BERTRAND SERVIN

Statistical Geneticist / Data Scientist

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EXPERIENCE

Research Associate
Institut National de la Recherche Agronomique - Animal Genetics

📅 Sep 2006 – Ongoing   📍 Toulouse, France

Leader of the *Genome and Population Dynamics* group in the GenPhySE Lab.
- Development of statistical methods for genetic data analysis
- Analysis of large scale population genomics data

Postdoctoral Fellow
University of Washington - Department of Statistics

📅 Feb 2004 – Aug 2006   📍 Seattle, WA, USA

Development of statistical methods for genome-wide association studies using genotype imputation. Supervisor : Matthew Stephens

RESEARCH

Genetics of Adaptation
- Methods for the detection of local adaptation. Software `hapflk` (`http://forge-dga.jouy.inra.fr/projects/hapflk`)
- Analysis of large scale population genomics datasets in livestock

Genome Cartography
- Data integration for the improvement of whole genome assemblies
- Characterization of recombination rates in animal genomes

Genetics of Complex Traits
- Statistical methods for genome-wide association studies
- Genetic determinism of recombination
- Adaptation of honeybees to *Varroa destructor*

PRODUCTION

- 📖 46 publications
- 🔬 **h-index:** 23   **i10-index:** 37

SKILLS

Population Genetics

Quantitative Genetics   Statistics

Bioinformatics   Reproducible Research

C   python   numpy/scipy   R   Linux
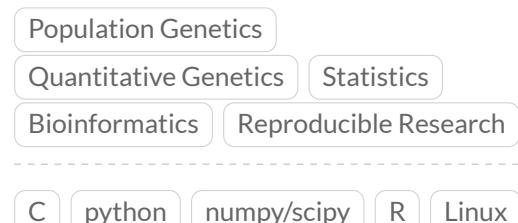
LANGUAGES

French   ●●●●●

English   ●●●●○

EDUCATION

Ph.D. in Genetics
Université Paris-Sud

📅 Dec 2000 – Dec 2003

Thesis title: Optimization of marker assisted gene pyramiding

M.Sc. in Agronomy
AgroParisTech

📅 Sept 1997 – Sep 2000

Specialization in Genetics and Plant Breeding

SELECTED PUBLICATIONS

- Bertolini, Francesca et al. (2018). "Signatures of selection and environmental adaptation across the goat genome post-domestication". In: *Genetics Selection Evolution* 50.1, p. 57.
- Rochus, Christina Marie et al. (2018). "Revealing the selection history of adaptive loci using genome-wide scans for selection: an example from domestic sheep". In: *BMC genomics* 19.1, p. 71.
- Petit, Morgane et al. (2017). "Variation in recombination rate and its genetic determinism in sheep populations". In: *Genetics* 207.2, pp. 767–784.
- Boitard, Simon et al. (2016). "Uncovering adaptation from sequence data: lessons from genome resequencing of four cattle breeds". In: *Genetics* 203.1, pp. 433–450.
- Du, Xiaoyong et al. (2014). "An update of the goat genome assembly using dense radiation hybrid maps allows detailed analysis of evolutionary rearrangements in Bovidae". In: *BMC genomics* 15.1, p. 625.
- Fariello, Maria-Ines et al. (2014). "Selection signatures in worldwide sheep populations". In: *PLoS One* 9.8, e103813.
- Fariello, Maria Inés et al. (2013). "Detecting signatures of selection through haplotype differentiation among hierarchically structured populations". In: *Genetics* 193.3, pp. 929–941.
- Servin, Bertrand, Thomas Faraut, et al. (2012). "High-resolution autosomal radiation hybrid maps of the pig genome and their contribution to the genome sequence assembly". In: *BMC genomics* 13.1, p. 585.
- Tortereau, Flavie et al. (2012). "A high density recombination map of the pig reveals a correlation between sex-specific recombination and GC content". In: *BMC genomics* 13.1, p. 586.
- Bonhomme, Maxime et al. (2010). "Detecting selection in population trees: the Lewontin and Krakauer test extended". In: *Genetics* 186.1, pp. 241–262.
- Servin, Bertrand, Simon de Givry, and Thomas Faraut (2010). "Statistical confidence measures for genome maps: application to the validation of genome assemblies". In: *Bioinformatics* 26.24, pp. 3035–3042.
- Servin, Bertrand and Matthew Stephens (2007). "Imputation-based analysis of association studies: candidate regions and quantitative traits". In: *PLoS genetics* 3.7, e114.
- Servin, Bertrand, Olivier C Martin, Marc Mézard, et al. (2004). "Toward a theory of marker-assisted gene pyramiding". In: *Genetics* 168.1, pp. 513–523.

SUPERVISION

PhD Students

Alice Danguy des Déserts
INRA, Clermont-Ferrand

📅 2019 – Ongoing

Recombination landscape in Bread Wheat

- -

Klavdija Poklukar
KIS, Slovenia

📅 2018 – Ongoing

Determinism of Pig fatty acid metabolism

- -

Cyriel Paris
INRA, Toulouse

📅 2016 – 2020

Estimation of selection parameters from time-series data

- -

Morgane Petit
INRA, Toulouse

📅 2014 – 2017

Genetics of recombination in Sheep

- -

Christina Rochus
SLU, Sweden

📅 2013 – 2017

Genetic diversity of domestic sheep

- -

Jason Lapeyronnie
INRA, Toulouse

📅 2014 – 2017

Statistical methods for the detection of local adaptation

- -

Maria-Ines Fariello
INRA, Toulouse

📅 2009 – 2013

Statistical methods for detecting selection signatures

- -

Postdoctoral Fellows

Sonia Eynard
INRA, Toulouse

📅 2017 – Ongoing

Genetics of honeybee resistance to *Varroa destructor*.