



Training and research in *Listeria monocytogenes* adaptation through proteomic and transcriptome deep sequencing analysis

Workshop: Introduction to statistical analysis of expression data with R

10-12 October 2016

Allée de Vilvert, Jouy-en-Josas, France

Agenda

General information:

- The workshop will take place in building 233 of the INRA campus in Jouy-en-Josas.
- Each day will start at 10 am and will end around 5 pm (5 to 6 hours of training + lunch at the restaurant of the INRA campus).
- ESRs are strongly encouraged to bring their own laptops and to install R (ideally Rstudio) before coming. INRA laptops will also be available if needed. ESRs will have access to wifi via eduroam.

Monday, 10th

Introduction to R language for data analysis (instructor: Sophie Schbath)

10:00 am

- introduction to the R and Rstudio environments;
- basic data structures (from vector to dataframe);
- subsetting data with logical operators: [], \$, which, (%in%);
- descriptive statistics (mean, var) et simple graphs (plot, histogram, boxplot, barplot,...);
- the for loop;
- writing in a file;
- applying a function to a margin of an array (apply);
- transition to Day 2 : introduction to hypothesis testing (p-values).

5:00 pm

Tuesday, 11th

Differential gene expression analysis of RNA-Seq data using R (instructor: Julie Aubert)

10:00 am

- Analyses will be illustrated on a data-set with 2 factors (growth medium x strain) obtained on *L. monocytogenes* (Lobel et al., 2016 PMID: [26895237](#)); introduction to experimental design;



- model for counts data including normalization;
- the DESeq2 pipeline;
- multiple hypothesis testing (q-values).

5:00 pm

Wednesday, 12th

Exploratory analysis and graphical representation of expression data with R (instructor: Pierre Nicolas)

10:00 am

- exploratory data analysis will be illustrated on small and large data-sets (*S. aureus* data-set combining 156 RNA samples taken under 44 experimental conditions from Mäder et al., 2016 PMID: [27035918](#));
- clustering, principal component analysis;
- more plotting (from basic to customized and advanced graphs);
- programming with R (loops, user-defined functions);
- functional enrichment analysis, searching for DNA motifs.

At the end of the day, a time will be taken to discuss and evaluate the workshop

5:00 pm



