**To Do List**

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**Project: SPAGO**

Note: This is not a sequential list.

1. Human assembly labels the connected components.
   1. Find a source for the genome assembly (it’s not available in DNA Zoo)
   2. Once we have the gff3 file:
      1. Run OrthoFinder to assign orthogroups to each gene.
      2. Run DAGChainer for Human vs the other 100 species.
      3. Add the homology-synteny human links to the network.
      4. Label the connected components.

Note: Mouse is not in the DNA ZOO assemblies either.

1. Analyze the connected components that share orthogroup.
2. Analysis of orthogroups:
   1. For a couple of species, check how many orthogroups there are and how many genes per orthogroup. The numbers should be matched with the numbers in the network.
3. Same as point 2.a) but for the OrthoFinder file.
4. Build the network with TOGA annotations and analyze the differences between our SPAGO network and TOGA network.
   1. Study TOGA annotations and see what information they have and how it is presented.
5. Take off the ostrich from the network. (Why was this? Because we only want to keep the mammals(?))
6. Redo the network considering different parameters for DAGChainer.
7. Read carefully Zoonomia papers 9,11,TOGA.

**Project: Genome distances**

1. Once SPAGO be ready, we can track gene distances across species.