

API Call to BCO Records	
ARGOS_000022	
organism_name	
infraspecific_name	
lineage	
assembled_genome_acc	
genome_assembly_id	
taxonomy_id	
bco_id	
ARGOS_000012	
organism_name	
infraspecific_name	
lineage	
assembled_genome_acc	
genome_assembly_id	
taxonomy_id	
bco_id	

Assembly QC NCBI
This script will parse an XML for a single feature and return a list via terminal or file, if an output is supplied.

Assembly XML From NCBI

efetch -db assembly -id {ids} -format docsum

Parse Assembly XML

Creates dictionary based on definition

Get Lineage

NCBI full taxonomic lineage is grabbed and sent back to parse XML function

Download Assembly Stats and parse

Stats are sent back to the Parse Assembly XML function

Create Output file

If output path is supplied file will be created at location

JSON DUMPS to terminal

If no output is supplied will dump result to terminal

