

FFW: Deploying scalable interactive Bioinformatics analyses via VICE

Description: This webinar by Peter Rose (San Diego Supercomputer Center, UCSD) will demonstrate how the Structural Bioinformatics Lab deployed a prototype of their mmtf-pyspark project for scalable data mining of the Protein Data Bank (PDB) on VICE (Visual Interactive Computing Environment), an extension to the CyVerse Discovery Environment (DE). As an example, Peter will show how his team mapped genetic variants onto 3D protein structures and visualized them in Jupyter Notebooks. This webinar is aimed at researchers and developers interested in using or deploying reusable scientific methods on VICE through the Jupyter Lab UI and biologists who would like to learn how to data-mine the Protein Data Bank or map genomic and proteomic data onto 3D protein structures in a zero-install, interactive notebook environment.

Presenter: Peter Rose, Director, Structural Bioinformatics Lab, SDSC, UC San Diego

Tutorials+Documentation+Apps:

* Online tutorial: <https://github.com/sbl-sdsc/mmtf-workshop-2018>

* Documentation: <https://mmtf-pyspark.readthedocs.io/en/latest/>

* Structural Bioinformatics Lab @SDSC Github link: <https://github.com/sbl-sdsc>

* Peter's paper on 10 Simple Rules for Reproducible Research in Jupyter Notebooks: <https://arxiv.org/abs/1810.08055>

* Peter's app in the DE (launch):

mmtf-genomics-vice 0.3.6: <https://de.cyverse.org/de/?type=apps&app-id=ad36b1e4-2dae-11e9-af23-008cfa5ae621&system-id=de>

mmtf-pyspark-vice-0.3.6-16: <https://de.cyverse.org/de/?type=apps&app-id=0c25cbcc-4a74-11e9-b417-008cfa5ae621&system-id=de>

YouTube video:

Chat text from webinar:

chat.txt

Presentation Slides:

Peter Rose: Deploying scalable, interactive bioinformatics apps to mine the PDB