**Title:** Fluent genomics: a plyranges and tximeta case-study

**Presenters:**

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**Key words:**

genomics, RNA-seq, tidyverse, R programming, Bioconductor

**Description:**

In this workshop, we will give an overview of how to perform exploratory analyses of genomic data using the grammar of genomic data transformation defined in the plyranges package. In the first half of the workshop, we will introduce the GRanges data structure and provide an overview of the core verbs for arithmetic, restriction, and aggregation of GRanges. In the second half of the workshop, we will work through case study of integrating differential expression and differential chromatin accessibility results from an experiment of macrophage cell lines. We will learn how to use the tximeta package for automatically preparing data from an RNA-seq experiment with correct reference annotations.

**Requirements:**

Laptop with the latest version of R and Rstudio installed. Further setup instructions will be provided in the workshop. A familiarity with the basics of R/tidyverse would be a plus but is not strictly necessary.

**Relevance:**

This workshop will be beneficial to new learners of R who would like to understand more about Bioconductor and learners who are already familiar with the tidyverse suite of packages and would like to apply those concepts to bioinformatics data analysis. It is also recommended for biological scientists who would like to start looking at data from their own experiments but are not sure how to begin.