Computational efficiency of software for the analysis of Next Generation Sequencing data

Magda Mielczarek¹, Joanna Szyda¹, Artur Gurgul², Kacper Żukowski², Monika Bugno-Poniewierska²

joanna.szyda@up.wroc.pl

¹ Biostatistics Group, Department of Genetics, Wrocław University of Environmental and Life Sciences, Wrocław, Poland
² National Research Institute of Animal Production, Cracow, Poland

CONCLUSIONS

whole genome NGS data editing & alignment are possible on a small server
BOWTIE2 software showed the best performance

MATERIAL & METHODS

whole genome NGS of a dog generated by Illumina

RESULTS

BOWTIE2
Langmead & Salzberg (2012)

SOAP2
Luo et al. (2012)

BFAST
Homer et al. (2009)

DATA EDITING

READ ALIGNMENT

not enough memory