Hands-on:
Automatic functional annotation of metabarcoding and shotgun metagenomic data by using Galaxy (A-Game, ..)

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Environmental DNA (eDNA) represents a rich source of genetic diversity that may be exploited for the identification of novel genes encoding activities of biotechnological interest. Many recent "targeted functional metagenomics" studies have employed high throughput sequencing of eDNA expression library inserts that have previously been identified through functional screens to characterize such genes. To minimize the costs of library construction multiple inserts can be pooled in single libraries, although this approach requires careful sequence assembly and quality control to avoid the recovery of chimeric contigs/scaffolds.

In this practical, we will introduce A-GAME, a web based resource built on the Galaxy framework, designed to assist users with limited bioinformatics skills to reconstruct and characterize desired genes from pooled insert libraries.

The practical will provide a general introduction to Galaxy (data upload, data sharing, histories and workflows) with a particular focus on tools and resources for the assembly and annotation of metagenomic data. Attendees will learn the basic principles of short NGS reads assembly and annotation, and become familiar with the most common bioinformatics tools and pipelines.

No strong background in bioinformatics is required. Participants are encouraged to bring their own data.