



Working with genomics sequences and features in R with Bioconductor

Thursday 23 September, 10am - 1 pm AEST

Lead Trainer: Dr Paul Harrison, Monash Bioinformatics Platform

Facilitators:

Dr Nandan Deshpande, Sydney Informatics Hub
Dr Andrew Perry, Monash Bioinformatics Platform
Ms Adele Barughare, Monash Bioinformatics Platform
Dr Nick Wong, Monash Bioinformatics Platform
Mr Benjamin Reames, Monash Bioinformatics Platform

Hosts: Dr Melissa Burke, Australian BioCommons

*Timings are approximate and subject to change

Time	Topic
9:45 am AEST 9:15 am ACST 7:45 am AWST	Instructors online to help with setup
10:00 am AEST 9:30 am ACST 8:00 am AWST	Welcome and housekeeping
10:10 am AEST 9:40 am ACST 8:10 am AWST	Presentation: Introduction to the workshop Overview of Bioconductor
	Demonstration: Finding documentation DNA sequences
	Breakout room: DNA sequences challenge ~ 10 minutes
	Demonstration: Using Genomic Ranges Loading data files

	Seqinfo and genome versions Representation of genes
11:00 am AEST 10:30 am ACST 9:00 am AWST	Break (5 mins)
11:05 am AEST 10:35 am ACST 9:05 am AWST	Demonstration: Operations on GRanges
	Breakout room: Transcript initiation sequence challenge ~ 15 minutes
	Demonstration: PolyAdenylation Signal example
12:00 pm AEST 11:30 am ACST 10:00 am AWST	Break (5 mins)
12:05 pm AEST 11:35am ACST 10:05am AWST	Demonstration: BAM and bigWig files
	Presentation: File types and reference resources
	Demonstration: AnnotationDbs, TxDb, and several ways to obtain reference data in Bioconductor
12:55 pm AEST 12:20 pm ACST 10:50 am AWST	Wrap up and feedback
1:00 pm AEST 12:30 pm ACST 11:00 am AWST	Close

Useful links

Training materials: <https://monashdatafluency.github.io/r-bioc-2/>