Snakemake & notebooks integration

HANDS ON WEBINAR

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Are you interested in learning how to streamline and automate bioinformatics workflows? This hands-on webinar, will dive deep into the integration of **Snakemake** with **Jupyter** and **R notebooks** to boost reproducibility, scalability and sustainability in your data analyses.

Date: Oct 21 2024

Time: 2pm – 4pm

Platform: webex

Speaker: Johannes Köster, developer of Snakemake and group leader at the University of Duisburg-Essen, Germany. Johannes has extensive experience in bioinformatics and computational reproducibility. He has led groundbreaking work in bioinformatics tools, including the widely used Snakemake workflow management system, and is a co-founder of BioConda

Register now: https://bit.ly/snmkweb

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What You'll Learn:

- ▶ How to integrate Snakemake workflows with Jupyter notebooks and R notebooks for reproducible bioinformatics pipelines

- ▶ Best practices in workflow design and automation

- ▶ Real-world bioinformatics case studies demonstrating these techniques.

Who Should Attend:

Bioinformaticians, biologists, data scientists, developer and any kind of researchers/analysts having:

- ▶ Basic knowledge of Snakemake

- ▶ Basic knowledge of Jupyter or R notebooks

- ▶ A working installation of Snakemake on their laptop

- ▶ A working installation of Jupyter and/or Rstudio in their laptop.