

AIMs of CAMI

-set of metrics that allow to assess different usecases (no tool is best for all purposes), usecases are for instance draft genome reconstruction, taxonomic profiling from shotgun data..

-shared data formats (binning, profiling)

-common evaluation framework for developers

- give people a realistic expectation to what the limitations are. Many non-experts are using metagenomics for all sort of crazy stuff. The best tool sometimes is not good enough.

Simulated microbial communities

Empirical abundance distributions: Mike Imelforts script to generate genome coverage from input OTU abundance table: <https://github.com/minilininim/symCalc>

Which read simulators?

-Art (MiSeq, HiSeq). We need an uptodate ART HiSeq error profile.

- <https://github.com/lh3/wgsim>

-Illumina read simulator

Advertise:

Aaron Darling could advertise on the assemblathon mailing list

Prize:

-free sequencing, or money?