High perfomance computing FOR Next Generation Sequencing

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Valencia 21-22 May 2012

Next Generation Sequencing has brought unprecedented volumes of data to the bioinformatics arena. Cost reduction in NGS forecasts massive adoption of these technologies by the genome research community. High Performing Computing might be a necessary choice for an efficient processing and analysis of this daunting amount of data. The HPC4NGS SeqAhead workshop presents recent advances in the application of High Performing Computing solutions for NGS. The workshop covers HPC developments for assembly, mapping, RNA-seq, variant analysis, and more and it is targeted to bioinformaticians and computer scientists with interest in NGS.

Organizes: COST Action SeqAhead
Local organizers: Ana Conesa, Ignacio Medina, Joaquín Dopazo
Venue: Centro de Investigación Príncipe Felipe, Valencia, Spain
Registration fee: 70€ (includes material, lunch and coffee breaks)
Registration: http://bioinfo.cipf.es/courses/registration/hpccourse
Further info: aconesa@cipf.es and http://bioinfo.cipf.es/courses/hpc4ngs

PROGRAM (next page)

PROGRAM

21st May

09:00-09:30 Registration and welcome

09:30-10:00 *Introduction to HPC for NGS*. **Juan Manuel Orduña**, UV, Spain

10:00-11:00 *HPC pipeline for NGS alignment and data analysis*. **Ignacio Medina**, CIPF, Spain

11:00-11:30 Coffee break

11:30-13:00 *HPC technologies applied to the BTW transformed to enhance short read assembly*. **Ignacio Blanquer**, UPV, Spain

13:00-14:00 Lunch

14:00-16:00 *GPGPU for NGS data analysis*. **Brian Lam**, University of Cambridge, UK

16:00-16:30 Coffee break

16:30-18:00 *HPC for de novo assembly*. **Martin Simonsen**, CLC bio, Denmark.

22nd May

09:30-10:15 *Speeding up Smith Waterman by SSE/AVX and Open MP* **Joaquín Tárraga** CIPF

10:15-11:00 *HPC solutions for Variant Analysis.* **Cristina Gonzalez**, CIPF, Spain

11:00-11:30 Coffee break

11:30-13:00 *Parallel programming with StarSs*. **Rosa Badia**, BSC, Spain.

13:00-14:00 Lunch

14:00-15:00 *HPC solutions for RNA-seq*. **Enrique Salvador Quintana**, UJI, Spain

15:00-16:00 *Genome-wide nucleosome positioning using Next Generation Sequencing and High-Performance Computing: from peaks to reads*. **Oscar Flores,** BSC, Spain

16:00-16:30 Coffee break

16:30-17:15 *IT infrastructures for NGS data analysis* **Pablo Escobar**, CIPF, Spain

17:15-18:00 *The road to the Exabyte TBA*, **Oscar de Bustos,** BULL Spain