making

/'meikin/

noun

the process of making or producing something.

metametrics

/'metrik/

adjective

a system or standard of measurement.

more

/moː/

determiner & pronoun

a greater or additional amount or degree.

meaningful

/ˈmiːnɪŋfʊl,-f(ə)l/

adjective

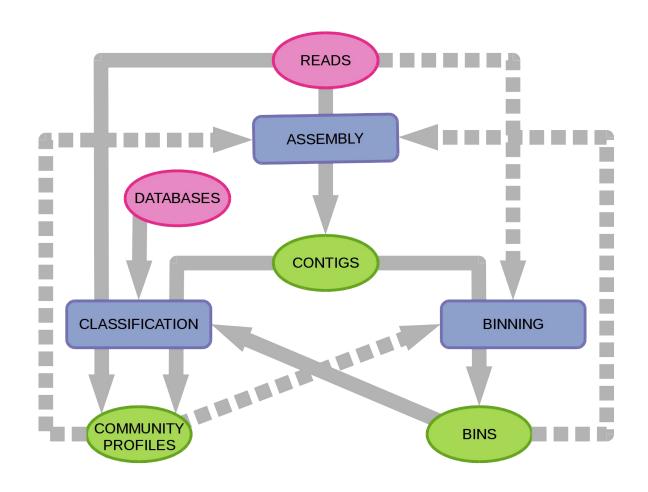
having meaning.

serious, important, or worthwhile.



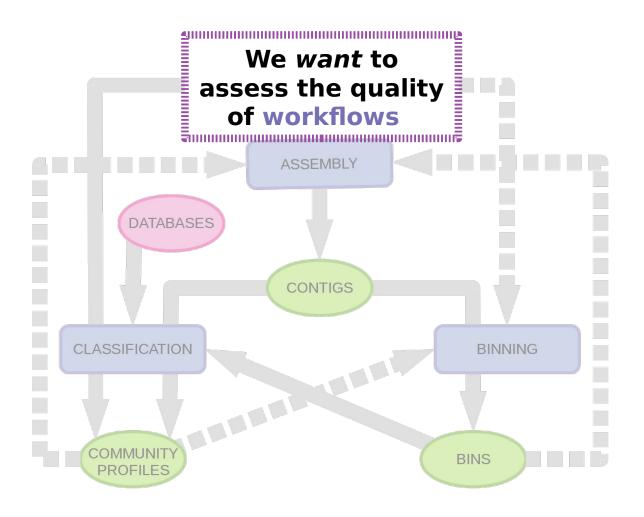




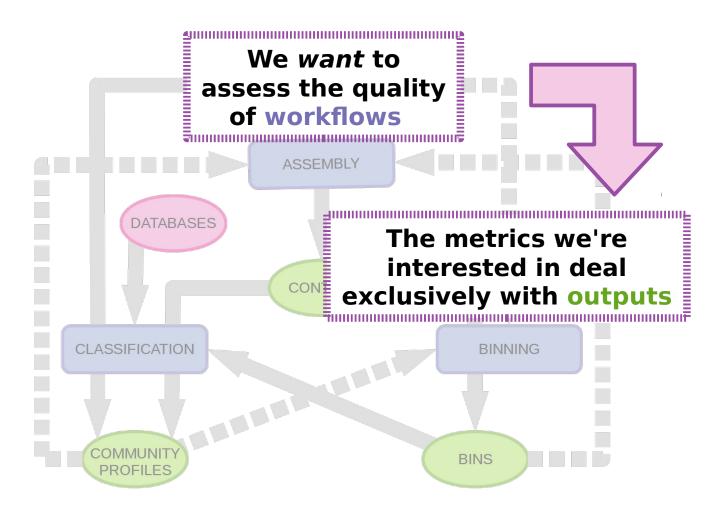


Initial CAMI targets: Assembly, taxonomic binning and profiling

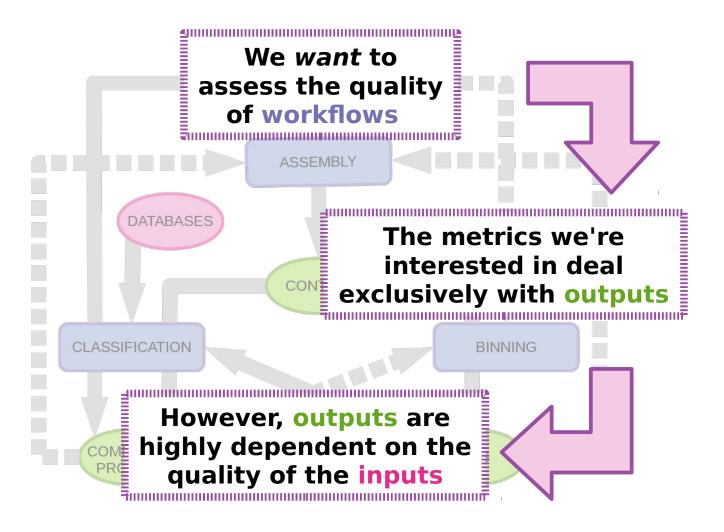




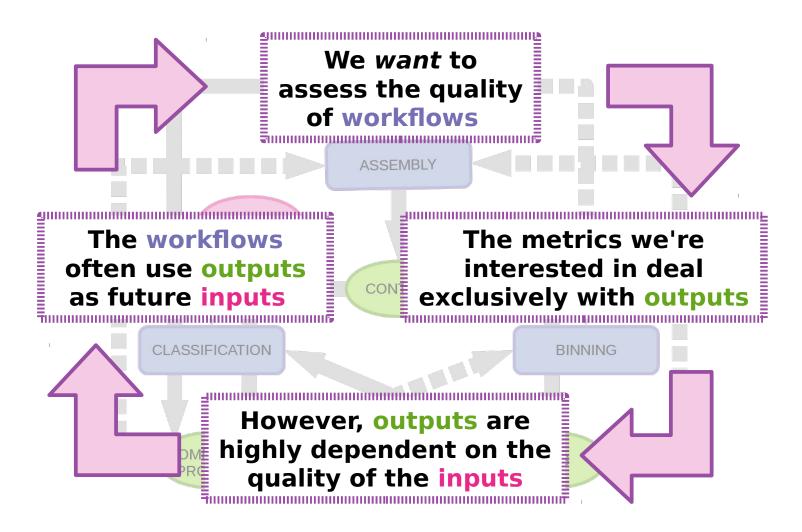














Metric mixing must be managed!

We must render unto the assembly algorithm the things that are caused by the assembly algorithm, and unto the binning algorithm the things that are caused by the binning algorithm

Good metrics should have clear domains

Some amount of mixing is unavoidable

We must be very careful



Must metametrics have domains?

How much of the final result can be attributed to community structure? Good outcomes: Rare / novel species recovered Bad outcomes: Strain nightmares

How much of the final result can be attributed to the strucure of / bias in the reference databases?

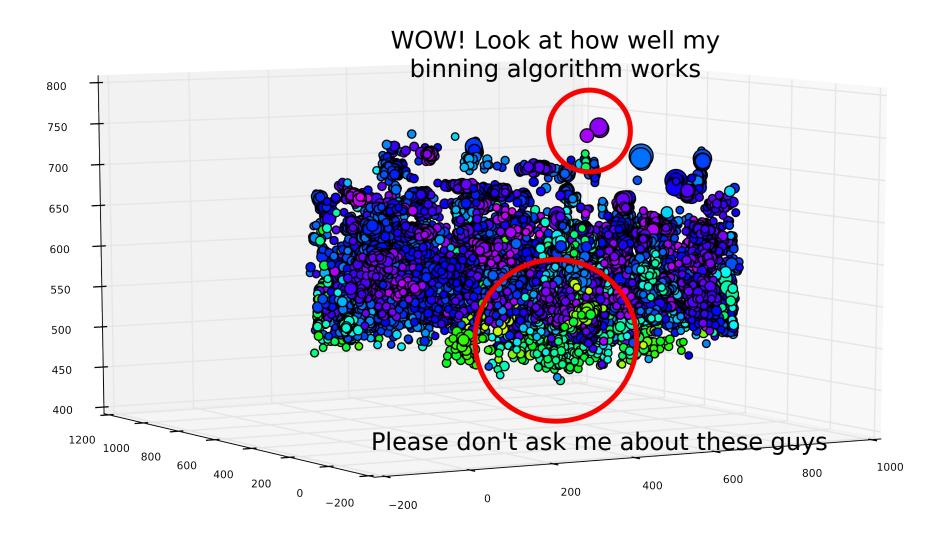
Who's to blame in the strain game?

Do we care about "rare" or "novel" species?

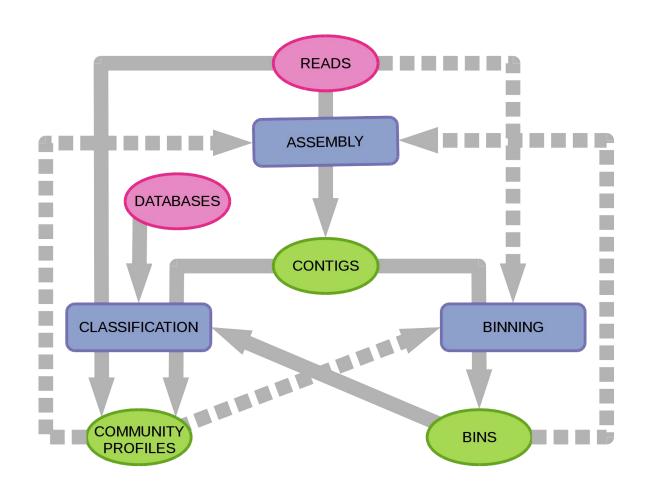
(from a metrics perspective)



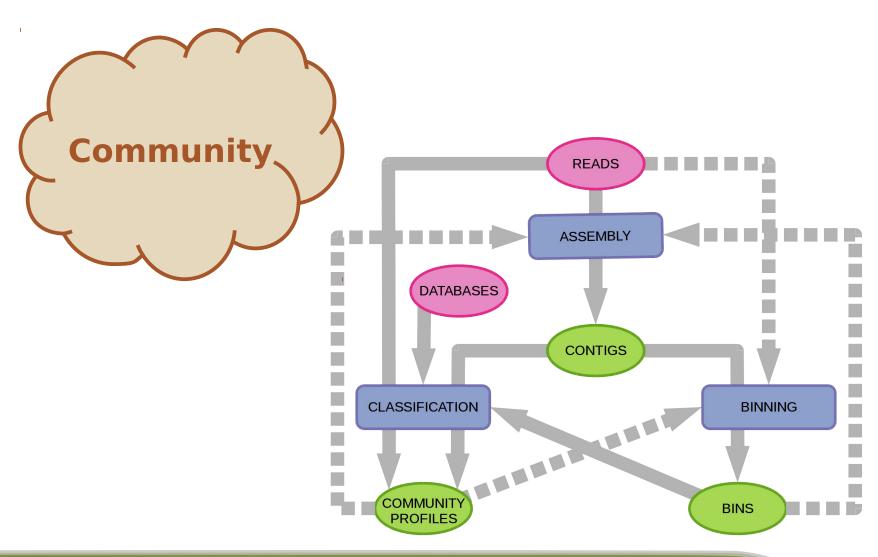
The strain game is THE game



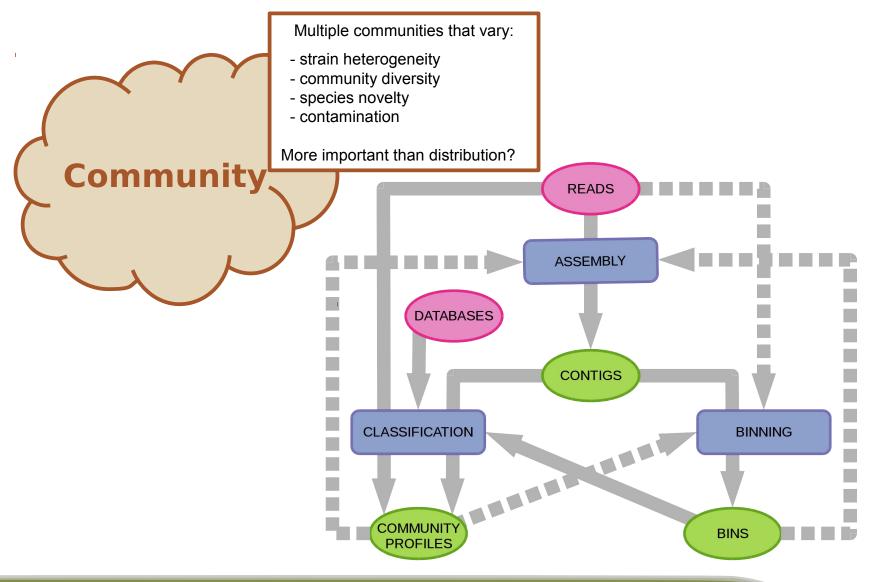




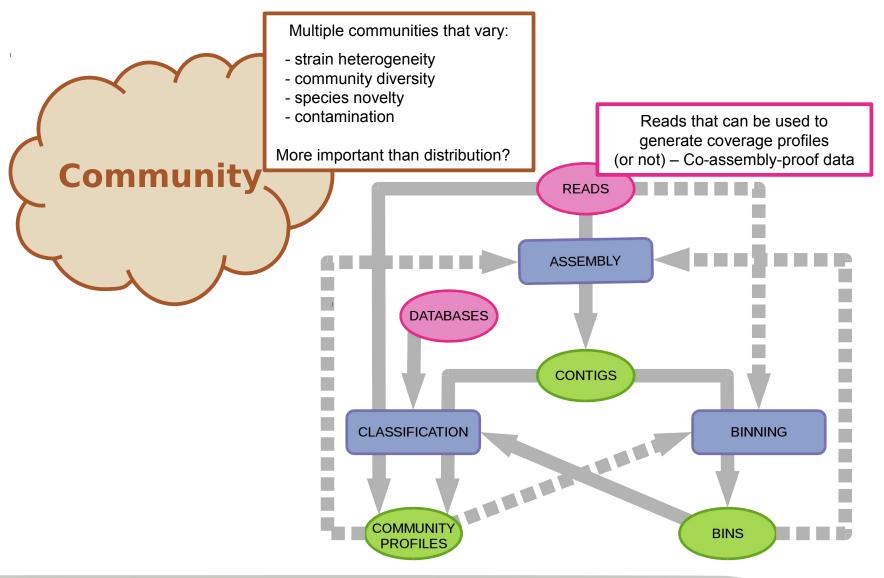




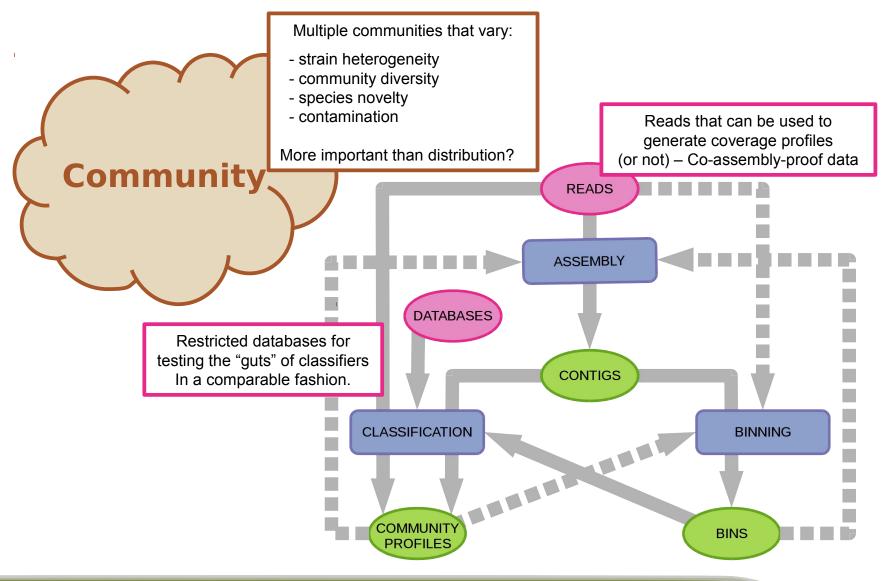




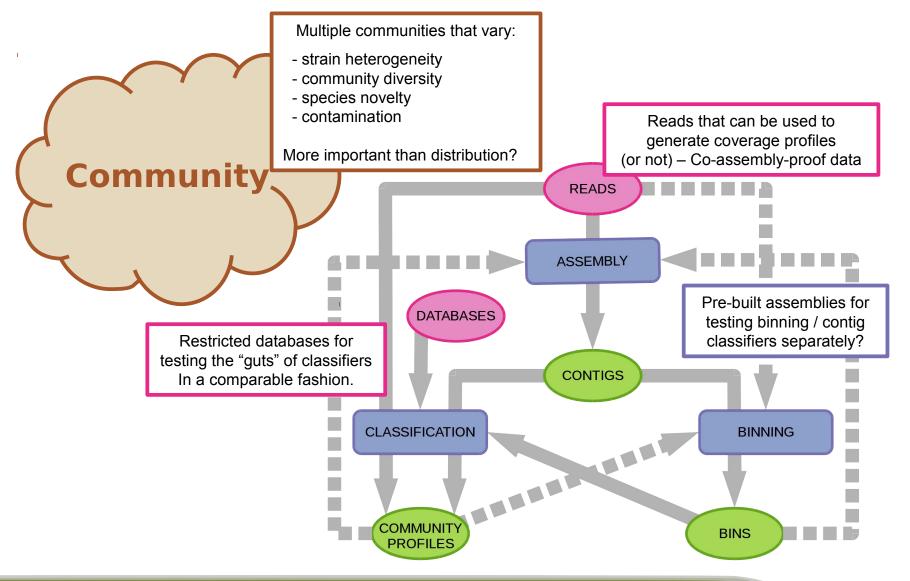




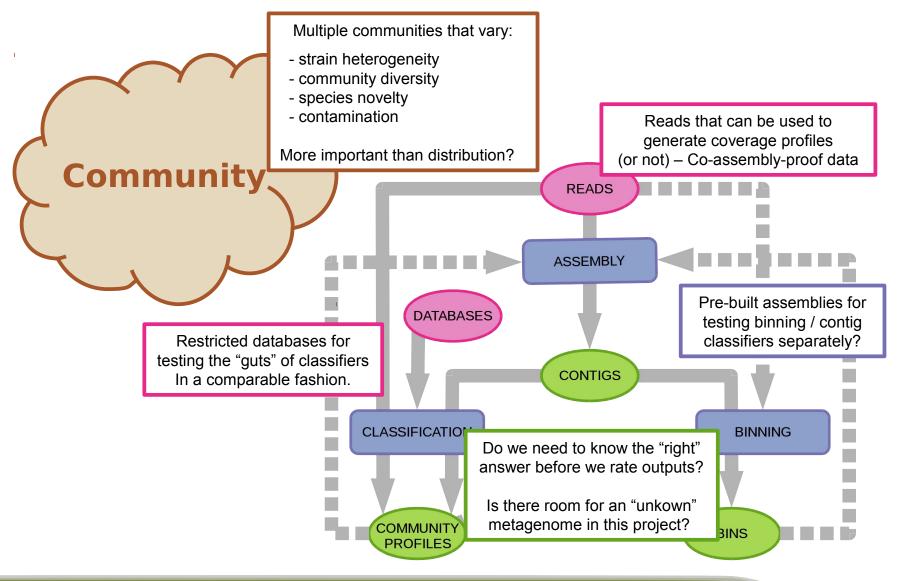














Test Data

Competition

Metrics



Test Data

- Intentional / unintentional biases
- Value of "real" Vs synthetic data
- Accessability / scalability
 (compute requirements etc.)

Competition

- Who are the consumers? What are their needs?

Developers Vs Users

Metrics

- Minimise mixing
- Accessability / explanatory value



Final thoughts

An algorithm is not an island

Metric mixing must be managed

Good metrics should have clear domains

Knowing what we intend to measure must *drive how* we build the test data

We shouldn't be distracted by "rare" or novel species

Strains are the issue facing metagenomics



