

# Laboratory of Biometry

**Leader: Prof. Paweł Krajewski**

## **Staff:**

**Prof. Zygmunt Kaczmarek**  
**Dr Grzegorz Koczyk**  
**Dr Aneta Sawikowska**  
**Pedro Madrigal Bayonas, M.Sc.**  
**Hanna Ćwiek, M.Sc.**  
**Wojciech Frohmberg, M.Sc.**  
**Joanna Stasiak, M.Sc.**  
**Bernadeta Borucka**

## **Research topics:**

The Laboratory of Biometry conducts research in the area of statistical and informatic methods applicable in the analysis of results of biological experiments, with the special stress on genetic and genomic research and on plant breeding. The most important statistical methodologies which are used are: linear mixed models, semiparametric models and multivariate methods. Among bioinformatic methods are: biological database exploration, profile sequence analysis, analysis of biomolecule interactions, homology and *ab initio* modelling of biomolecule structure. The results are applied in: planning and analysis of genetic and breeding field trials and laboratory experiments, statistical analysis of genotype x environment interactions, gene expression analysis, analysis of DNA sequencing data and protein structure as well as phylogeny reconstruction. The group cooperates with numerous research and breeding units. At present the research program is focused on:

- Statistical methods in gene expression analysis and in analysis of protein-DNA interactions, in cooperation with [Research Institute of Integrative & Comparative Biology](#), Faculty of Biological Sciences, Leeds University i and other partners in the projects Marie Curie RTN Sysflo and COST Action TD0801 [StatSeq](#),
- Methods of integrative analysis of results of genetic experiments in the projects: [POLAPGEN-BD](#) and transplant,
- Development of algorithms for the analysis of breeding and varietal experiments, in cooperation with the Department of Mathematical and Statistical Methods, Poznań University of Life Sciences, Polish breeding companies, the Research Centre for Cultivar Testing and other partners, and implementation of these algorithms in the programs [SERGEN](#) and [EKSPAN](#),
- Theoretical and methodological studies aimed at the simplification of presently applied methods of analysis for the inheritance of measurable characters by substitution of segregating generations with populations of homozygous lines, in cooperation with the Department of Quantitative Genetics, IPG PAS, and the Department of Mathematical and Statistical Methods, AU Poznań,
- Analysis of coevolution of protein structure and function, in cooperation with Computational Biology Unit, University of Bergen, Norway.

## **Main research achievements:**

- Development of statistical and bioinformatic methods for analysis of data obtained by using chromatin immunoprecipitation and high-throughput DNA sequencing (ChIP-Seq).
- Development of methods to utilize doubled haploid lines in the assessment of genetic parameters, detection of non-allelic interaction and linkage of genes controlling quantitative traits, and a proposal of a general formula for the calculation of the number of genes (effective factors) in case of the occurrence of a non-allelic interaction.
- Development of an algorithm and computational software [LINKGEN](#) facilitating the detection of genes and non-allelic interactions on the basis of DH lines and SSD.
- Theoretical and numerical comparisons of methods to assess additive gene effects on the basis of phenotypic observations and on the basis of molecular markers.
- Development of methods to localize genes controlling quantitative characters, taking into consideration environmental interaction and nonallelic interaction in one- and multidimensional

models.

– Development of methods to utilise protein structural data in establishing functional annotation and designing cross-species specific molecular markers for homologous genes.