TITLE : High Performance Computing for Big Biology

ABSTRACT : Biological data is growing at an exponential rate, driven mainly by the rapid progress of high-throughput sequencing technology. The scientific community has now generated data beyond the exabyte level, leading to Big Biology. Major computational resources, which are storage and compute intensive, are needed to store, organize, manage and analyse these massive data. In this talk, we present how high performance computing opens up great opportunities in solving the challenges in Big Biology.