







## MAGs Hackathon Event

Our colleagues in Europe are running a hackathon aimed at ***Optimising Metagenome-Assembled Genomes (MAGs) Workflows in Galaxy*** and we will join from Australia!

### What is it?

This event will connect you to a group of professionals with diverse skills and support your collaboration to:

-  Enhance FAIR MAGs building Workflows
-  Develop user-friendly training materials
-  Advance workflow evaluation methods (using CAMI infrastructure & real data)
-  Build intelligent computational resource estimation tools

You will connect in person with a national group and online with international experts and enthusiasts. More details about the objectives of this event are [here](#).

### Why you should participate

- **Collaborative group work:** work with people outside your usual network.
- **Expert connections:** connect with a national and international group of experts and enthusiasts.
- **Workflow enhancement:** contribute to enhancing MAG workflows.
- **Training material development:** participate in developing related training materials.
- **Skill development:** enhance your knowledge of microbiome data analysis or MAGs.
- **International participation:** work alongside colleagues in Europe on globally important projects.



### **How it works**

Our group will be in Melbourne from Tuesday to Friday 7th to 10th October, 2025 working from 1pm - 7pm AEST . We will mostly work asynchronously, but align with the European hackathon team in Freiberg, Germany for a live discussion each day. BioCommons will cover your accommodation and food expenses while you are at the event.

Please email us to share why you would like to participate, and tell us about any relevant experience. Make sure to provide your name, organisation and role.

Email Tiff at [tiff@biocommons.org.au](mailto:tiff@biocommons.org.au) no later than 5 Sep 2025.