Marcus

1. Do you know what redbiom is? (if not, briefly explain)

I have a rough idea. Searching for study information in qiita, don’t need taxonomy for searching features. Haven’t used in practice, think can be fast and useful.

1. What are you most interested about RB?

How it would be used in practice. Noticed the tab of redbiom in qiita. Want to try sometimes

1. What do you think is most confusing about RB?

On backend not sure how it works. Looking at substring of words?

1. Can you give 3 scenarios where redbiom could be helpful?

* Study sequence that appeared in the sample which is not expected, food to know more about
* Metadata analysis of all infants, search broadly
* Run rb outside qiita

1. (choose one scenario) How would you do this task without redbiom?

* (1 OTU) all info on qiita: go thru biome tables I have. Run biome table dump ids. Grab info from features. Mapping feature id to sample using python

1. Is there a task that redbiom could help you with your recent work?

* Nothing comes to mind

1. If you search for “Water” in RB, what do you expect to see in results?

* Samples with metadata
* Table of Sample ids, with location
* See water samples, marine studies

1. If you search for “H. pylori” in RB, what do you expect to see in results?

* Same thing, but features instead of samples
* Name confusions may occur (normalization)

1. If you search for a specific DNA sequence “ATTCAAT” in RB, what do you expect to see in results?

* List of features associated
* Subset of studies it occurs in with links

1. Can you tell us an interesting or handy feature you found in tools you used?

* Emperor to drag around and see the 3d model

George

1. Do you know what redbiom is? (if not, briefly explain)

* I’ve heard of it. You can use it to retrieve information. I forget what kind of info. Metadata maybe? Filtering features in qiita.

1. What are you most interested about RB?

* No

1. What do you think is most confusing about RB?

* I don’t know. Concept makes sense. Used a long time ago, but I don’t remember what the experience was like.

1. Can you give 3 scenarios where redbiom could be helpful?

* Looking for samples/studies with specific criteria
* Filtering for specific features
  + Studies have specific sequences

1. (choose one scenario) How would you do this task without redbiom?

* First to cry. A lot of queries in qiita. Maybe go to qiita, do a lot of searching. Currently qiita doesn’t allow many filtering options.
* Go through a lot of metadata tables to dig on myself

1. Is there a task that redbiom could help you with your recent work?

* There are some potential directions I could use rb to develop my project further. Rn im training feature classifiers for shotgun data. I could pull down some shotgun data, subset of reference genomes. Search for if these references appeared in other samples before.

1. If you search for “Water” in RB, what do you expect to see in results?

* Depends for index
* Studies that involve water in any capacity
* Environmental samples of water
* A list of matching results
* A list of samples seems… early
* Quick numbers
  + Number of time water appears in description of studies
  + Number of samples found
  + Histogram of number of features in samples
* Quality plots

1. If you search for “H. pylori” in RB, what do you expect to see in results?

* Any sort of sample where hp has been identified
* Studies involved hp
* A list of matching results
* Similar to water
* Difference from water
  + Taxonomy summaries
  + Functionalities for searching for related/neighboring taxonomy

1. If you search for a specific DNA sequence “ATTCAAT” in RB, what do you expect to see in results?

* Samples/studies that contain that sequences
* Summary statistics
* A list of matching results
* (predicted)Taxonomy info about the sequence
* Where is the sequence coming from?
* More usually search for a set of sequences

1. Can you tell us an interesting or handy feature you found in tools you used?

* Tensor board? Hyper parameters. Interactive line plots for monitoring visualization of hyperparameters in your model. Can see how changes could affect the model.
* Torch is easier for people to install.

Aries

1. Do you know what redbiom is? (if not, briefly explain)

* Yes. I’ve heard of it but might not all the functionality.
* A place where you can interact with other studies in microbial analysis in qiita

1. What are you most interested about RB?

* Meta analysis recently. How can I use RB to help me in learning about these data
* Educational aspects

1. What do you think is most confusing about RB?

* Not very prevalent in educational aspects
* Learning curve, people might be more willing to spend time to know it after learning about all the functionalities

1. Can you give 3 scenarios where redbiom could be helpful?

* Multi-study analysis
* Microbial interactions
* Multi-omic level tools
* Understanding how relation evolves over time

1. (choose one scenario) How would you do this task without redbiom?

* Meta analysis of microbial studies in breast milk
  + Qiita for meta analysis
  + Stastical analysis acquired from other people
  + Find 16s region related to studies/disease phenotype

1. Is there a task that redbiom could help you with your recent work?

* Comparing my 16s seq to a controlled dataset.

1. If you search for “Water” in RB, what do you expect to see in results?

* Expect error message
* If searchable, maybe studies analyzing 16s reads/microbial analysis from water
* Concept map
  + Criteria in testing water
* Different populations of studies

1. If you search for “H. pylori” in RB, what do you expect to see in results?

* A m studies concerning hp

1. If you search for a specific DNA sequence “ATTCAAT” in RB, what do you expect to see in results?

* Bacteria strains related, and studies
* Priorer knowledge/studies
  + If you don’t know about the seq or bacteria before, it might be helpful to have a quick and general idea

1. Can you tell us an interesting or handy feature you found in tools you used?

* Unixlinux website. Right explanations for questions

Danial

* UI needs to be improved
* Thing like to see
  + Take out the v4 sequences and associate meta data with it
  + A lot of other lookups we can do
* Usibility
  + To facillitate discovery of metadata
  + Type in a word: list results in hierarchy structure and provide explorative menus for people
    - Consistent terminologies (currently not available for qiita)
    - Type in a name, and list all studies using it with frequencies
  + CLT can achieve this by
    - Search for category
    - Search summary for a specific category of interest
  + Qiita gives summarization in different associated categories
  + Navigating taxonomy
  + Learning more about what you have
  + What is the best ways to present these information
  + Visualization about the environment (latitude and longitude)
  + Need to think about
    - The same set of information with shotgun information
    - Cross context comparison
    - Data model is fully reading
    - Need UI to enable people doing these tasks
    - Websockets
    - Indexing of private and public studies
      * Different authorization level of users
      * Firewalls and data security
* CLT vs Graphic
  + Visualizations of the environment and features
  + HDF5 library not available in javascript level (biome tables)
    - Might be able to produce cmd for user to use in CLT instead
    - Or can use third party producing a download link to go around
* Redbiom select
  + Restrict search options with criteria
* Explore
* On developer’s side
  + Habitual formats and grammar
  + Embedding in other tools and transformation of data
* V4 is a region on 16s rRNA sequence
  + Need to use the same region for comparisons
  + 16s rRNA highly conserved region (not under selective pressure/not changed over the past millions years)
  + Primer used targeted v4 region
* Websocket
  + Keep the http request open for a long time (1hr/20min)
  + Might need this for frequent data request
* Biom tables
  + Biological observation matrix