Amaury Vaysse

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PROFESSIONAL EXPERIENCES

Research engineer – omics data processing and statistical analysis (2020-)
Hub of bioinformatics and biostatistics, Institut Pasteur

Post-doc/Researcher in genetics of autism (2019)
Human Genetics and Cognitive Functions, Institut Pasteur

Post-doc/Researcher in statistical genetics (2018)
Statistical Genetics G5, Institut Pasteur

Post-doctoral fellow in genetic epidemiology of melanoma and asthma (2012-2017)
UMR-946, Inserm-Université Paris Diderot, Paris, (director: Florence Demenais)

PhD in Bioinformatics (Defended in 2011)
« Identification des signatures génétiques de la sélection chez le chien », under the supervision of Christophe Hitte. IGDR UMR-6061, CNRS-Université de Rennes 1, Rennes (France),

Developer (2006-2008)
Creation of a relational database with a web interface for the handling of biological samples

EDUCATION

PhD « Identification of genetic signatures of selection in dog » (2011)
Université de Rennes 1, Rennes (France)
Master - M2 Complementary skill in informatics (2005)
Institut de Formation Supérieure en Informatique et Communication, Rennes (France)
Master - M2 Biology and health (2004)
Université de Rennes 1, Rennes (France)

COMPLEMENTARY TRAINING

- Convolutional Neural Networks (deeplearning.ai on Coursera) Apr. 2018
- Structuring Machine Learning projects (deeplearning.ai on Coursera) Dec. 2017
- Improving deep neural networks (deeplearning.ai on Coursera) Nov. 2017
- Neural Networks and Deep Learning (deeplearning.ai on Coursera) Nov. 2017
- Workshop on Machine Learning for Personalized Medicine, Barcelona (Spain), 2016
- The 5th International Workshop on Genomic Epidemiology, Paris (France), 2013
- Atelier INSERM 222: Méthodes statistiques et nouvelles stratégies de recherche de gènes impliqués dans les maladies communes à l'ère du séquençage haut débit, Bordeaux (France), 2013
- The 3rd International Workshop on Genomic Epidemiology, Paris (France), 2009
- Workshop on data management and association analysis (BC|SNPmax), Uppsala (Sweden), 2008

SKILLS AND EXPERTISE

In-depth knowledge of methods and tools of statistical genetics

- Sequence data processing (GATK, smoove)
- Imputations of genetic data (Shapeit2, IMPUTE2)
- Single and multi-marker analyzes on individual data (PLINK, GEMMA, script to test gene-gene interactions, meta-analyzes, survival analyzes)
- Multi-marker (GCTA, VEGAS) and Pathways-based (GSEA, DAVID) analyses.
- Functional annotation (use of eQTL chromosome conformation data bases)

Computer skills

- General programming (mainly in Shell, Python and PERL languages, notions of Java, C ++)
- Statistical programming (R and STATA)

LANGUAGE

- English (read, write and speak fluently)
- French (native)

MAIN RESEARCH PROJECTS IN STATISTICAL GENETICS

Study of Autism

Search of genetic factors influencing autism in the non-coding part of the human genome. Development of strategy and pipeline including variant calling (SNV, CNV …), genome annotation and statistical analysis

Study of genetic mechanism using summary statistic from GWAS

Development of a strategy extending the Mendelian randomization approach to classify genetic variants according to their effect on correlated phenotypes. Application on Body Mass Index and Waist-to-Hip Ratio.

Genetic study of melanoma in human

Development of a multi-marker strategy combining pathways analysis on summary statistics from pan-genomic association studies (GWAS) and tests of the interactions effects between DNA markers to identify sets of genes that jointly influence the trait: Application to the risk of melanoma (6,803 subjects in two studies) and to the Breslow index, a prognosis factor (2,506 subjects in two studies)

Cross-species comparative genomic study of melanoma

Development of an inter-species comparative genomic strategy (human-pig-dog) to identify new genes for susceptibility to melanoma in humans (project funded by INCa).

- GWAS adapted to related populations (mixed model), meta-analyzes..
- Comparative mapping to define orthologous regions and compare the results between species.

Contribution to other multifactorial disease study projects

- Identification of rare mutations of a new gene (POT1) associated with the risk of familial melanoma (Nature Genetics, 2017, in collaboration with an American team at NCI).
- Pathway analysis to contribute to the discovery of the association between the gene RAB27A and the exhaled nitric oxide fraction in families of asthmatics.
- Integration of interaction analyzes among genes selected by text mining in a study that identified an interaction between two genes involved in allergy using data from 3,244 subjects.
- Functional annotation of the results of the Trans-National Asthma Genetic Consortium (meta-analysis of 66 GWAS of asthma totaling 142,486 subjects) using public results from SNPs-gene expression (eQTL) assays and chromosome conformation (HiC).

Development and dissemination of pipelines and procedures to

- Detect genomic regions with differences in allele frequencies of markers between populations
- Implement pathway and gene interaction methods
- Implement pan-genomic analysis methods adapted to canine populations
- Establish orthologous regions between two the human and dog genomes and produce the integrated graphical representation of the results of pan-genomic association studies for both species.

SCIENTIFIC PRODUCTION

Publications in peer-reviewed international journals

1. Ziyatdinov A., Parker MM., **Vaysse A**, *et al.* Mixed-model admixture mapping identifies smoking-dependent loci of lung function in African Americans. 2019. *Eur J Hum Genet*. (doi:10.1038/s41431-019-0545-8)
2. Gallois A., Mefford J., Ko A., **Vaysse A**. *et al* A comprehensive study of metabolite genetics reveals strong pleiotropy and heterogeneity across time and context. 2019*, Nature Communications; 10(1):4788*
3. Bourneuf E, Estellé J, Blin A, *et al.* Mapping of susceptibility loci for cutaneous melanoma occurrence and progression using a porcine model. 2018*, Oncotarget. 9(45):27682-27697.*
4. Demenais F, Margaritte-Jeannin P, Barnes KC, Cookson W *et al.* Multi-ancestry genome-wide association study identifies new asthma susceptibility loci that co-localize with immune cell enhancer histone marks. 2017, *Nat Genet. 2018;50(1):42-53*
5. Sugier P-E, Brossard M, Sarnowski C, **Vaysse A**, *et al.* A novel role for cilia function in atopy: ADGRV1 and DNAH5 interactions. 2017, JACI, *doi:10.106/j.jaci.2017.06.050*
6. Liu Y*, Brossard M* (co-1er auteurs), Sarnowski C, **Vaysse A**, *et al.* Network-assisted analysis of GWAS data identifies a functionally-relevant gene module for childhood-onset asthma. *Sci Rep. 2017;7(1):938.*
7. Fang S*, **Vaysse A*** (co-1er auteurs), Brossard M, *et al*. Novel melanoma expression genes identified through genome-wide association study of Breslow tumor thickness. *J Invest Dermatol. 2016 doi: 10.1016/j.jid.2016.07.032.*

8. **Vaysse A***, Fang S*, Brossard M* *et al.* A comprehensive genome-wide analysis of melanoma Breslow thickness identifies interaction between *CDC42* and *SCIN* genetic variants. *Int J Cancer. 2016. 139(9):2012-20.*
9. Brossard M*, Fang S* (co-1er auteurs), **Vaysse A** *et al.* Integrated pathway and epistasis analysis reveals interactive effect of genetic variants at *TERF1* and *AFAP1L2* loci on melanoma risk. *Int J Cancer, 2015, 137(8):1901-9.*
10. Plassais J, Guaguère E, Lagoutte L *et al.* A spontaneous KRT16 mutation in a dog breed: a model for human focal non-epidermolytic palmoplantar keratoderma (FNEPPK). *J Invest Dermatol. 2015; 135(4):1187-90.*
11. Bouzigon E, Nadif R, Thompson E *et al.* A common variant in RAB27A is associated with fractional exhaled nitric oxide levels in adults. *Clin Exp Allergy, 2015, 45(4):797-806.*
12. Shi J, Yang XR, Ballew B, *et al.* Germline POT1 mutations predispose to familial cutaneous malignant melanoma. *Nat Genet. 2014; 46(5):482-6.*
13. Derrien T, **Vaysse A**, André C, Hitte C. Annotation of the domestic dog genome sequence: finding the missing genes. *Mamm Genome. 2012, 23(1):124-131.*
14. **Vaysse A***, Ratnakumar A*, Derrien T, *et al.* Identification of loci governing common and rare phenotypic traits in dog breeds using selection mapping. *PLoS Genet. 2011; 7(10):e1002316.*
15. Rimbault M, Robin S, **Vaysse A**, Galibert F. RNA profiles of rat olfactory epithelia: individual and age related variations. *BMC Genomics. 2009;10:572.*
16. Abadie J, Hédan B, Cadieu E, *et al*. Epidemiology, pathology, and genetics of histiocytic sarcoma in the Bernese mountain dog breed. *J Hered. 2009;100 Suppl 1:S19-27.*
17. Derrien T, Thézé J, **Vaysse A**, *et al*. Revisiting the missing protein-coding gene catalog of the domestic dog. *BMC Genomics, 2009 Feb, 10:62*.
18. Robin S, Tacher S, Rimbault M, **Vaysse A**, *et al*. Genetic diversity of canine olfactory receptors. *BMC Genomics, 2009 10(1):21*.
19. Hubert JF, Duchesne L, Delamarche C, **Vaysse A**, *et al.* Pore selectivity analysis of an aquaglyceroporin by stopped-flow spectrophotometry on bacterial cell suspensions. *Biol Cell, 2005 97(9):675-86.*

Publications and Communications in national and internationals congresses

1. Aschard H, **Vaysse A**, Bzili A. Identifying disease subtypes from genotype data. *American Society of Human Genetics*, Oct. 2018, San Diego(USA) – *Abs. published online*
2. Brossard M, Liu Y, **Vaysse A**, *et al*. The SigMod network analysis method identifies gene modules for cutaneous melanoma and nevus count that share relevant candidates. *International Genetic Epidemiology Society* (IGES), Sept. 2017, Cambridge (UK).
3. Brossard M, **Vaysse A**, Mohamdi H, *et al*. Genetic analysis of the telomere interactome pinpoints new candidate genes for melanoma risk *International Genetic Epidemiology Society*, 2016, Toronto (Canada).
4. **Vaysse A**, Fang S, Brossard M, *et al*. A comprehensive genome-wide analysis of melanoma Breslow thickness identifies interaction between *CDC42* and *SCIN* genes. 49th annual meeting of the *European Society of Human Genetics* (ESHG), May. 2016, Barcelone (Spain). *Abs. published online.*
5. Liu Y, Brossard M, Sarnowski C, *et al*. Network-based analysis of genome-wide association data identifies a gene sub-network underlying childhood onset asthma. *American Society of Human Genetics*, Oct. 2015, Baltimore (USA) – *Abs. published online*
6. Sugier PE, Brossard M, **Vaysse A**, *et al*. Combining text mining and epistasis analyses identifies new atopy genes. *American Society of Human Genetics* (ASHG), Oct. 2015, Baltimore (USA) - *Abs. published online*
7. Liu Y, Brossard M, Margaritte-Jeannin P, *et al*. Network-Assisted Investigation of Signals from Genome-Wide Association Studies in Childhood-onset Asthma. *Capita Selecta on Complex Disease Analysis* (CSCDA), Nov. 2014, Liège (Belgium). *Abs. published online*
8. Sugier P-E, **Vaysse A**, Sarnowski C, *et al*. Integration of gene-based and text mining analyses to discover genes underlying atopy. *Capita Selecta in Complex Disease Analysis* (CSCDA), Nov. 2014, Liège (Belgium). *Abs. published online.*
9. **Vaysse A**, Fang S, Brossard M, *et al*. Combined pathway and gene-gene interaction analysis pinpoints biologically relevant genes for a major melanoma prognosis factor. 64th annual meeting of the *American Society of Human Genetics* (ASHG), Oct. 2014, San Diego (USA). *Abs. published online*
10. Brossard M, Fang S, **Vaysse A**, *et al*. Integrated pathway and gene-gene interaction analysis reveals novel candidate genes for melanoma. 64th annual meeting of the *American Society of Human Genetics* (ASHG), Oct. 2014, San Diego (USA). *Abs. published online.*

11. **Vaysse A**, Fang S, Brossard M, *et al.* Integration of pathway and gene-gene interaction analyses reveal biologically relevant genes for Breslow thickness, a major predictor of melanoma prognosis. *International Genetic Epidemiology Society* (IGES), Août 2014, Vienna (Austria). *Abs. published online.*

12. Brossard M, Fang S, **Vaysse A** *et al.* Pathway and gene-gene interaction analysis reveals new candidate genes for melanoma, *International Genetic Epidemiology Society* (IGES), Août 2014, Vienna (Austria). *Abs. published online.*

13. Brossard M, **Vaysse A**, Corda E, *et al.* Comparison of permutations strategies to assess gene-set significance in gene-set-enrichment analysis, *International Genetic Epidemiology Society* (IGES), Sept. 2013, Chicago (USA). *Abs. published online*

14. Sugier PE, **Vaysse A**, Loucoubar C *et al.* Identification of common and specific genetic determinants to skin prick test reactivity using genome-wide association study and gene-based test approaches. 62nd annual meeting of the *American Society of Human Genetics* (ASHG), Nov. 2012, San Francisco (USA). *Abs. published online.*

15. Loucoubar C, Brossard M, Sugier PE, **Vaysse A**, *et al.* Performances of single-SNP and pathway-based analyses of genome-wide data to detect genetic factors shared by eosinophil and basophil counts in asthma ascertained families. 62nd *Annual Meeting of the American Society of Human Genetics* (ASHG), 6-10 Nov. 2012, San Francisco (USA**).** *Abs. published online*

16. Brossard M, **Vaysse A**, Corda E, *et al.* Pathway-based analysis of genome-wide SNP data reveals new candidate genes for susceptibility to melanoma. 62nd Annual Meeting of the *American Society of Human Genetics* (ASHG), Nov. 2012, San Francisco (USA). *Abs. published online.*

17. Jean-Baptiste-Adolphe H., Emily M, **Vaysse A**, André C, Hitte C. Haplotype-based method for detecting regions under selection in the domestic dog. Journées Ouvertes en Biologie, Informatique et Mathématiques(JOBIM), Juil. 2012, Rennes (France).

18. Derrien T, **Vaysse A**, Hennuy B, *et al.* Computational detection and expression profiling of conserved long non-coding RNAs in the domestic dog. Journées Ouvertes en Biologie, Informatique et Mathématiques(JOBIM), Juil. 2012, Rennes (France).

19. Hitte C, Ratnakumar A, **Vaysse A**, *et al.* Identification of loci governing phenotypic traits in dog breeds highlights disease genes of relevance to human health. *European Human Genetics Conference*, May 2011, Amsterdam (the Netherlands). *Abs. published online*

20. Webster MT, **Vaysse A**, Ratnakumar A, *et al.* Identification of common and rare selective sweeps in 36 dog breeds. *The 5th Advances in Feline and Canine Genomics,* Sept. 2010, Baltimore (USA).

21. Hitte C, Ratnakumar A, **Vaysse A**, *et al.* Functional impact of artificial selection in the domestic dog. *The 5th Advances in Feline and Canine Genomics*, Sept. 2010, Baltimore (USA).

22. Grall A, **Vaysse A**, Escriou C, *et al.* Recherche des bases génétiques d'une épilepsie canine : un modèle pour les épilepsies humaines. 5èmes *Assises de Génétique Humaine et Médicale*, Jan. 2010, Strasbourg (France). *Abs. published online.*

23. **Vaysse A**, Ratnakumar A, Derrien T, *et al.* Differentiation of allelic frequencies analysis identifies short genomic regions with signatures of artificial selection between canine breeds. Journées Ouvertes en Biologie, Informatique et Mathématiques(JOBIM), Sept. 2010, Montpellier (France).

24. **Vaysse A**, Galibert F, André C, Hitte C. Comparative patterns of positive selection between human and five mammalian genomes. 5èmes *Assises de Génétique Humaine et Médicale*, Jan. 2010, Strasbourg (France). *Abs. published online*

25. **Vaysse A**, Derrien T, André C, Galibert F, Hitte C. Lineage-specific pseudogenes identification through selective constraints analysis in the canine genome. Journées Ouvertes en Biologie, Informatique et Mathématiques(JOBIM), Juin 2009, Nantes (France).

26. André C, Chaudieu G, Herbin L, **Vaysse A**, *et al.* CaniDNA : a French initiative for the collection and distribution of dog DNA samples and distribution of dog DNA samples. *4th International Conference: Advances in canine and feline genomics and inherited diseases*, May 2008, St Malo (France).

OTHER ACTIVITIES

Advisory and expertise activity:

- Advisory activity for the development and computerized management of the Canine Biological Resource Center for the "Dog Genetics" group (IGDR-UMR6290, Rennes, France)
- Reviewer for PLoS One and BMC vet
- Grant reviewer for the « Netherlands Organisation for Scientific Research » (NWO)

Popularisation of science:

During October 2018 & 2019, I participated to the “fêtes de la science” with the association JeBiF. We went to the “cite des sciences” and to l'université Pierre-et-Marie-Curie to explain several aspects of the bioinformatics field through games tailored for people above 5-7 years old
I participate this year to the conception of the

Formal nationals and internationals collaborations:

- **Cooperative group MELARISK for the study of melanoma un human:** UMR-946 (INSERM/université Paris Diderot), CHU Cochin, Institut Gustave Roussy and national network of et le réseau national de dermatologists et d’onco-geneticists.
- **Comparative genomic of melanoma in three species (human/pig/dog) :** UMR-946, UMR-6290 (CNRS/Université de Rennes 1), UMR-1314 (INRA/CEA).
- **Study of the selection in the dog genome:** Institut of biology from the “école normale supérieure”, Paris.
- **Exome sequencing for familial melanoma:** National Cancer Institute, Rockville; McGill University, Montréal.
- **Genetics of melanoma and Breslow thickness based on pathway analysis** : MD Anderson Cancer Center, Texas; Dartmouth College, New Hampshire, USA
- **Genetic Epidemiology of Melanoma:** International Melanoma Genetics Consortium (GenoMEL) : over 20 groups from Europe, North America and Australia (http://www.genomel.org)
- **Genetic Diversity in Dog:** Department of Medical Biochemistry and Microbiology (IMBIM), Faculty of Medicine, Uppsala University as a member of the European consortium LUPA (over 20 groups from 12 European countries)

Oral presentation in research seminar and workshops:

1. Identification of genetic signatures of selection in dog. Mar. 2011, Rennes.
2. A Knowledge-Integration System for the Multi-Locus Analysis of Genome-Wide Association Studies. Feb. 2012, Paris.
3. Gene ontology: tool for the unification of biology. Mar. 2013, Paris.
4. Integration of GWAS results across species: analysis strategy. Jul. 2013, Rennes.
5. Genome-wide pathway-based analysis. Nov. 2014, Paris.
6. “Etudes pan-génomiques du mélanome dans l’espèce canine”. Jul. 2015, Rennes.

Collective life of the different teams I worked with

- Presentations in internal seminars and working groups
- Participation to the Monitoring of scientific literature
- Presentations at journal club organised as part of the “Cercle francilien de Recherche en génétique EPidémiologique et Evolutive” (CREPE)

TEACHING AND TRAINING

Teaching:

From 2015 to 2018 in the Master M2 of Public Health "Epidemiological Genetics and Biomarkers within the teaching units « *Logiciels d’analyse génétique* » and *« Liaison, Association, Génétique Quantitative et Formelle ».*

Supervision and training:

I contributed to the supervision and training of a master student, 4 engineers and 3 doctoral and post-doctoral students from the laboratory or coming to the laboratory for international exchanges organized within the European network Marie -Curie "Machine Learning for Personalized Medicine".

AWARDS

- Thesis Prize, Rennes 1 Foundation "Progressing, Innovate, Initiate," University of Rennes 1, Rennes (France), 2012
- Winner of a grant from the French Society of Genetics, Montpellier (France), 2010