Presentation Type: Talk

Presentation Topic: Tools

Presentation Title (70 characters max):

Using Galaxy and Integrated Genome Browser to study tardigrade biology

Abstract (500 words max, must demonstrate relevance to Galaxy, must be compelling, make sure to highlight that IGB is open-source):

Tardigrade species are micro-animals found in nearly every environment on Earth and are famous for their ability to survive extreme environmental stresses. Studying how these organisms survive extreme environmental stress could provide new insight into how organisms overcome toxic environments. In recent years, new scaffold-stage genome assemblies have been published for two tardigrade species: *Hypsibius exemplaris* and *Ramazzottius varieornatus*. However, advanced genomics visualization resources for tardigrades are currently difficult to find and use. To improve access to tardigrade genomic resources, we developed a new genome visualization resource using the Integrated Genome Browser, an open-source, desktop genome browser well-suited for visual analysis of functional genomics data sets, especially data from scaffold genome assemblies. We also provide published RNA-Seq datasets downloaded from public archives as original sequence data and then re-aligned to tardigrade genome assemblies downloaded from GenBank. The re-processed data includes sequence alignments, useful for comparing genetic differences across species, and scaled coverage graphs, useful for observing differentially expressed genes between experimental samples, created using deepTools bamCoverage. Thanks to an existing, long-standing connection between Integrated Genome Browser and Galaxy, researchers can upload their own experimental data to Galaxy, create their own sequence alignments and scaled coverage graphs within Galaxy, and then use the IGB-to-Galaxy connection to display and visually analyze their data alongside the publicly accessible data sets we provide via the Integrated Genome Browser system. In this short talk, we will describe the connection between IGB and Galaxy, and describe lessons learned from our experience working across the two systems.

Briefly state how is this work related to Galaxy? (50 words max):

We are creating a new genome visualization and data analysis system for tardigrade research, prioritizing easy access and low cost by using IGB for visualization and Galaxy for data analysis. Together, IGB and Galaxy provide almost everything researchers need to understand and process genomic data.