

WANT TO PREDICT RISK OF COMPLEX DISEASE OR RESPONSE TO MEDICAL TREATMENT?

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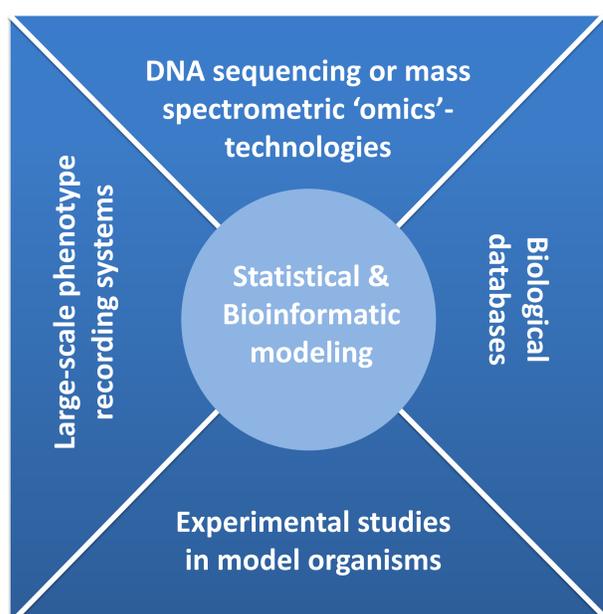
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WHY PREDICT?

Predicting individual disease risk and response to treatment provide better diagnostic tools and targeted treatments

NEW OPPORTUNITIES IN DISEASE PREDICTION

Large data sets generated through rapid advances in large-scale phenotype recording systems (e.g. medical measuring devices, gadgets, wearables), as well as in nucleotide sequencing or mass spectrometric 'omics'-technologies, will dramatically change our health care system in the near future.



CURRENT RESEARCH PROJECTS

- identify genetic factors and predict risk for schizophrenia and ADHD
- identify genetic factors for response to exercise in humans
- predict treatment response using phenotypic and whole genome sequence data from *Drosophila Melanogaster*
- predict cancer drug combination synergies using different layers of molecular data (e.g. copy number variations, exome sequencing, gene expression and methylation).

WHO ARE YOU?

A student who wants to:

- discover the genetic factors underlying complex traits and diseases
- learn how to predict disease risk or treatment response using advanced statistical and bioinformatic methods

WHAT ARE COMPLEX DISEASES ?

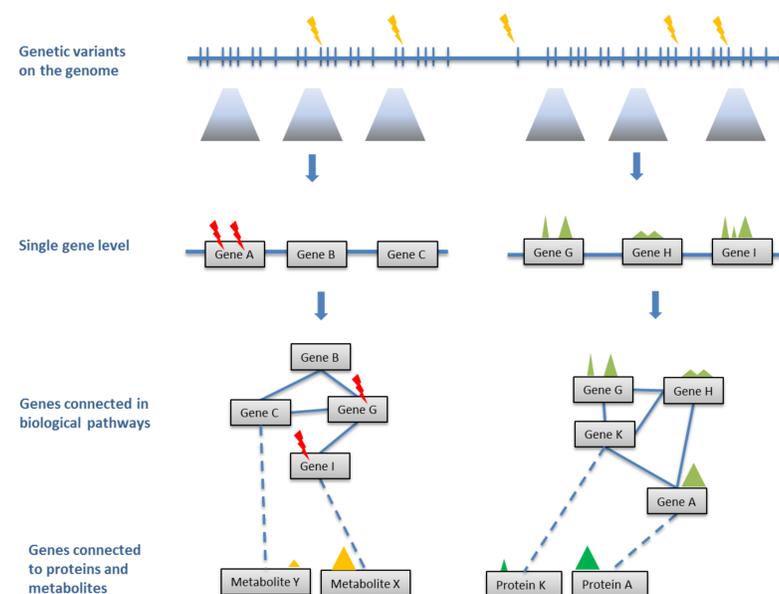
Examples of complex diseases are **high blood pressure, diabetes, mental disorders and obesity**

They are complex because they **likely caused by many interacting genes in combination with lifestyle and environmental factors.**

They are difficult to predict because the effects of the majority of genes affecting the disease are too small to be individually detected.

PREDICTION MODELS USING INFORMATION FROM DIFFERENT LEVELS OF BIOLOGY

A key to take advantage of these "Big data" resources is to develop novel predictive tools, which combine sophisticated quantitative statistical models with fundamental biological knowledge of molecular mechanisms, to generate novel models, which will accurately predict disease risk or treatment response.



WHO ARE WE?

An international group of researchers with expertise in development, optimization, and implementation of genetic and statistical models for identifying the underlying genetic factors and prediction of phenotypes for complex traits and phenotypes in animals, plants and humans.