

Propositions accompanying the thesis

“Computationally Fast Approaches to Genome-Wide Association Studies”

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1. The necessity of involving large computing resources in the genome-wide association analyses is often a consequence of using inefficient algorithms. **(this thesis)**
2. To determine important SNPs in GWAS, it is sufficient to obtain the approximate p-values. **(this thesis)**
3. To make full use of fast algorithms, proper organization of SNP data storage is essential. **(this thesis)**
4. Simple rearrangements of matrix operations can speed up algorithms by several orders of magnitude. **(this thesis)**
5. The performance of some of the approximate procedures for longitudinal data is highly dependent on whether the data is balanced or unbalanced. **(this thesis)**
6. With the growing amount of collected data, computational statistics becomes an integral part of contemporary clinical research.
7. Despite the large number of scientific articles published on GWAS results, their relevance for the individual remains debatable.
8. In a computer game GWAS means “Game Was A Success”. In association studies this is seldom the case.
9. Computers have lots of memory, but no imagination. (Author unknown)
10. Whenever anyone says, 'theoretically', they really mean, 'not really'. (David Parnas)
11. Advisors are like parrots. With one you look like a cool pirate. With more you look like a fool.