Propositions

1) Published population–level genetic datasets contain more population-specific variation than they share with the other populations. (*this thesis*)

2) Many genetic variants we currently consider "pathogenic", will be revealed to show incomplete penetrance by sequencing of healthy populations. (*this thesis*)

3) Standardization of dynamic genomic data has been challenging due to the large range of applications, but most data analysis methods will yield similar results. (*this thesis*)

4) To avoid out-of-context interpretation and conclusions, expression differences of individual genes or pathways must be reviewed as part of the whole gene expression network. (*this thesis*)

5) To understand all disease-relevant genetic variation, somatic DNA variants should be studied much more widely then is currently done. (*this thesis*)

6) The accumulation of somatic variants with age - genosenium - differs per tissue, tissue region, disease-state and is likely relevant for human age-associated diseases. (*Lodato et al, 2018, Science*)

7) High-throughput genotyping, for example by genome sequencing, yields medically relevant results for each individual and will become commonplace in healthcare to prevent disease (based on results of the MEDseq project, *Machini et al, 2019, AJHG*).

8) In the case of multiple competing theories, the simplest hypothesis should be preferred. (*the law of parsimony, William of Ockham*)

9) Not everything that can be counted counts, and not everything that counts can be counted. (*Albert Einstein*)

10) To obtain anything, something of equal value must be lost - equivalent exchange. (*Alphonse Elric*)

11) *non blaterare sed polire*.