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KeyGene – the crop innovation company

KeyGene is the go-to AgBiotech company for higher crop yield & quality. With our intellectual capital, solution driven approach and collaborative spirit, we work for the future of global agriculture with partners in the AgriFood sector. With our proprietary technologies and non-GM approaches, we support our customers with the development of new, improved crops. Our goal is to help organizations with their toughest R&D challenges, combining our cutting edge breeding technologies, bioinformatics & data science expertise and plant-based trait platforms. At KeyGene, we work in an international environment with more than 140 professionals from all over the world. Our company is based in Wageningen, Netherlands and Rockville, MD, USA. www.keygene.com

The Breeding Solutions team is looking for talented students in some of the current areas of research:

INTERN Crop Molecular Breeding

New approaches to Genomic Prediction in Crop Breeding

Driven by the development of high-throughput genotyping methods, genomic selection is quickly developing itself into an important breeding strategy for many crops thanks to its ability to speed up the development and release of new varieties. The key component of a genomic selection program is the genomic prediction method, a statistical method to predict the performance of individuals based on genome-wide variation data, which is used to select the best ranking individuals according to the model. An accurate genomic prediction method is of utmost importance for genomic selection, as otherwise wrong individuals are selected.

Conventional genomic prediction methods can be inaccurate though, ultimately leading to an ineffective genomic selection program. To make genomic selection more widely applicable KeyGene is currently developing new improved methodologies for genomic prediction, using contemporary machine learning methods that make use of all data as efficiently as possible.

The research carried out by the selected candidate will contribute to the development of new predictive methods to make best use of SNP marker, phenotype and pedigree information to accurately estimate the genotype-phenotype relationship in complex traits.

The Grand Selection

Selecting the best plants from large populations is a fundamental step in plant breeding practice. The selection process to obtain the best genotype typically spans multiple rounds of selection in successive plant populations. This combination of iteration and the stochastic element of Mendelian allele segregation makes the result of even a relative simple selection process surprisingly difficult to predict. For a plant breeder, it would be of great benefit, if an optimal selection process could be determined in advance, as growing and selecting large populations of plants is costly. In the context of a challenging research program in collaboration with several breeding companies, KeyGene is developing and testing algorithms to predict optimized breeding strategies.

The selected student will focus on the further development of algorithms based on stochastic optimization, dynamic programming or genetic algorithms.

Breeding support simulation platform

ProSpect is a decision support system developed by *KeyGene* to help breeders explore and optimize their breeding strategies by simulation with user-defined biological and economic constraints. *ProSpect* is an R package that provides a proper environment to simulate populations, traits and breeding strategies and advanced tools to compare alternative strategies. The platform allows users to flexibly create their own strategies through the integration of phenotype information, molecular markers, pedigree structure, and different trait architectures. Users can subsequently choose to perform phenotype selection, pedigree-based evaluation, marker assisted selection, genomic selection or combinations of these. Strategies can be evaluated and compared based on genetic progress towards a trait or breeding goal and cumulative costs.

The selected student will focus on the platform improvement, especially with regards to data simulation, computational time and ease of use of the platform.



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Genetic analyses in polyploid species

Great advances have been made in breeding of diploid species by making use of the many genetic analysis tools/methods currently available for these species. Genetic mapping, QTL mapping, GWAS analyses and genomic prediction are widely available for diploid species, but have been lagging behind for more complex polyploid species. Additionally, there is a challenge for genetic analysis, namely genotyping, which is at the basis of all aforementioned analyses. While for diploid species simple SNP scoring can be applied, for polyploid species we have to think about accurate dosage for multiple alleles and how to make best use of this information.

The selected student will focus on assessing publicly available tools to perform such genetic analysis and will contribute to the development of new tools with special regards to genetic mapping and QTL analysis (population and family based).

Genetic analysis in multi-parental populations

Bi-parental crosses have been extremely helpful in plant breeding for QTL detection and markers development for indirect selection. One of the drawbacks while working with bi-parental populations is the limited genetic variation generated by the two parents drawn from the population of interest. This limitation can be reduced by making more complex crosses (involving more parents) in which the same type of analyses can be performed as for the bi-parental cases. For example, in Multi-parent Advanced Generation Inter-Cross populations (**MAGIC**) several parental lines can be used to generate a single segregating population. However, tools and methods needed for analyses are less well explored and not as readily available as for the bi-parental cases.

The selected candidate will explore and test tools available in the public domain for analyses of multi-parental crosses and will contribute to the current internal effort in developing new methods for multi-parent genetic analysis.

The research will be carried as an internship at KeyGene's Wageningen facilities. For more information contact Nicola Bacciu (nicola.bacciu@keygene.com).

