

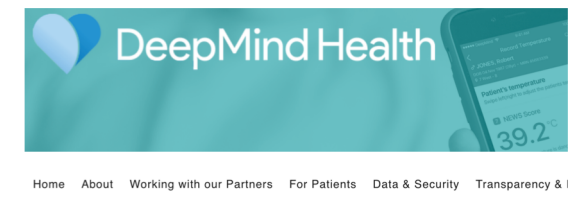
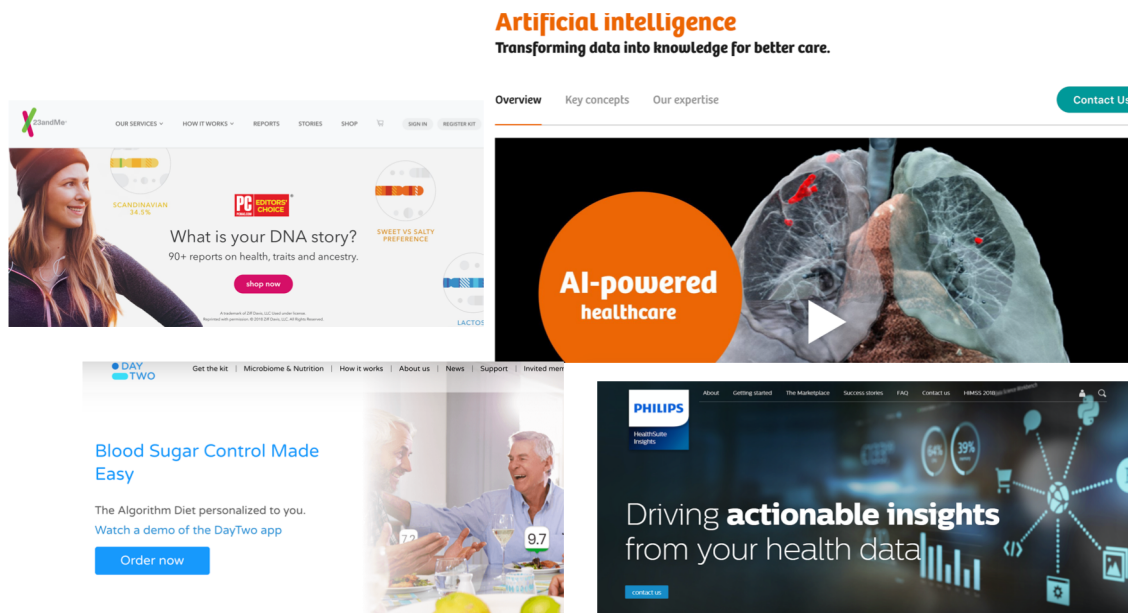
ARTIFICIAL INTELLIGENCE FOR CARDIOMETABOLIC DOMAIN

Evgeni Levin, PhD



AI REVOLUTION IN HEALTHCARE

During the last years AI has increasingly attracted attention in biomedical research

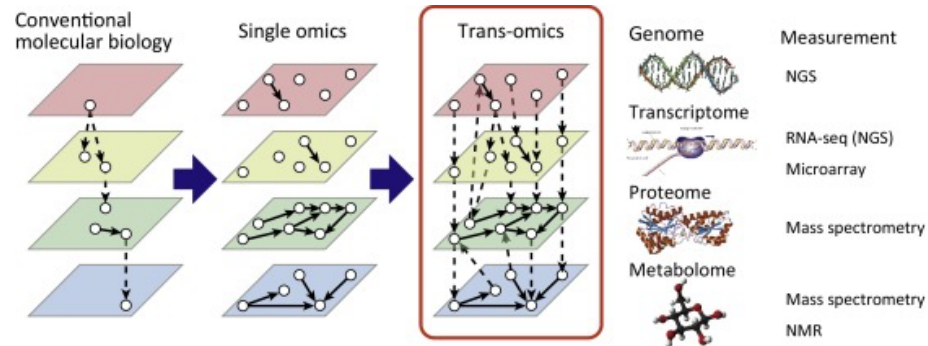


Helping clinicians get patients from test to treatment, faster

BIG DATA IN HEALTHCARE

We are witnessing explosion in availability of various data sources/information on nutrition, growth, health, etc.

It is becoming increasingly difficult to process and utilize these data – but at the same time health care professionals more and more rely on outcomes of complex multi-omics data analysis



AI IN CARDIOMETABOLIC DOMAIN

Metabolic syndrome - metabolites, microbes (Cell met 2017), IBD – microbes, fungi (Gastro 2017), Multi-ethnic microbiome (Nature Medicine 2018), CAD – targeted proteomics (European Heart), etc.



New biological hypotheses and biomarkers

New paradigms on personalized treatment

New non-invasive technologies

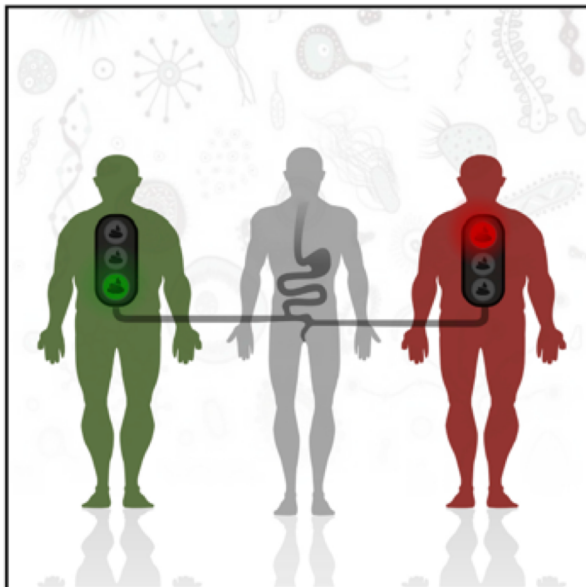
IMPROVING INSULIN SENSITIVITY

Clinical and Translational Report

Cell Metabolism

Improvement of Insulin Sensitivity after Lean Donor Feces in Metabolic Syndrome Is Driven by Baseline Intestinal Microbiota Composition

Graphical Abstract



Authors

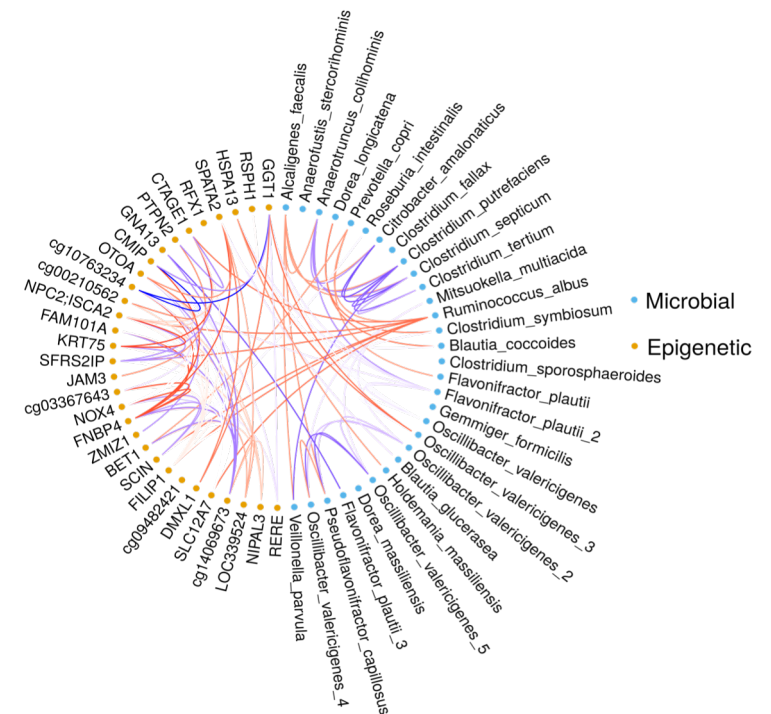
Ruud S. Kootte, Evgeni Levin, Jarkko Salojärvi, ..., Erik S.G. Stroes, Albert K. Groen, Max Nieuwdorp

Correspondence

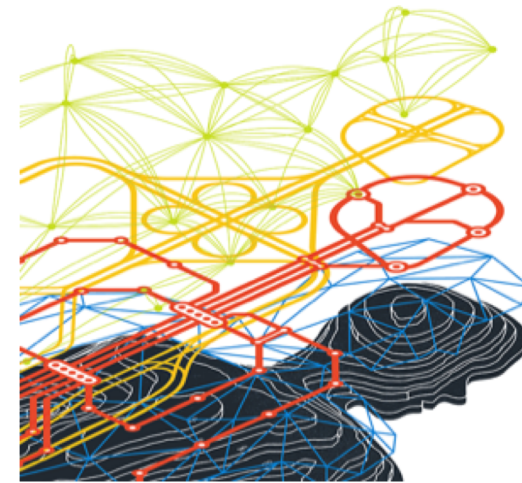
m.nieuwdorp@amc.uva.nl

In Brief

Kootte et al. show that fecal microbiota transplantation from lean donors to obese patients with metabolic syndrome improves insulin sensitivity, a transient effect associated with changes in microbiota composition and fasting plasma metabolites. Baseline fecal microbiota composition in recipients predicts the response to lean donor fecal microbiota transplantation.



MULTI-ETHNIC PROFILES / MULTI-OMICS



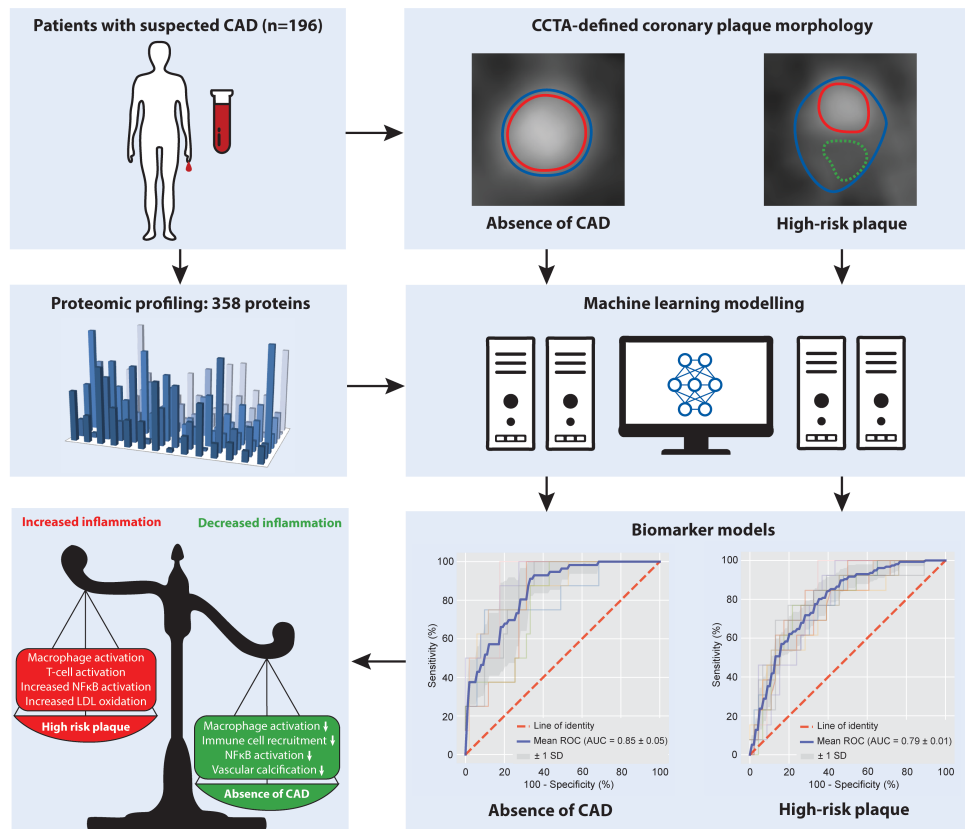
Samples are being analyzed on various platforms: sequencing – metagenome, 16s data, various measurements on relevant clinical parameters, etc.

OUR APPROACH: Identify predictive biomarkers and make a new predictive model for clinicians and patients (model suggests: best treatment strategy, response to treatment, best diet based on microbiome)

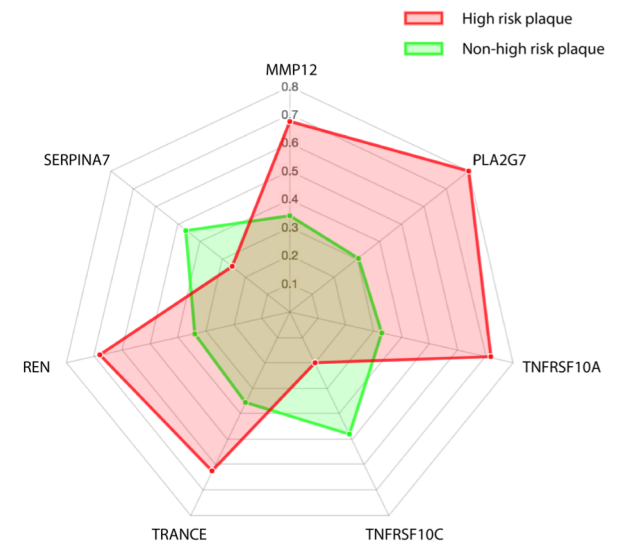
HIGH RISK PLAQUE PREDICTION



Michiel J. Bom, Evgeni Levin, et al
 Max Nieuwdorp, Albert Groen, Erik Stroes,
 Paul Knaapen



Standardized mean protein levels



SUMMARY

AI is becoming essential for biomarker discovery and predictive modeling in cardiometabolic domain

We develop cutting edge AI methodologies for multi-omics analysis: allowing us to gain new, relevant biomedical insights and support clinicians in decision making

Artificial intelligence



Omics Data

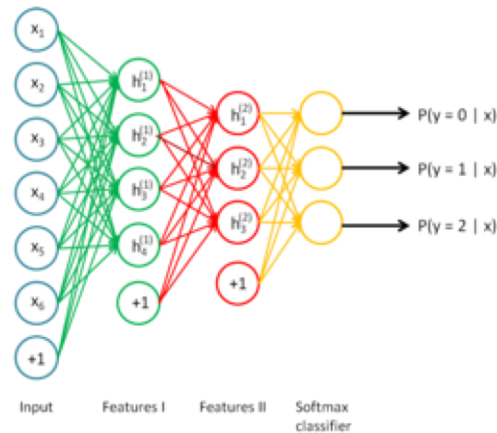


Personalized therapy



OUR AI METHODOLOGY

$$\begin{aligned}
 K_{\cdot,R} A_R &= \\
 K_{\cdot,R} (K_{\cdot,R}^t K_{\cdot,R} + \lambda K_{R,R})^{-1} K_{\cdot,R}^t Y &= \\
 K_{\cdot,R} \left(\frac{1}{\lambda} K_{R,R}^{-1} - \frac{1}{\lambda} K_{R,R}^{-1} K_{\cdot,R}^t \left(\frac{1}{\lambda} K_{\cdot,R} K_{R,R}^{-1} K_{\cdot,R}^t + I \right)^{-1} \right. \\
 \left. \frac{1}{\lambda} K_{\cdot,R} K_{R,R}^{-1} \right) K_{\cdot,R}^t Y &= \\
 (\hat{K} - \hat{K} (\hat{K} + I)^{-1} \hat{K}) Y &= \\
 (\hat{K} (I - (\hat{K} + I)^{-1} \hat{K}) Y &= \\
 (\hat{K} ((\hat{K} + I)^{-1} (\hat{K} + I) - (\hat{K} + I)^{-1} \hat{K}) Y &= \\
 \hat{K} (\hat{K} + I)^{-1} (\hat{K} + I - \hat{K}) Y &= \\
 \hat{K} (\hat{K} + I)^{-1} Y. &
 \end{aligned}$$



Models can handle large-scale, heterogeneous, high-dimensional multi-omics data

Standard methodology does not lead to reliable solutions

Predictive models at the individual level