

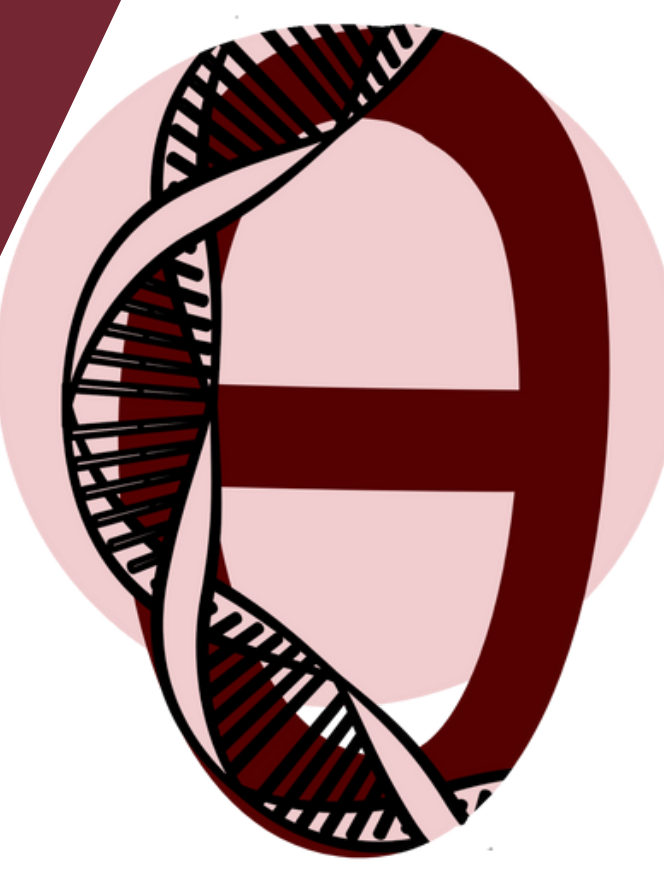


Nextflow vs Naïve Bash: Different approaches to SNP calling parallelisation on the Whole Genome Bovine Sequence

M. Sztuka, P. Hajduk, J. Liu, K. Kotlarz, M. Mielczarek and J. Szyda

Wroclaw University of Environmental and Life Sciences

Biostatistics Group, Department of Genetics, Wrocław
University of Environmental and Life Sciences



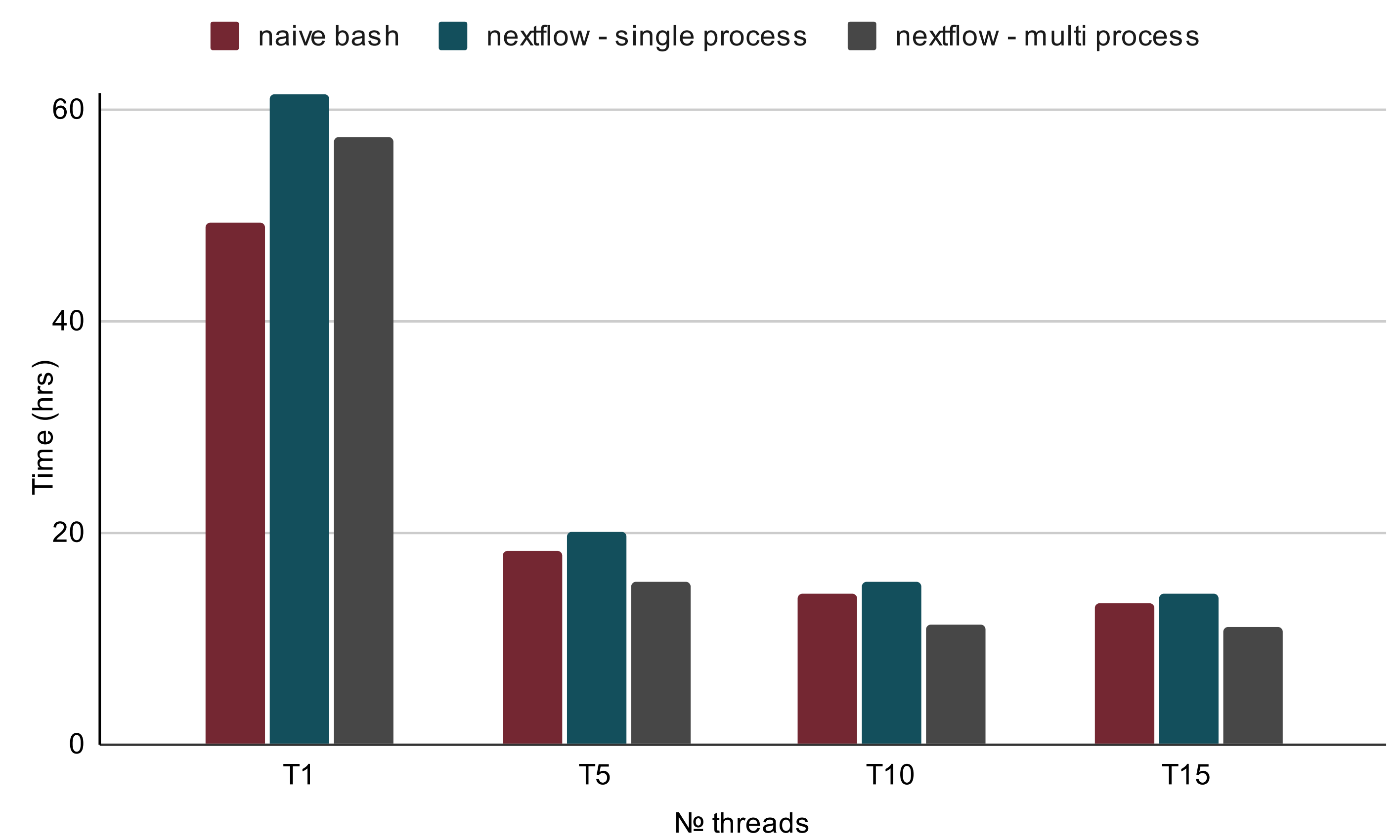
BIostatistics GROUP
WROCLAW, POLAND

Objective

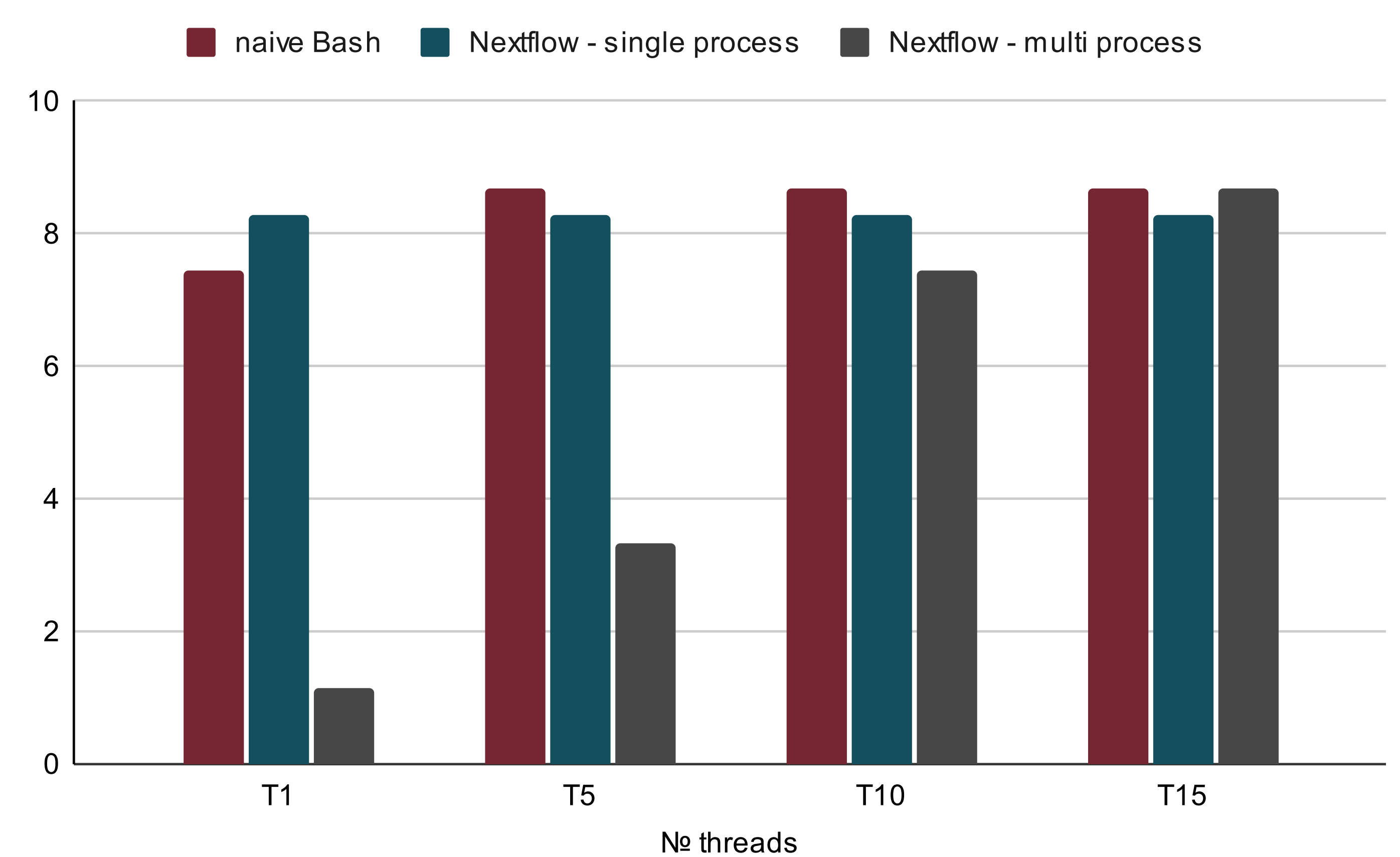
Comparing variant calling efficiency in WGS data under various parallelisation strategies

Results & Conclusions

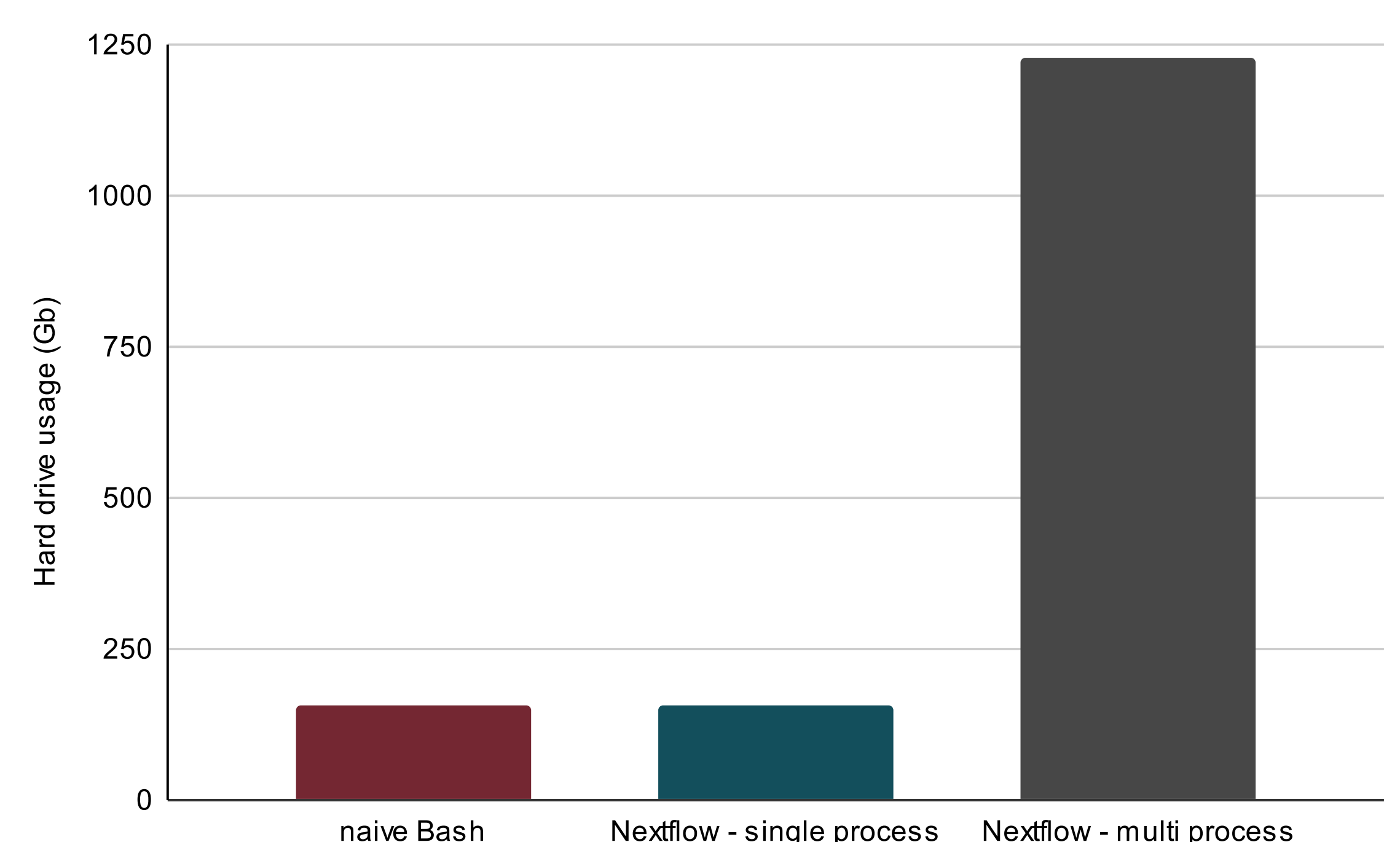
- Lower execution times with multi-process nextflow



- Significantly lower memory usage with multi-process nextflow



- Drastically larger hard drive usage of multi-process nextflow



Marek Sztuka
mareksz19@gmail.com
THETA Biostatistic Group

Three approaches

