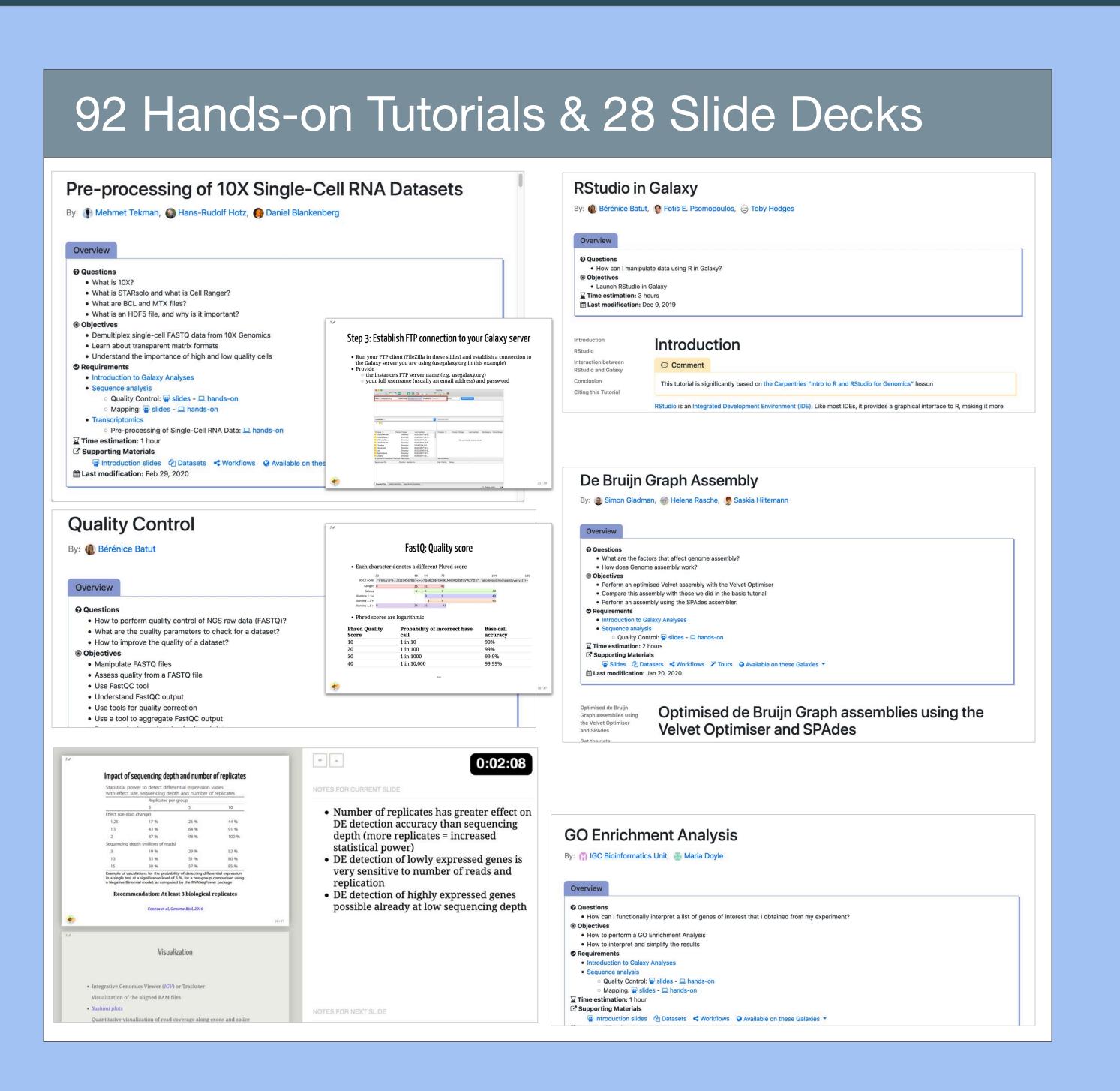
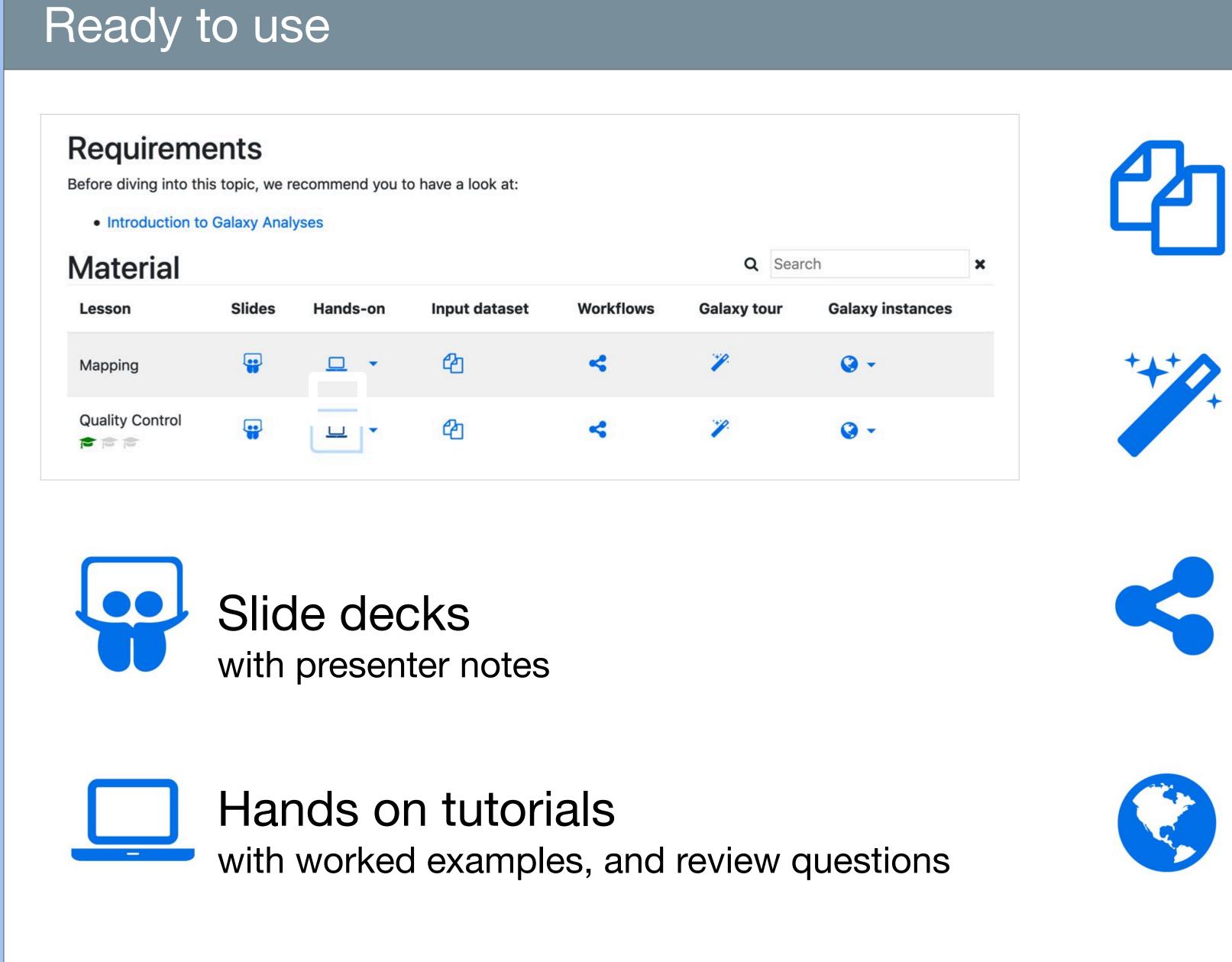
Using the Galaxy Training Network Tutorial Library for Bioinformatics Training Programs

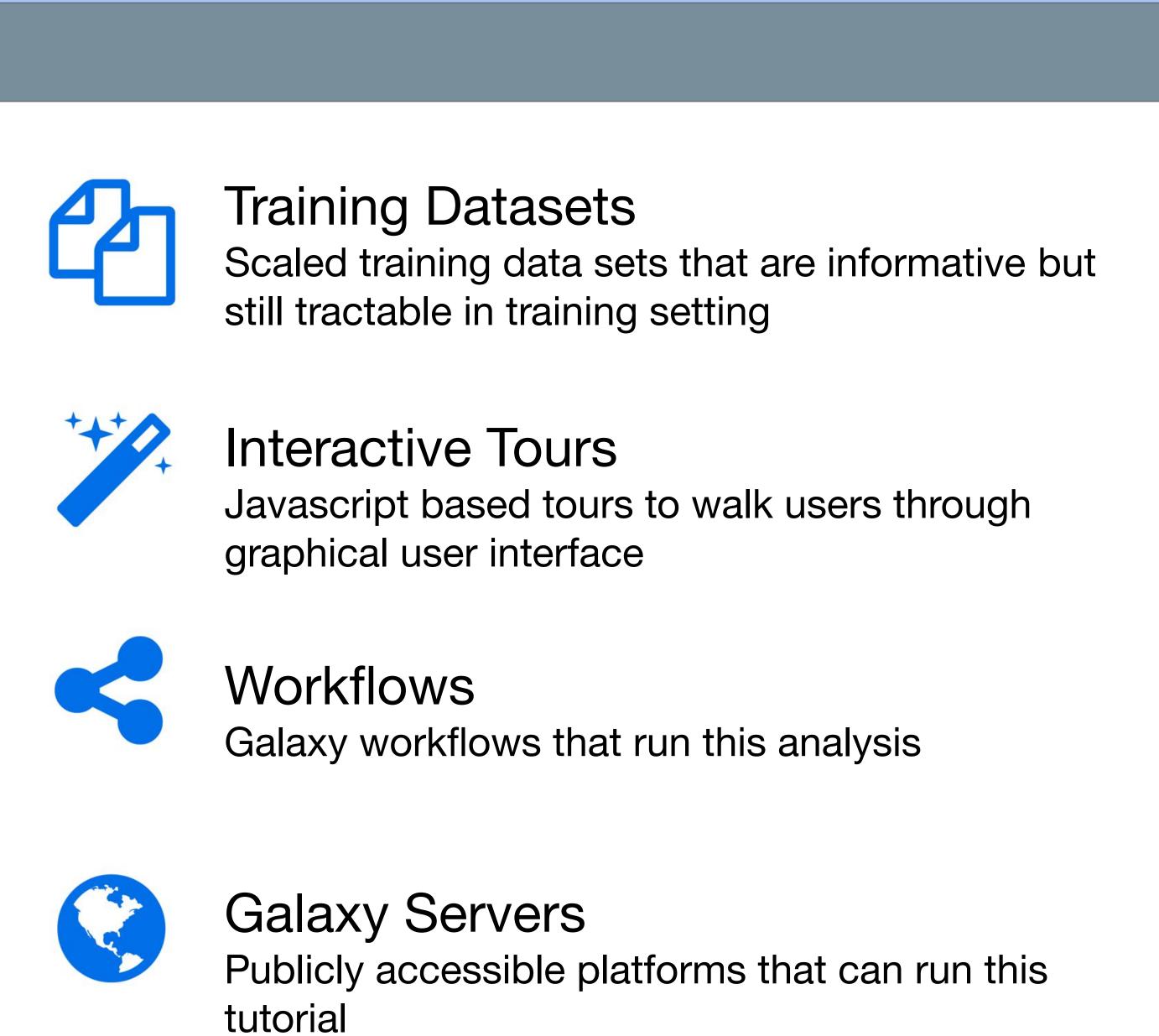
The Galaxy Training Network¹, Bérénice Batut², Saskia Hiltemann³, Helena Rasche⁴, Dave Clements⁵, Björn Grüning² ¹ training.galaxyproject.org/training-material/hall-of-fame ² University of Freiburg ³ Erasmus University Medical Center ⁴ Independent ⁵ Johns Hopkins University

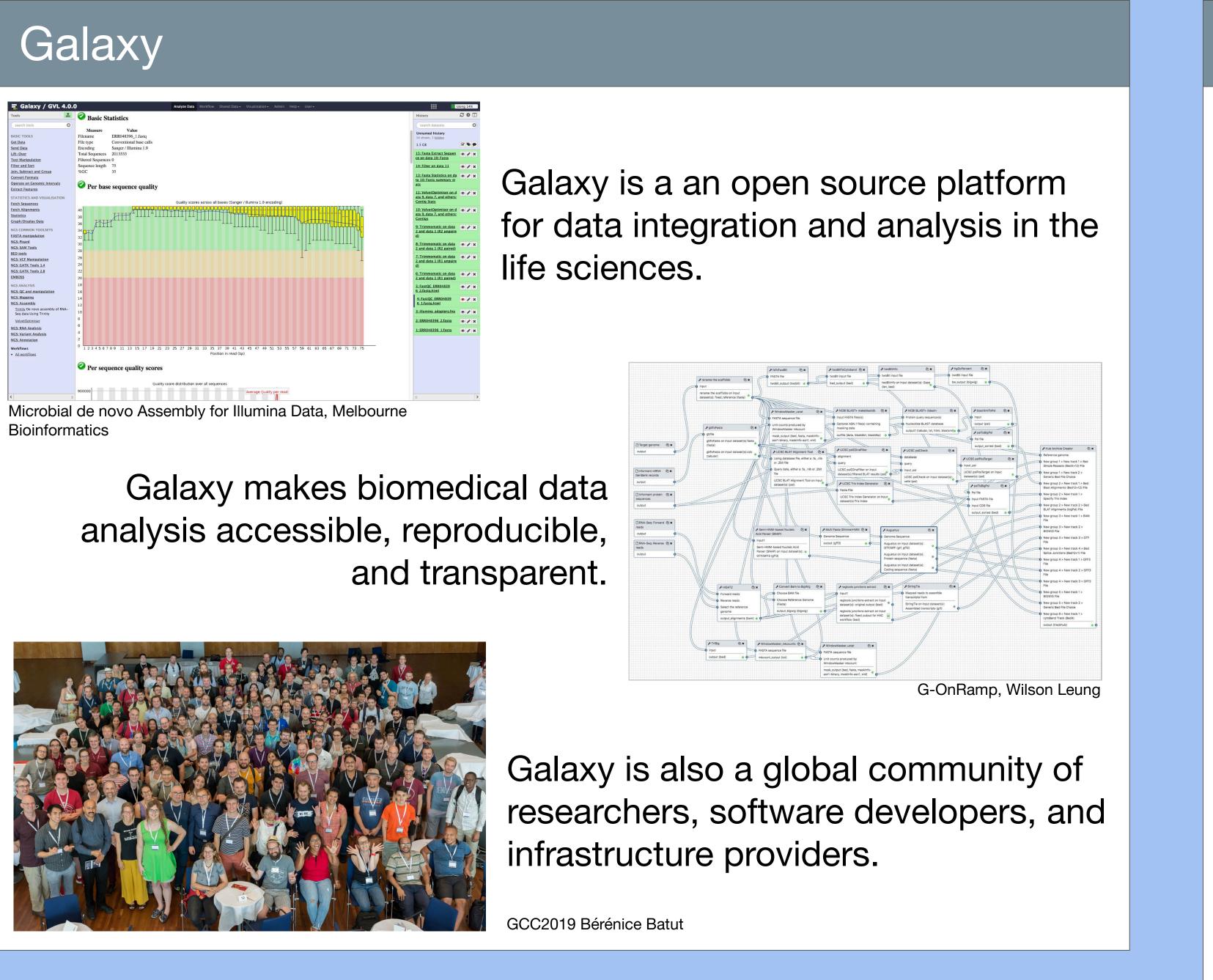
Workshop Support

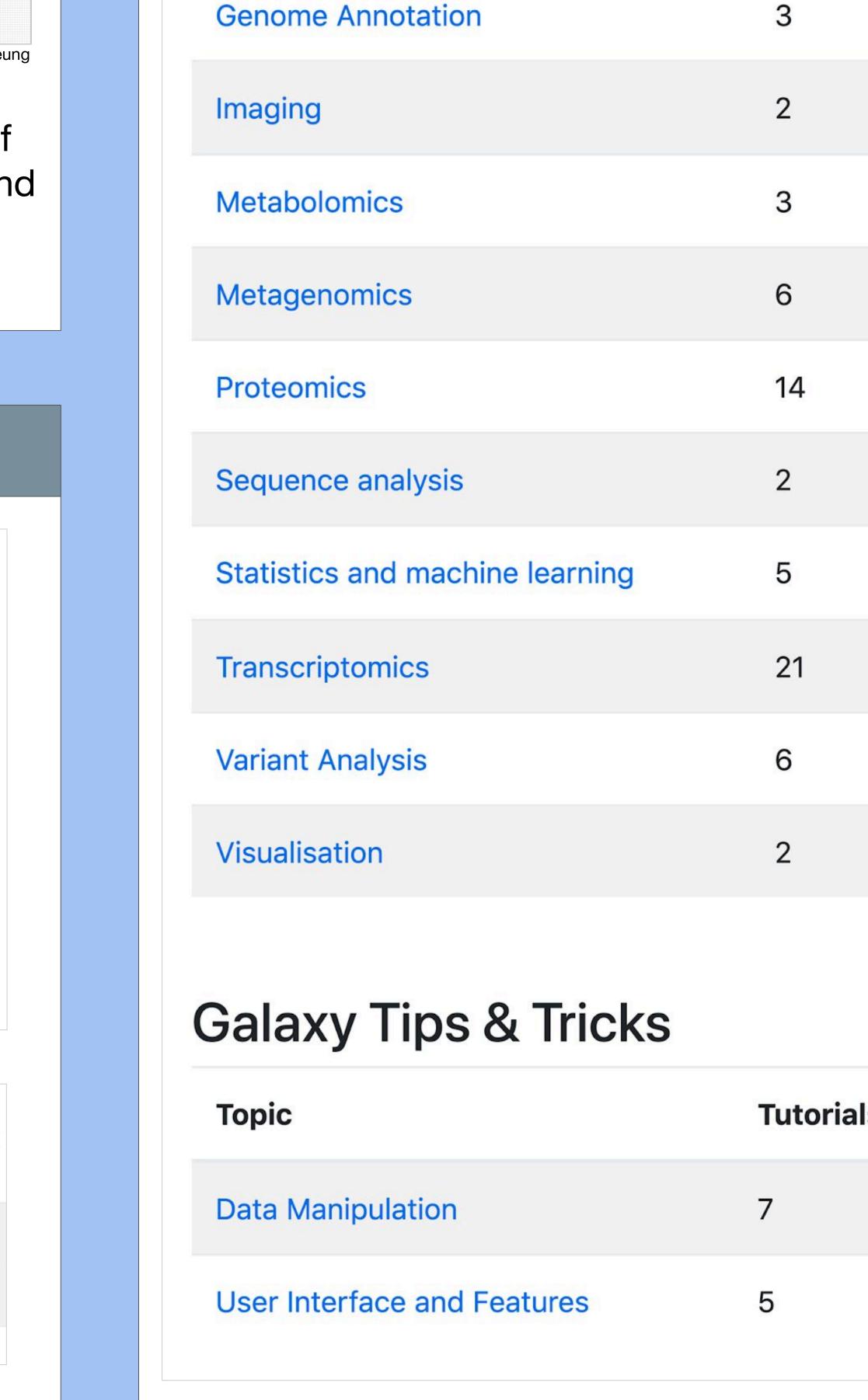
(TlaaS) provides dedicated











Breadth of topics

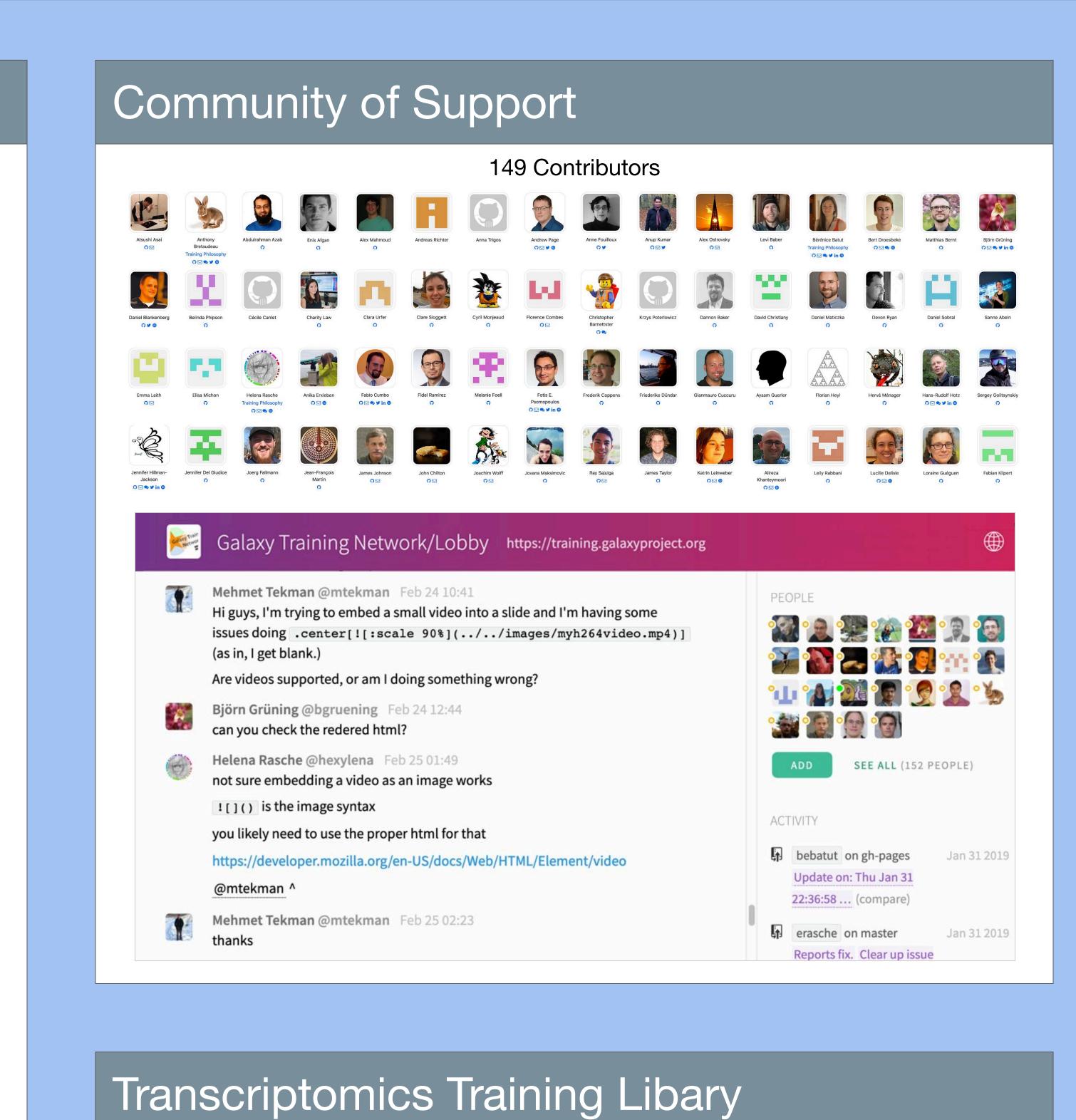
Introduction to Galaxy Analyses

Computational chemistry

Ecology

Epigenetics

Tutorials



Pre-processing of 10X Single-Cell RNA Datasets single-cell 10x

control with scater

RNA Clustering

Understanding

RNA-Seq results

with Volcano Plot

RNA-Seq results

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□ • 4

RNA-Seq results 😛 🚨 🔻 🖆

Transcriptomics

Introduction to Galaxy Analyses

Transcriptomics

analysis from pre-

transcriptome

RNA-Seq

reconstruction wit

abundance testing

Downstream Single-

Plates, Batches, and

Barcodes

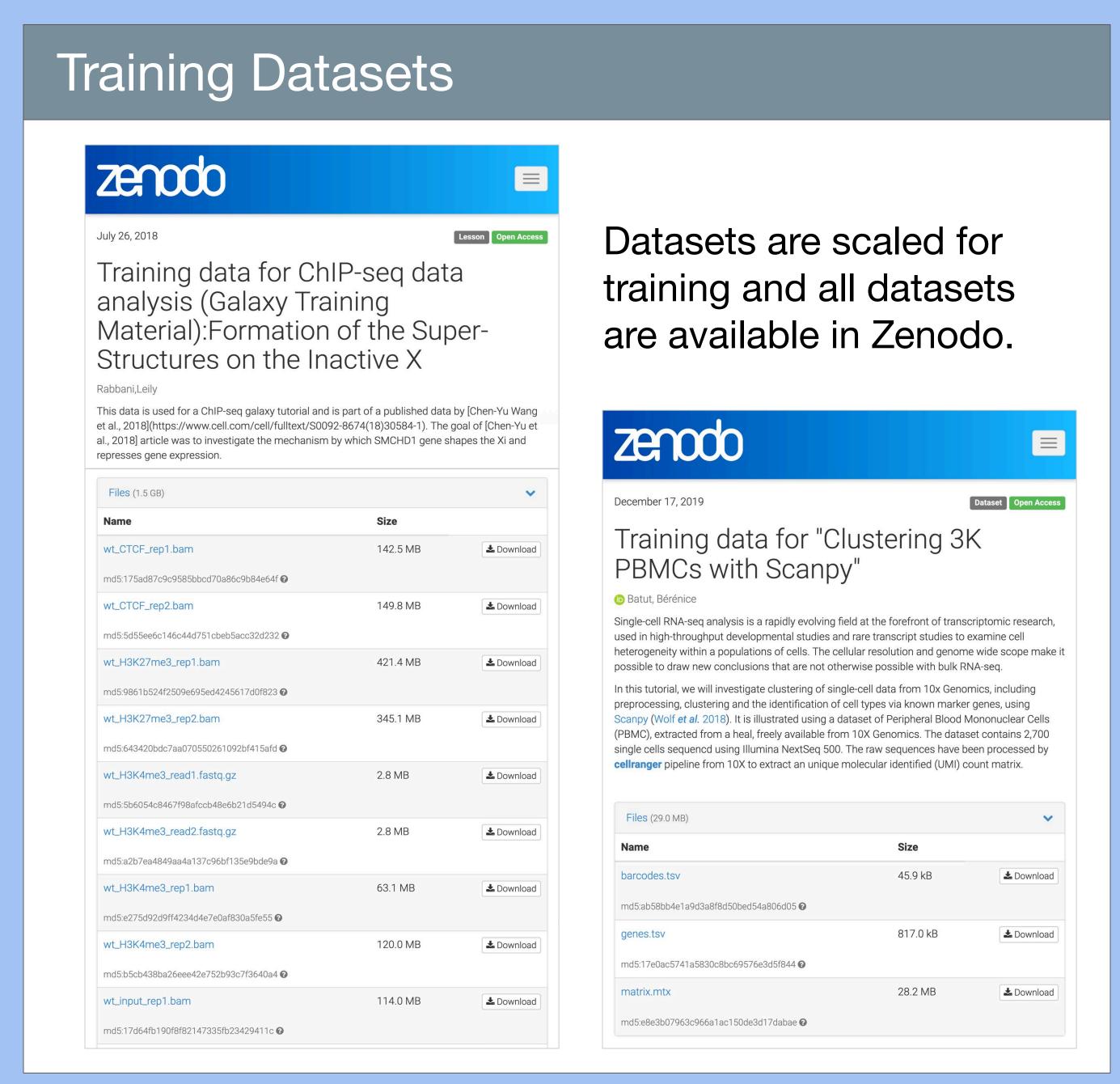
Training material for all kinds of transcriptomics analys

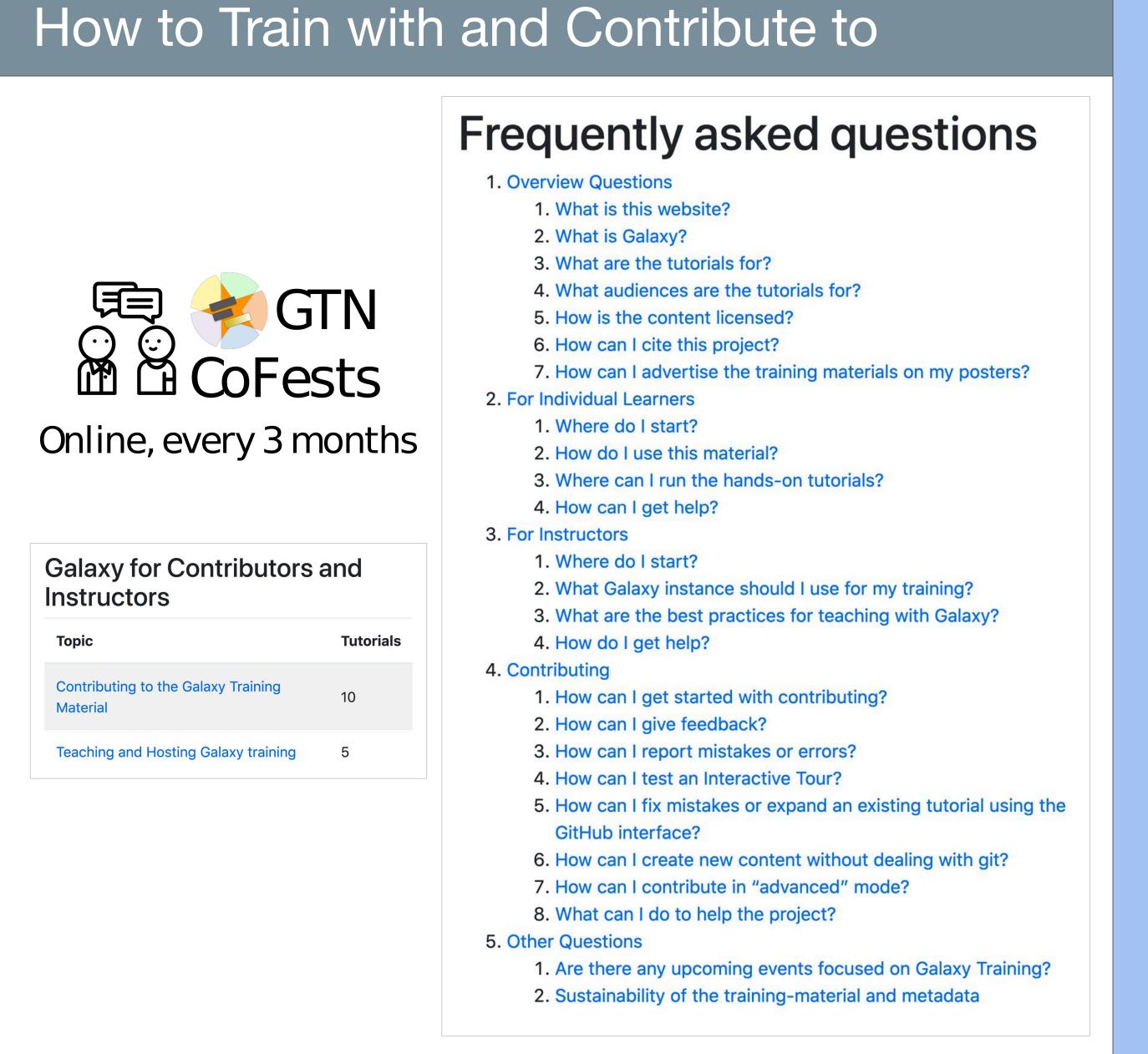
Before diving into this topic, we recommend you to have a look at:

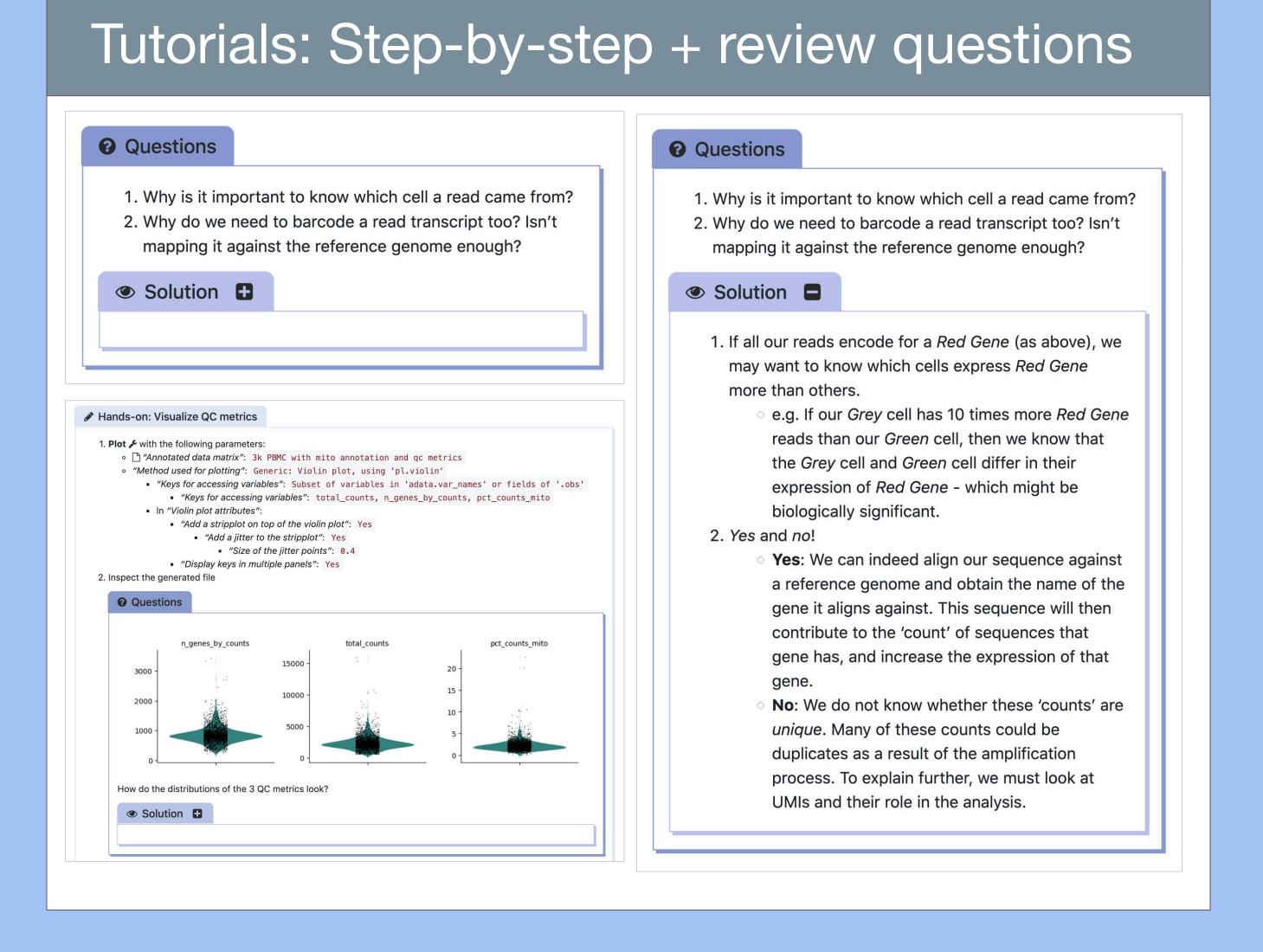
PBMCs with Scanpy 🔐 🚨 🔻 🖆

Quality Control: slides - hands-on

Mapping: slides - hands-on







nttps://training.galaxyproject.org/

