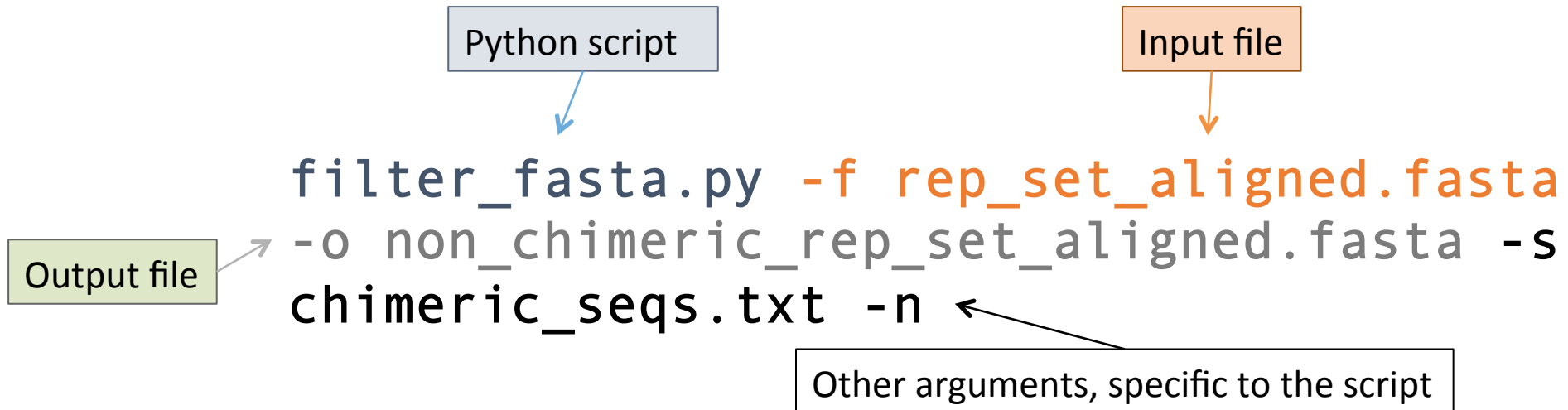


# Amplicon Analysis Using Quantitative Insights Into Microbial Ecology (QIIME)

# A look at **python** syntax & common arguments in QIIME



## Other common QIIME arguments

- m analysis method, metric (sometimes map file)
- t tree file
- a alignment template file
- v verbose = good for troubleshooting
- h help
- f force overwrite of an existing directory

# Tutorial: What we're about to do

- Practice subsampling a dataset to make it manageable for workflow development
- Merge paired end reads in QIIME
- Pick OTUs open reference - includes:
  - Quality control/ chimera check
  - Cluster at 97% identity
  - Pick representative sequence for the whole OTU
  - Assign taxonomy to the rep. sequence
  - Make an alignment of the rep. sequence
  - Build a tree from the alignment
  - Made OTU tables (biom + classic): **make\_otu\_table.py**
- Rarefy to an equal sequencing depth
- Calculate & visualize alpha and beta diversity

# How will we use QIIME?

- Using a community AMI on Amazon.
  - An operating system with a set of software and data installed on one computer that can be copied onto an users' personal instance.
  - To circumvent installation issues, the QIIME community AMI has everything you need to get the ball rolling!