UNIVERSITY of FLORIDA

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April 22th, 2021

Bayer Crop Science
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To whom it may concern,

I am writing to apply for the position of Quantitative Geneticist II (Job Number 383788) in Bayer. I am currently a Ph.D. candidate in Horticultural Sciences at the University of Florida focusing on quantitative genetics, and I am also pursuing a PhD. minor in Statistics. The objective of my present research is to build and evaluate quantitative genetics tools to enhance molecular breeding and data-driven decisions. Before coming to UF, I earned an M.Sc. degree in Plant Genetics and Breeding from the University of Sao Paulo, where I worked on different Quantitative Genetics topics as relationship coefficient estimation, genetic data simulation, and software development. My areas of expertise are genomic prediction & selection, Bayesian data analysis, QTL mapping, population structure analysis, and mating optimization. Furthermore, I have developed specific software to assist gene discovery and breeding decisions. I am very excited for the opportunity to work as a quantitative geneticist in Bayer. I believe I am a strong candidate for this position because of my quantitative genetics knowledge, research and communication skills, demonstrable capacity to complete projects, and ability to collaborate widely are valuable assets that will contribute to Bayer's innovation in agriculture.

With the recent drop in genotyping price, the use of DNA information to guide breeding programs is now a reality; however, there is a lack of adapted and user-friendly tools to assist breeders to do precise selections and gene discovery. In 2016, I released the AGHmatrix software, an R package that builds genomic relationship matrices using different methods and information sources. These matrices are essential for breeding values prediction, GWAS analysis, and breeding population parameters estimation (e.g., inbreeding). This software has a global impact and is used by the industry and in academia with more than 60 citations. Nowadays, the software is used in breeding companies such as CTC, the most prominent private Brazilian sugarcane breeder, and by VSNi (ASReml). AGHmatrix has been applied in a variety of species, from traditional crops (as wheat and maize) to specialty crops (forages and blueberry) and animals (pigs and cattle). Over my career, I have developed software that helped in the breeder's decision-making process and improved our capacity to understand the molecular mechanisms of essential traits in standard and complex backgrounds (e.g., autotetraploids). Currently, I have three software (diaQTL, PedigreeSimR, fullsibQTL) under review in the journals Genetics and Journal of Heredity, and I am collaborating in a fourth (PolyOrigin) also under review in the journal Genetics. My ability to translate real quantitative genetics problems faced by geneticists and breeders into user-friendly software and accessible reports has had a tangible and broad impact, and I look forward to working with Bayer's Product Design team continue contributing in this area.

I have established fruitful collaborations in multi-disciplinary project that resulted in nine articles published in leading journals such as BMC Genomics, Frontiers, G3, Heredity, and GigaScience. I contributed to improving methodologies, performing statistical analyses, and enhancing the manuscript discussions. From

metabolomics in sugarcane to signatures of selection in sheep, my expertise and adaptable communication have allowed me to collaborate in a range of studies with different species and designs. I also led the publication of four manuscripts and six software in various topics as genomic selection, QTL mapping, and population genetics. My flexibility to work in multi-disciplinary teams will be a strength I will continue to pursue in this position.

I strongly believe that my work would contribute to the Bayer to shape the future of sustainable agriculture through quantitative genetics and breeding.

Sincerely,

Rodrigo Rampazo Amadeu