

	Monday	Tuesday	Wednesday	Thursday	Friday
9:00 – 9:30	Registration				
9:30 – 10:00	Course Overview				
10:00 – 10:30	Introduction to Linux (Rafael Hernández)	Managing and visualizing NGS data → Samtools & IGV (Pedro Furió)	Introduction to R and NGS Bioconductor packages (Patricia Sebastián)	Functional annotation of novel transcripts → Blast2GO (Ana Conesa)	Consulting morning: Setting up a project + closing (Ana Conesa)
10:30 – 11:00					
11:00 – 11:30	CAFE				
11:30 – 12:00	Introduction to NGS: Technologied for Expression Analysis (Ana Conesa)	Quality Control for Mapped sequences → Qualimap (José Carbonell)	Differential expression → NOISeq, edgeR ... (Sonia Tarazona)	Functional annotation of novel transcripts → Blast2GO (Ana Conesa)	
12:00 – 12:30					BRUNCH
12:30 – 13:00					MASCLETÀ (Fireworks exhibition)
13:00 – 13:30	LUNCH				
13:30 – 14:00					
14:00 – 14:30					
14:30 – 15:00	Quality Control for RAW Data → FastQC (Pedro Furió)	Transcript Assembly → Cufflinks and trinity (Rodrigo Lomas)	Functional enrichment with RNASeq → GOSeq (Sonia Tarazona)	Time series analysis with RNASeq → nextmaSigPro (M ^a José Nueda)	
15:00 – 15:30					
15:30 – 16:00					
16:00 – 16:30	CAFE				
16:30 – 17:00	Mapping reads for Expression Data → Tophat; SAM-BAM, BED; GTF .. (Rodrigo Lomas)	Extracting RNASeq counts → Cufflinks, htseq, qualimap ... (Ana Conesa)	DNASE-seq analysis (Sonia Tarazona & Pedro Furió)	Chip-Seq analysis (Lorena de la Fuente)	
17:00 – 17:30					
17:30 – 18:00					