

## **Analysis of genetic variety of human gut metagenome**

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Most of modern metagenomic study are limited to functional and taxonomic content comparison, while genome differences of individual-specific strains are left unattended. We developed an approach for identification of different statistical measures of genetic variety of human gut microbiota. This approach was applied to 322 faecal metagenomes of individuals from USA, Denmark, China and Russia. For 93 most abundant microbial species we analyzed how various factors especially place of residence of individuals are related with genome differences. Despite of complication caused by distinction in coverage profiles we managed to compare mutation rates and strain diversity of dominant species.