KBase
PREDICTIVE BIOLOGY

DOE Systems Biology Knowledgebase

Q & A for Australian BioCommons KBase Webinar

9:00 am AEST 22 Sept 2021 / 4:00 pm PDT 21 Sept 2021

Presenters: Ellen Dow, PhD; Elisha Wood-Charlson, PhD
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Facilitator: Melissa Burke

Create a free KBase account: https://narrative.kbase.us/#signup

Webinar Feedback Form: https://forms.gle/9Bji1MDqm399Qdjv9

Slides: 2021-09-21: Aust BioCommons webinar

Narrative Links:
Australian BioCommons webinar
Live Demo

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KBase Technical Support: https://www.kbase.us/support/

Use this document to ask questions about KBase! KBase staff will answer your questions below.

Pre-webinar:

Question: Is there an easy tool to analyze horizontal gene transfer (fastq files) or a pipeline?

Answer: Not at the moment, but we are open to recommendations, as well as supporting community developers that would like to contribute their tools to the platform.

Question: Tools and guidelines for network analysis by cytoscape

Answer: We have a prototype cytoscape tool in development that is based on Arabidopsis, with work underway to explore how to adapt the tool for other model plants. If anyone is interested in beta-testing, please email engage@kbase.us, and we will contact you when it is ready for UX feedback.

Webinar:

Question: Is there a tool to remove Eukaryotic contamination from metagenomes (without binning)?

One option could be to try the JGI RQCFilter that we have on-system. Although I've not used, believe it works well for removing contamination from model organisms like human, monkey, mouse, … Another option is the tool EukRep, which isn't available today in KBase, but we do have a version in development. Would you be willing to reach out to the engage email address and let us know if you'd like to help test it?

Question: Which resources are available for single cell analysis?

Answer: All our tooling is post-read library generation. So anything you can do with an isolate read library or genome, you can do with the single-cell data. That includes assembly, gene annotation, functional gene analysis, pangenomics, and metabolic reconstruction. That said, most single-cell genomes are not very complete, so assembling from combined read libraries from multiple cells in the same lineage is best.

Question: does the platform have capacity to take in processed data (asv tables, count tables) for analysis or does it need to utilize raw data and process in full within the platform?

Answer: (answered live, Sean) - yes those tools are coming online now! See

Question: I might have missed it but can you identify KEGG modules as outputs?

Answer: You can get E.C. classification for genes as part of the RAST annotation