

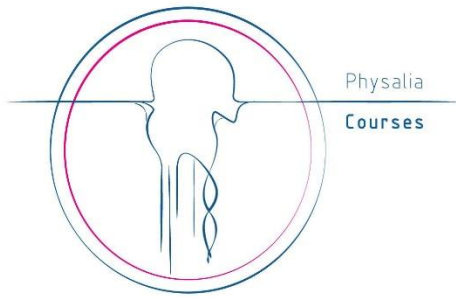
Using the Trinity Framework for De novo Transcriptome Assembly, Annotation, and Downstream Expression Studies

12-16 June 2017

**Instructor: Brian Haas
(The Broad Institute of MIT & Harvard)**



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12-18 June 2017
Instructor:
Brian Hauss



Genome Data Visualization and Software Solutions
10-15 September 2017
Instructors:
Dr. Oibi Griffith
Dr. Malachi Griffith



Substrata for Sequencing using Hi-C
18-25 September 2017
Instructor:
Dr. Kern Ahio



Practical GWAS using Linux and R
25-27 October 2017
Instructor:
Dr. Jing Hua Zhao



LeipzigGenome
8-10 November 2017
Instructor:
Stephane Jacob
Oliver Schmidt, NISC



Genes and experimental data
genome browser (IGV) and data analysis for population genetics, genome data reduction and phylogenetics
4-8 December 2017
Instructors:
Dr. Natalia Rodriguez-Cordero
Dr. Josephine Paris



Applied Substrata and Bioinformatics with Hi-C and Hi-C analysis for
22-28 January 2018
Instructor:
Dr. Lavi Waldron
Kempson



Data visualization and visualization with Python
1st
Instructor:
Dr. Martin Jones



10xRNA, gene mapping and
1st



Microbiome Data Analysis
July 2018
Instructor:
Dr. Paul 'Joey' McMurdie
Kempson



Data analysis in R
2018
Instructor:
Dr. January Weiner



Dr. Martin Jones
(Funder, Python for Biologists, UK)



Dr. Aedin Culhane
(Harvard University, US)



Dr. Owen S. Wangrambani
(University of Salford, UK)



Vasco Eberich
(University of Duisburg-Essen, Germany)



Dr. Paolo Cavalieri & Matteo Ghetti
(Parma, IT)



Dr. Lavi Waldron
(EMBL School of Public Health in Rome, UK)



Dr. Kern Ahio
(Idaho State University, US)



Dr. Lewis G. Spurgin
(University of East Anglia, UK)



Dr. Martin I. Taylor
(University of East Anglia, UK)



Dr. January Weiner
(Max Planck Institute for Evolutionary Biology, Germany)



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(Icahn Institute, Spain)



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(The Broad Institute at MIT & Harvard, USA)



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(Wellington University School of Medicine, UK)



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(Wellington University School of Medicine, UK)



Dr. Stephane Jacob
(EPFL, Switzerland)



Dr. Jing Hua Zhao
(University of Cambridge School of Clinical Medicine, UK)



Dr. Josephine Paris
(University of Paris, UK)



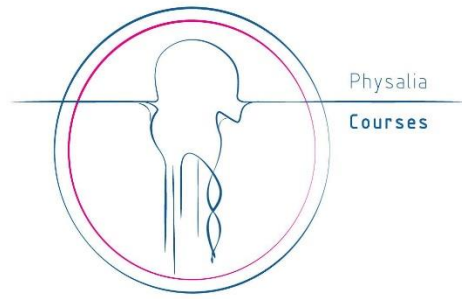
Dr. Alexander Suh
(Yonsei University, South Korea)



Dr. Paul 'Joey' McMurdie
(Edinburgh, San Francisco, UK)

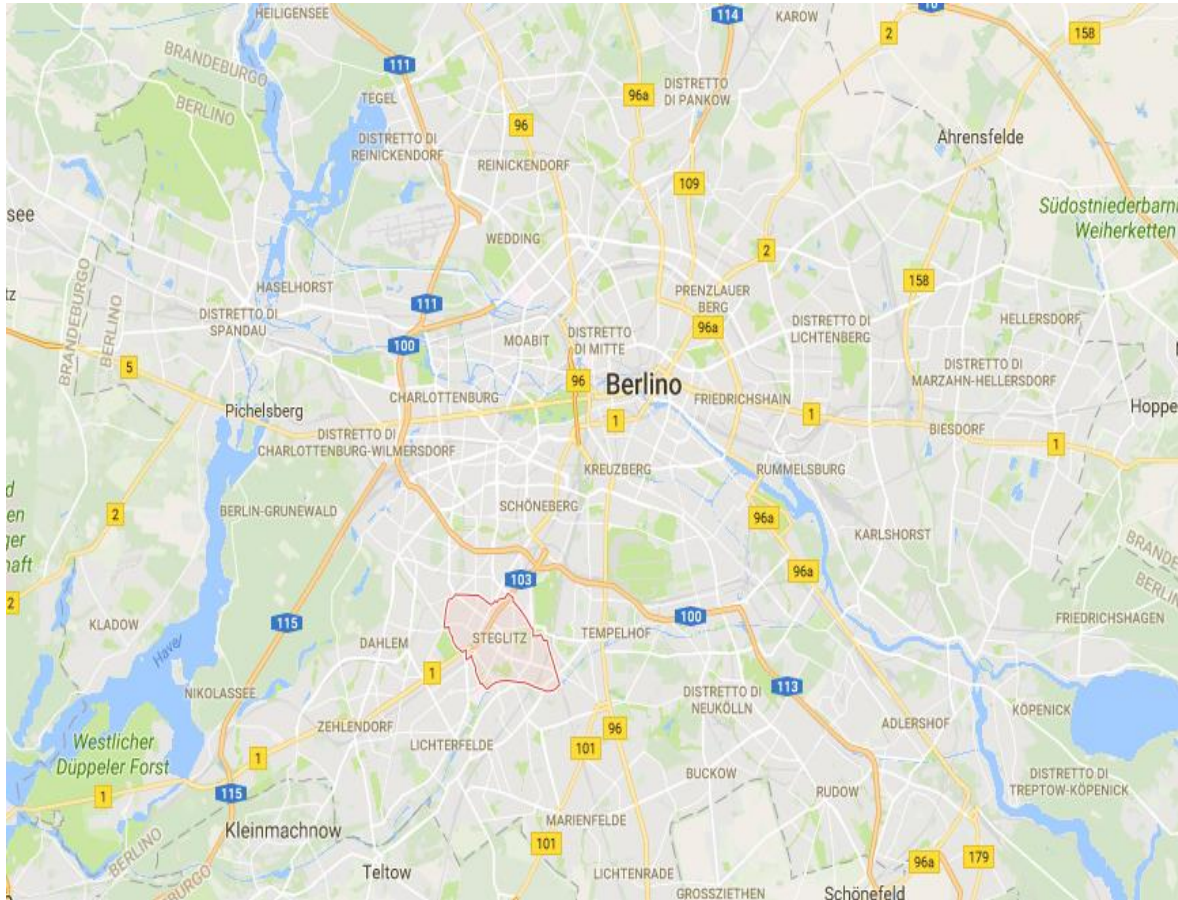


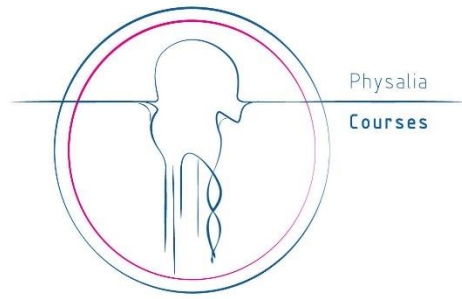
Dr. Carmelo Pruciani
(Queen's University of Belfast, Belfast, Northern Ireland)



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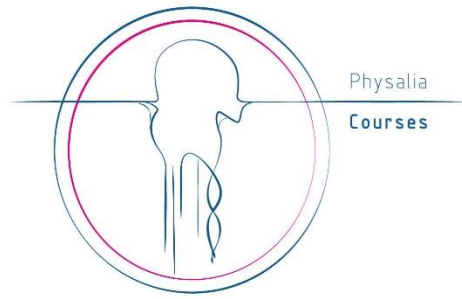
WELCOME TO BERLIN





About you



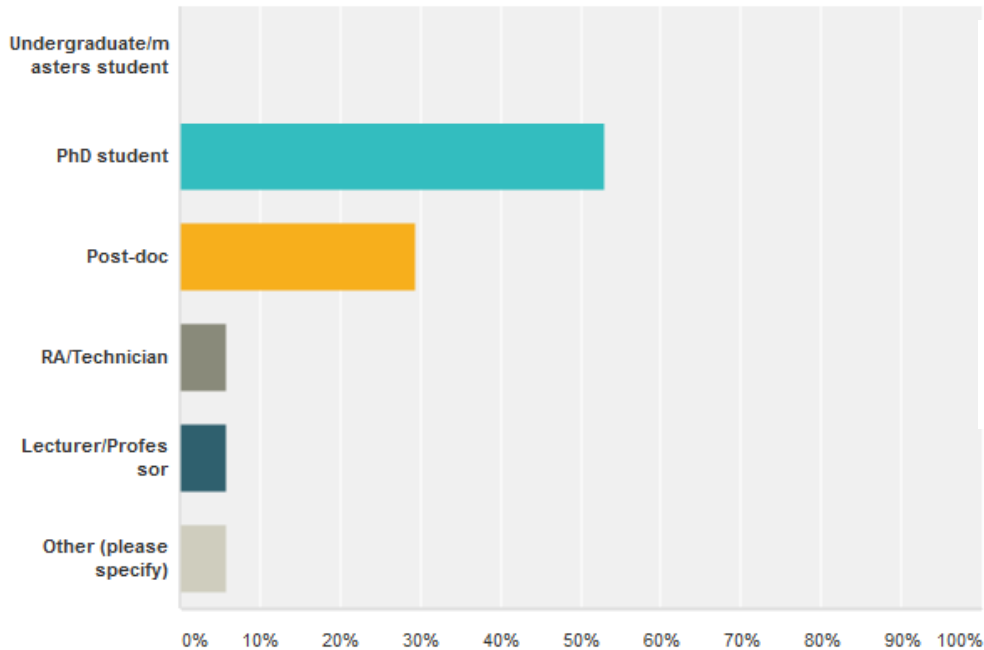


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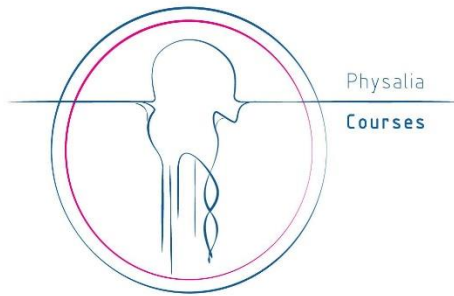
Your current position

Answered: 17 Skipped: 0



	Never heard of it	Heard of it but haven't used	Used a little	Used lots	Wizard!	Total	Weighted Average
Linux	0.00% 0	29.41% 5	64.71% 11	5.88% 1	0.00% 0	17	2.76
Python	0.00% 0	58.82% 10	41.18% 7	0.00% 0	0.00% 0	17	2.41
Perl	11.76% 2	64.71% 11	17.65% 3	5.88% 1	0.00% 0	17	2.18
R	0.00% 0	0.00% 0	70.59% 12	23.53% 4	5.88% 1	17	3.35

Workshop Agenda		
Day	Time	Activities
Monday 12th	09:30-10:00	Workshop introduction
	10:00-11:00	Intro to the Trinity RNA-Seq workshop
	11:00-11:20	Coffee Break
	11:20-12:50	Practical: exploring the computational infrastructure
	13:00-13:50	Lunch
	14:00-16:00	Practical: Unix command-line review
	16:00-16:20	Coffee Break
	16:20-17:30	Practical: using FASTQC and TRIMMOMATIC
Tuesday 13th	09:30-11:00	Overview of Trinity de novo transcriptome assembly
	11:00-11:20	Coffee Break
	11:20-12:50	Intro to expression quantification using RNA-Seq
	13:00-13:50	Lunch
	14:00-16:00	Initial data exploration: assembly quality, and QC samples and replicates
	16:00-16:20	Coffee Break
	16:20-17:30	Initial data exploration: assembly quality, and QC samples and replicates
Wednesday 14th	09:30-11:00	Overview of statistical methods for differential expression (DE)
	11:00-11:20	Coffee Break
	11:20-12:50	Overview of statistical methods for differential expression (DE)
	13:00-13:50	Lunch
	14:00-16:00	Transcript clustering and expression profiling
	16:00-16:20	Coffee Break
	16:20-17:30	Transcript clustering and expression profiling



Ice breaking session



- Who are you?
- Where are you from?
- What's your research project involving RNA-Seq?
- Did you bring RNA-Seq data with you?
 - Format of your data (fastq?)
 - Number of replicates?
 - Approx. number of reads, read length, paired end?