

# Bioinformatic platform “Binom”: parallel alignment

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Binom is the platform used by Genotek startup (DNA-diagnosis).



My task is to speed up alignment using parallelization.

Solutions:

- Proprietary solution started by Ignat
- Myrna: a cloud-computing pipeline for calculating differential gene expression in large RNA-Seq datasets
- Crossbow: a scalable software pipeline for whole genome resequencing analysis

## Preliminary results

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- Tested bowtie's speed
- Investigated Myrna solution
- Compared with Ignatiy's solution

# Plans

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- To measure Myrna's speed and scalability
- To hold a 2-days hackathon in Moscow to gain alpha-version of platform
- To deploy platform on Amazon cloud (Hadoop)

Thank you for attention!

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