Dear all,

Please join us for our November webinar:

14th November, 1 pm UK time

Steven Kemp:
Basic Introduction to Whole Genome Sequences and their Analysis – Part 2

This is a more practical session looking at different tools and most suited for those working with sequences themselves. The introduction will be split over two sessions and cover the topics below. We will go back to more scientific webinars from December.

1. Installing Linux (suggested distribution is BioLinux, which come pre-installed with many bioinformatics software)
2. Installing Linuxbrew + BioConda (for installing additional software we might need)
3. Quality control of raw reads (FastQC)
4. Alignment of reads to a reference file (BWA/Bowtie2/bbmap)
5. Sort and index (samtools)
6. Mark duplicate reads and remove (samtools)
7. What to do with BAM files

Dial-in details:

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