information on how your tester can get your code:

* https://github.com/chfal/investigating\_orthogroups

installation instructions

* git clone <https://github.com/chfal/investigating_orthogroups.git> into your working directory on Amarel

a description of dependencies (including version)

* on amarel:
  + OrthoFinder (.yml file in repository)
  + IQTree (shared app in Geneva bin, instructions in README)
  + ASTRAL (git clone this repo into the astral repository <https://github.com/smirarab/ASTRAL/raw/master/Astral.5.7.8.zip>)
* On local machine:
  + Figtree (https://github.com/rambaut/figtree/releases)
  + Java (FigTree will prompt you to download Java if you don’t have the right version)

a link to documentation for any other software that is used in the process

* N/A

a clear goal (what are they trying to do?)

* Make a phylogenetic tree of *Atadenoviruses* based on a bunch of gene trees that are then reconciled into one final species tree

directions (how should they do it?)

* Follow README.md in investigating\_orthogroups GitHub

example data or any other files they will need to satisfy the directions

* In investigating\_orthogroups/data

specific requests for feedback

* Were you able to get it to work without help?
* How can I make this more user friendly?

general estimates for how long it should take them to do it

* 30 mins max! PM me on Slack @chfal if you need help 😊