Introduction to Phoenix (UofA HPC) for Bioinformaticians

Who is this workshop for?

Does my work involve computational intensive tasks? Do I want to know more about the state-of-art computing facilities the University provide to use (for FREE)? Am I new to high performance computing (HPC) filed? Do I know some Linux/Unix and want to know how to operate under high performance computing (HPC) environment? If your answers to most of the questions are YES, then we are expecting to see you.

Objectives

1. Introduction to shared environment
2. Enable emergent users to determine need for HPC
3. Enable familiarisation with Phoenix
4. Edit the first Phoenix job script and submit the first job
5. Introduction to additional computing facilities and training resources for emerging bioinformaticians

Duration

90 mins

More Info

Additional Info and updates will be published on [Phoenix@BioHub Blog](#)

You can also subscribe to [Phoenix@BioHub Blog](#) @ https://goo.gl/1LvjL2