Bioada

POLYGENIC SCORE AND BIOMARKERS DISCOVERY MADE EASY!

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What is Bioada?

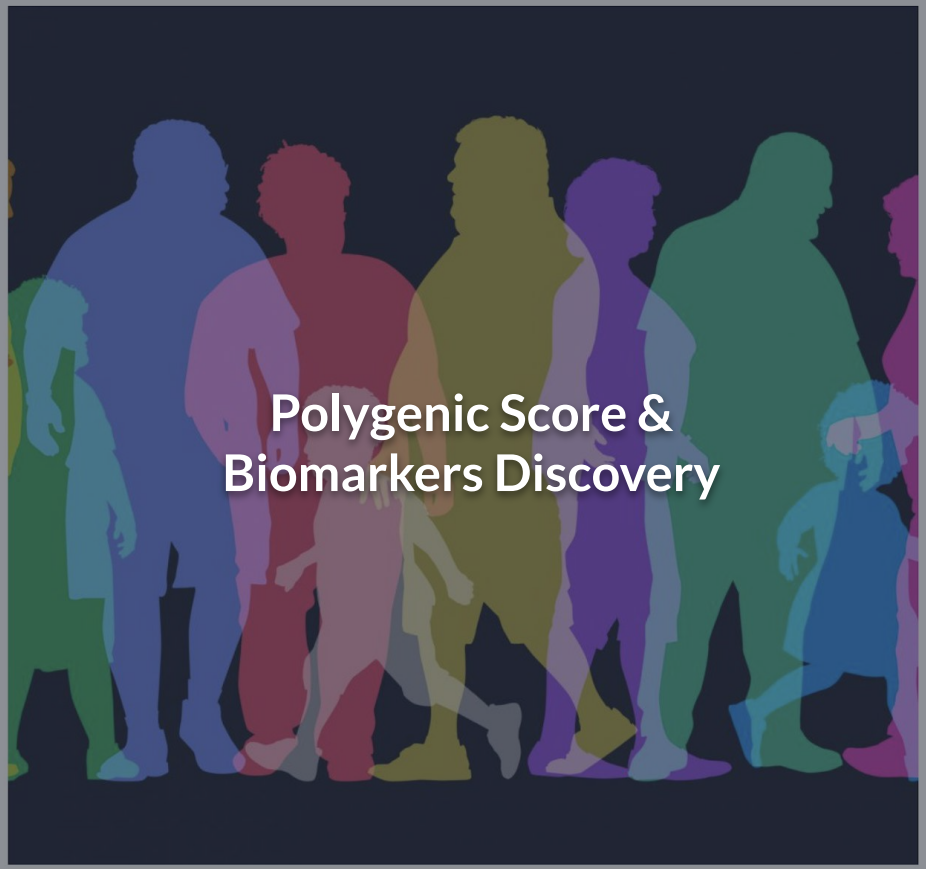
The Ultimate End-to-End Machine Learning Platform For Polygenic Score And Biomarkers Discovery

Understanding the problem

The scientific community is continuously trying to improve their understanding of genetic mechanisms in biological systems. With growing accessibility, still, only the minority of investigators in the life and medical sciences has the means to analyze and leverage this enormous treasure of data.

Bioada is an integrated, easy to use and interactive genomics data analysis platform for the broader community of life scientists.

Bioada Platform


Polygenic Score &
Biomarkers Discovery


SmartArray


Xarang


BIG
DATA
HappyReader

Bioada SmartArray

Database Management System

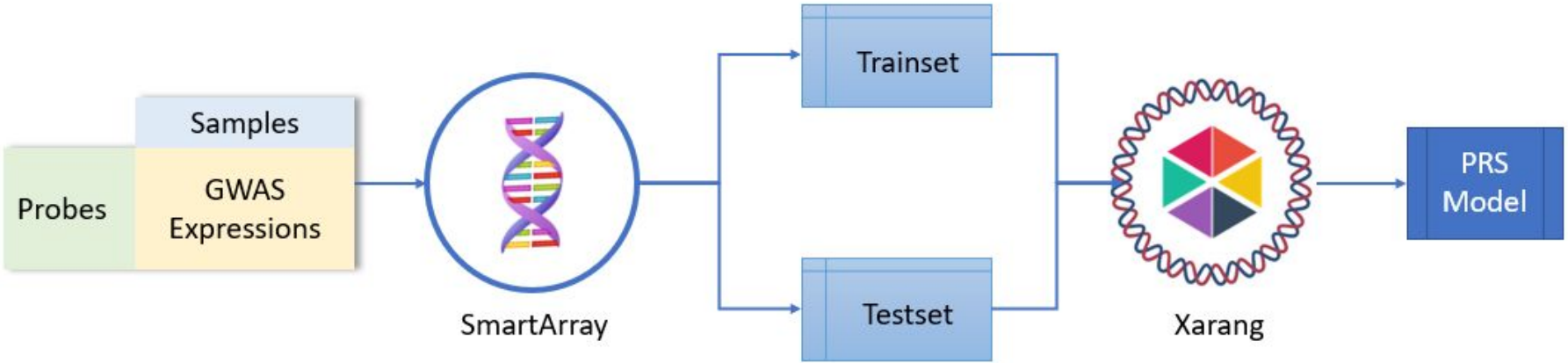
Interactive Visualization, Statistical Analysis and Enrichment

SmartArray - Database Management System

- Genomic data in database not flat files
- Data Integrity & Consistency
- Reduced Data Redundancy
- Robust Data Security & Recovery
- Significant improvement in productivity

SmartArray - Interactive Visualization & Statistical Analysis

- Univariate & Bivariate charts
- Volcano, Manhattan & t-SNE plots
- Descriptive & Inferential Statistical tests
- Correlation & Simulation analysis
- Pathway & Gene Ontology enrichment


Samples
Probes
GWAS
Expressions
SmartArray
Trainset
Testset
Xarang
PRS
Model

Bioada Xarang

- Data access (local disk, database or cloud)
- Classification and regression models
- Automated variable selection
- Extensive model evaluation
- One-click model deployment
- Federated Machine Learning

Bioada HappyReader

- **Quickly open** any delimited file; GBs in size!
- **Replace all** of one text with another.
- **Reorder** a selected subset of columns.
- **Extract** data using rows/columns **filters**.
- **Convert** files from one delimiter to another.
- **Clean** up a file by removing bad rows.
- **Append** multiple delimited files **by rows or columns**.
- **Split** any delimited file into smaller subsets.
- Perform univariate and bivariate **analysis**.

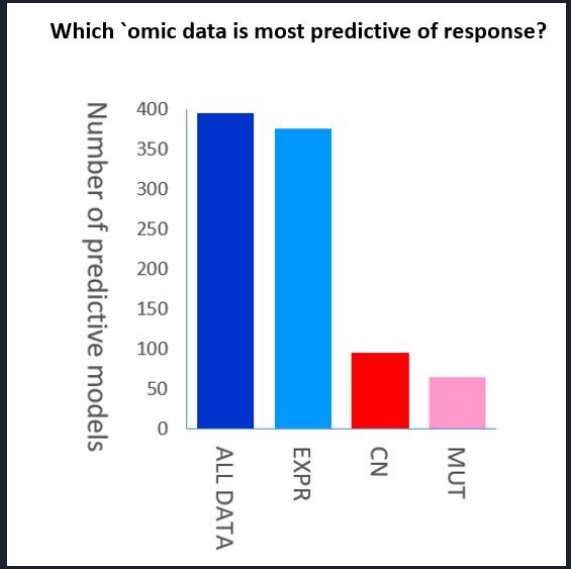
How is Bioada providing a better mousetrap?

Genome Wide Analysis

Traditionally, PRS models are built using the Genome-Wide Association Study (GWAS) of Mutations (MUT or SNP) or Copy Number Variations (CNV or CN). However, it has been shown that the gene expression data (EXPR) has much more predictability power compared to gene copy number (CN) or gene mutation (MU) data.

Bioada platform can analyse the following genomic data:

1. SNP (GWAS)
2. Copy Number
3. Gene Expression (RNA-seq and Microarray)

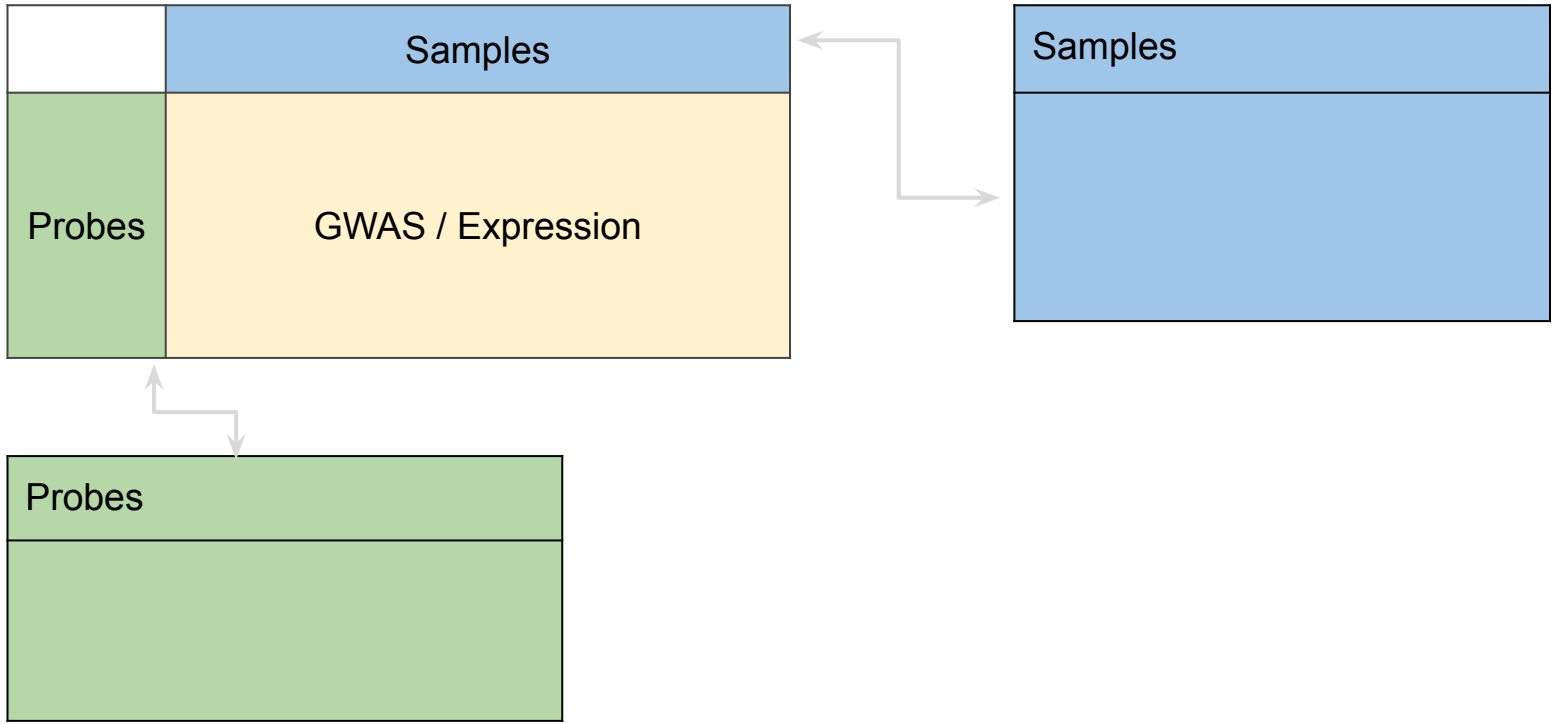


Bioada - 6 step methodology to build PRS model

Step 1 - Problem Definition

- To predict Pancreatic Cancer from Gene Expression Data.
- To predict Gastric Cancer from Genome Wide Association Studies data.

2. Data Preparation



DEMO

Thank You!

Learn more at
www.bioada.com

Q&A