

G-OnRamp: create genome browsers that enable undergraduate students to participate in collaborative genome annotations

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Genome annotation requires reconciliation of diverse sets of potentially contradictory experimental and computational evidence to produce gene models that are best supported by the available evidence. The Genomics Education Partnership (GEP; <http://gеп.wustl.edu>) is a consortium of over 100 colleges and universities that provide course-based research experiences in genomics for undergraduate students. Current GEP research focuses on the annotation and comparative analysis of the Muller F and D elements of multiple *Drosophila* species. While GEP faculty would like to apply this pedagogical approach to other eukaryotes that fit their research interests (*e.g.*, Puerto Rican parrot, parasitoid wasps), creating genome browsers is challenging and time-consuming — particularly for biology faculty with limited bioinformatics expertise.

To address this need, the GEP is collaborating with the Galaxy Project (<https://galaxyproject.org/>) to create G-OnRamp (<http://gonramp.org>). G-OnRamp is a suite of tools that scientists and educators can use to create genome browsers for interactive annotation of eukaryotic genomes. Galaxy is an open web-based platform for large-scale bioinformatics analyses. G-OnRamp extends Galaxy, providing tools and workflows to create UCSC Assembly Hubs and JBrowse genome browsers for eukaryotes with an assembled genome. These genome browsers include evidence tracks for transcript and protein sequence similarity, RNA-Seq data, gene predictions, and simple repeats. In addition to the G-OnRamp software, we have developed training materials and automated local and cloud deployment methods. We will host two G-OnRamp training workshops in Summer 2018. If you are interested in attending, please sign up for the G-OnRamp Workshop mailing list at <http://gonramp.wustl.edu/signup>. Supported by NIH 1R25GM119157.

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