

A large-scale metagenomic analysis using OSG

Tuesday, 7 March 2017 14:50 (20 minutes)

It is well known that exosomes play an important role in cell-to-cell communication by transferring all types of molecules from donor cells to recipient cells. The objective of this study was to assess the microbial mRNA cargos in exosomes of one type of body fluids. To identify the possible microbial species in the samples, we conducted a large-scale metagenomic analysis by using the Open Science Grid (OSG) and 4,742 microbial genomes were assessed on each of 6 samples. The result shows that, across all samples, microbial sequences consistently account for a large percentage of the mRNAs in exosomes. Moreover, through the highly efficient system of OSG, the tasks of ~81K CPU hours were completed in 17 days.

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Session Classification: OSG Users