

A HUMAN CYTOME PROJECT: FICTION OR CHALLENGE ?

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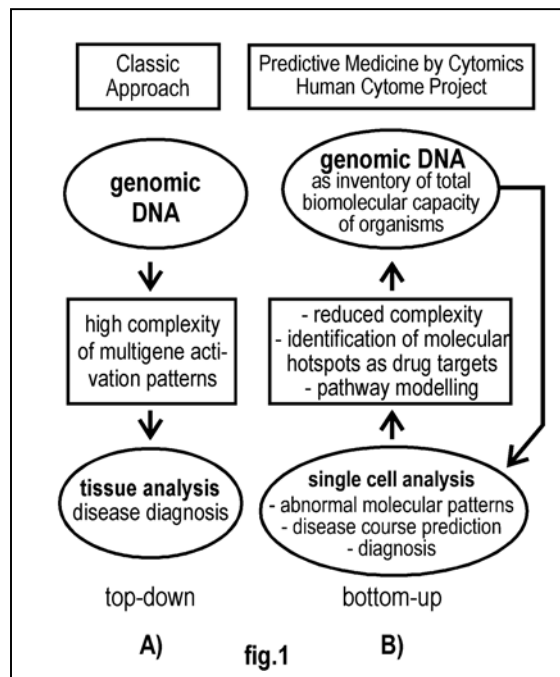
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BACKGROUND

The sequence information of the human genome does presently not explain the observed structural and functional multilevel biocomplexity (fig.1A) of cells and cellular systems (cytomes). Considering the still existing difficulties with the exact computer prediction of 3D protein structures from their known amino acid sequence containing the 20 most common amino acids, it seems out of reach to systematically understand the combinatorial complexity of the metabolic pathways of 20-30.000 gene products by classical deductive hypothesis formulation and experimental verification within reasonable time intervals.

CHALLENGES

In this situation, a *human cytome project* can simultaneously advance the biomedical sciences in *two* important directions. **1.** The newly established direction of individualised disease course



predictions and pretherapeutic identification of high risk patients [1] relies on the multiparametric differential screening of molecular cell phenotypes by image and flow cytometric single cell analysis in combination with the bioinformatic information enrichment strategies of molecular cell systems research (cytomics). **2.** The initial bypassing (fig.1B) of the complex mechanisms of genome realisation by differential molecular cell phenotype screening for medical purposes, represents a self focusing mechanisms for the identification of disease related molecular hotspots. This will permit the establishment of a standardized *relational framework* of disease associated data patterns as a kind of periodical system of characteristic molecular cell states. Unknown molecular interrelations can be identified without detailed a-priori hypothesis and new drug targets are detectable by this inductive *reverse engineering* like strategy of

functional genome analysis. A *human cytome project* constitutes a challenge for biomedical and bioinformatic scientists, clinicians and innovative technological developments [2].

[1] G.K. Valet, A. Tarnok, Cytomics in predictive medicine, *Cytometry* 53B, 1-3 (2003)

<http://www.biochem.mpg.de/valet/cellclas.html>

[2] G.K. Valet, J. Leary, A. Tarnok, Cytomics - New technologies: Towards a human cytome project. *Cytometry* (2004), in press