Analysis of RNA-seq data from bovine macrophages infected with Streptococcus agalactiae

Why was this stem important for you?

The main aim of the STSM was to obtain training on proper strategies and use of software for the analysis of a RNA-sequencing data. The purpose of data analysis was to identify differentially expressed transcripts in blood monocyte-derived macrophages form Norwegian Red (NR) cows infected in vitro with specific mastitis causing bacterial strains compared to uninfected controls. The results obtained during the STSM will contribute to better functional annotation of the bovine genome.

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