New Application: Locate your risk!

What are genome-wide polygenic risk scores (PRS)?

Many common disorders are characterized by a complex genetic component. The combined effects of many sequence variants contribute substantially to the risk of disease.

In a research setting, the inherited predisposition has already been analyzed in large case-control-studies for many phenotypes by means of polygenic risk modelling. Due to the low costs of genotyping, the resulting scores would be ideally suited for risk stratification on a population-wide scale. Indeed, most scientists do not ask themselves if but when the predictive value of genome-wide polygenic risk scores (PRS) will be robust enough to be used in personalized medicine. However, it is still unclear how a meaningful application of PRS in the clinic could look like.

We believe, that you - as a clinician scientist - will be able to develop innovative concepts, by gaining experience in PRS yourself. For that reason, we developed a platform that enables you to compute a growing number of PRS that are available from the literature.

"Locate your risk" is a new framework by GeneTalk that offers geneticists an easy way to integrate different polygenic risk scores from recent publications into their research. See details on the workflow on the back side.

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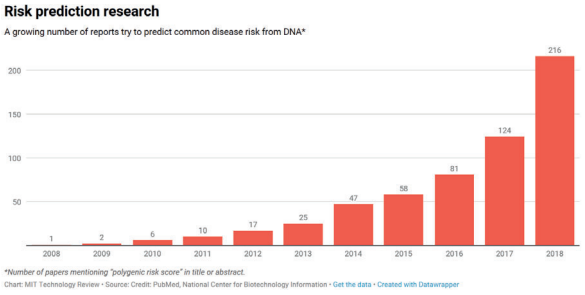
Bioinformatics of PRS and more

Starting from SNP data, it is possible to evaluate the genetic risk load for a specific trait by considering the additive cumulative effect of many common variants. The derived value, named polygenic risk score (PRS), can be compared with the scores obtained in a reference population. The quantile a given sample is located in can be used to stratify the genetic predisposition for a certain disorder as e.g. low, medium, or high.

The PRS is additional information that could also be used in combination with phenotypic features for risk assessment. For many disorders such as cardiovascular disease, diabetes mellitus, inflammatory bowel disease, breast cancer or atrial fibrillations "calculators" or "classifiers" are already available that evaluate the personal risk based on BMI, ECG, etc. The integration of PRS as a prior into these models is straightforward from a statistical point of view and might increase the accuracy of the predictions.

How does *Locate your risk* work?

A Choose a suitable PRS model for your research from hundreds of papers that are already available in the literature and we will take care of the implementation.
An example for a PRS on coronary artery disease (CAD) from Khera et al. can be found on www.prs.gene-talk.de.

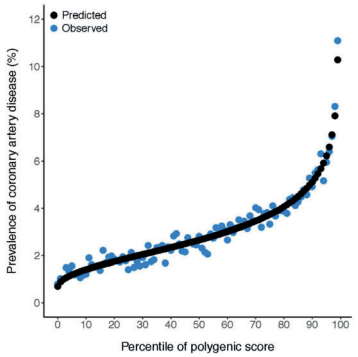


B You need to provide us with the SNPs, ideally from a chip such as the Global Screening Array (GSA) from Illumina. If you don't have the genotyping data already, Life&Brain will make you a good offer. ☺

In the demo account www.prs.gene-talk.de you could also work with your personal data from 23andMe®. You will find instructions on how to get your raw data here:
https://customercare.23andme.com/hc/en-us/articles/212196868-Accessing-and-Downloading-Your-Raw-Data.

C For each sample we will compute the PRS of your choice, assess the ethnicity and locate the risk in a suitable background population. The PRS could also be added to an existing risk calculator. Please see www.cvriskcalculator..com for some inspiration.

We are curious to learn about your ideas. Please tell us: info@gene-talk.de.



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