Computational models for clinical drug response prediction aligning transcriptomic data of patients and pre-clinical models

Mourragui, S.M.C.

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Propositions

accompanying the dissertation

COMPUTATIONAL MODELS FOR CLINICAL DRUG RESPONSE PREDICTION

ALIGNING TRANSCRIPTOMIC DATA OF PATIENTS AND PRE-CLINICAL MODELS

by

Soufiane Marc Charles MOURRAGUI

1. Cell lines form a reasonable, but limited, model system for clinical drug response prediction (This proposition pertains to this dissertation).
2. The signal in DNA-based measurements predictive of drug response is correlated with gene expression (This proposition pertains to this dissertation).
3. The expression of intrinsic immune pathways in lung cancer cell lines is aligned with the expression in epithelial lung tumor cells (This proposition pertains to this dissertation).
4. Kernel methods offer a comprehensive framework amenable to the interpretation, comparison and dissection of deep generative models (This proposition pertains to this dissertation).
5. Voter indecisiveness in democracies is a direct consequence of the curse of dimensionality.
6. Scientific trends follow patterns similar to the ones observed by behavioral economists in speculative markets.
7. Homo Deus does not constitute a Lyapunov stable equilibrium for humanity.
8. The political system in Western countries is gripped by a narrow-understanding of the notion of liberalism.
9. High impact journals would benefit from adding a general-public reviewer for all papers.
10. Due to the worldwide pervasiveness of fiat money, replacing taxes by a centralised monetary-based approach would strengthen our redistribution system.

These propositions are regarded as opposable and defendable, and have been approved as such by the promotors prof. dr. L.F.A. Wessels, prof. dr. ir. M.J.T. Reinders. and prof. dr. M. Loog