whether or not it has children
- **Tree navigation**: how much to display on default, and how to navigate when a tree is too large (expanding a child's children, and going back to originally searched tree)
- Add hover info on Sequence Ontology vis within the thorough info box
- Have a list of all descendents and their levels for each node (in case tree can't be shown), some indication of how much of a tree is shown and how much is omitted
- Average number of children per node… (how many children can be show on a level?)
- Display logistics of views (does tree move when thorough box shows up, or is there just white space where the thorough box would populate?, does thorough box go away upon tree navigation)

Next Steps:

- Find out the average number of levels in a tree or average level of inheritance in the dataset, if huge inheritance relationships are common (this tells us how big of an issue tree navigation will be)

  Average is 3, max is maybe 6
- Find out if it would be useful to target audience to be able to download a genetic part's data

  No , just include a link to part's webpage
- Average number of nodes in a level? (Average number of children in a parent part)

Average: 3, max is maybe 10 (when it's 10, then level is very small)

Average total tree size 4-5, max is 15

- Discuss default tree display if the tree is too large to display in its entirety (include from root to base and exclude middle layers, or omit lower levels after a certain number of levels is displayed)
- Possibility to have dual-view for inheritance/levels (horizontal tree design with collapsible rows of children), link it to the tree view??

No, trees are small enough, it would be redundant

Summary:

Ask Michael more questions about the data to determine how thorough we have to be about tree navigation and display. Also gauge how useful an additional view with the ability to show all of a node's inheritance is.