**Assembly of mammalian genomes using GemCode data**

1. Kekteeva1, I.Tolstoganov2, A.Bankevich2

*1 St. Petersburg Academic University, St. Petersburg, Russia*

*2 Center for Algorithmic Biotechnology, St. Petersburg State University*

*a*[*ngira.kekteeva@gmail.com*](mailto:Angira.kekteeva@gmail.com)

GemCode technology that was developed by 10X Genomics Company is actively used for assembly of mammalian genomes. CloudSPAdes is a genome assembly algorithm which was designed for metagenome assembly. However, algorithms in this tool, that were developed for resolving repetitions in the assembly graph, can be successfully used for assembly of mammalian genomes.

In this work we've examined exisiting metagenome assembly algorithms and analysed the disadvatages of using them for large genomes. Our analysis has shown that the average number of close edges in a human genome graph is more, than in metagenomes assembly graph, so it requires additional methods for sequencing long edges in the genomes of mammals.