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Languages English (fluent), French (native)

Education

- **Ph.D. in Computational and Molecular Biology** *(with highest honors)*   Jun. 2001 – Jan. 2005
  Paris VI (Pierre & Marie Curie) University. Paris, France

- **M.S. (french "DEA") in Molecular Biology** *(with honors)*   Oct. 2000 – Jun. 2001
  Paris VI (Pierre & Marie Curie) University. Paris, France

- **B.S. (french "maîtrise") in Biochemistry**   Oct. 1999 – Jun. 2000
  Paris VI (Pierre & Marie Curie) University. Paris, France

Experience

- **Assistant Research Professor, Dept. of Microbiology**   Dec. 2010 – Present
  Department of Microbiology. Montana State University. Bozeman, MT, USA
  Structure and evolution of metabolic networks organization at two scales—intracellular, and within microbial communities.

- **Director, Bioinformatics Core**   Sep. 2009 – Present
  Bioinformatics Core. Montana State University. Bozeman, MT, USA
  Involvement in various genomics and metagenomics projects as consultant or co-PI, including: Characterization of archaeal virus population structure and dynamics in acidic hot springs using metagenomics (Mark Young, PI, MSU); Transcriptional profiling of *Pseudomonas aeruginosa* under various experimental conditions, including biofilm formation (1 article; Philip Stewart, PI, MSU); Characterization of, and biomarkers identification for hypoxia response in *Aspergillus fumigatus* using microarrays, RNA-seq and ChIP-seq (Robert Cramer, PI, MSU); Characterization of host cell response to *Toxoplasma gondii* infection (Sandra Halonen, PI, MSU); Characterization of lipid accumulation in *Phaeodactylum tricornutum* using RNA-seq (Matthew Fields, PI, MSU); Mutagenesis of honey bee olfactive receptors (Kevin Wanner, PI, MSU).

- **Senior Post-Doctoral Research Fellow**   Nov. 2006 – Jul. 2009
  Systems Biology Unit. Institut Pasteur. Paris, France. PI: Benno Schwikowski, Ph.D.
  Impact of evolutionary pressures on metabolic network organization (1 article); Identification of functional modules from genome-scale, high-throughput data.

- **Post-Doctoral Research Fellow**   May. 2005 – Oct. 2006
  Center for the Study of Biological Complexity. Virginia Commonwealth University. Richmond, VA, USA. PI: Gregory A. Buck, Ph.D.
  Relationship between phylogeny and metabolic network organization (1 articles, 1 book chapter); Inference of gene essentiality from post-genomics data (1 article); Characterization of metabolic capabilities from expression data (1 article); Comparative genomics of two *Cryptosporidium* species.

- **Ph.D. Candidate**   Oct. 2001 – Jan. 2005
  Laboratoire de Génétique de la Neurotransmission (CNRS UMR 7091). Hôpital Pitié-Salpêtrière. Paris, France. Advisor: Jacques Mallet, Ph.D.
  Small-scale organization of gene regulatory networks (1 article, 1 book chapter); Inference of gene regulatory networks structure from expression data (1 article, 2 book chapters; Florence d'Alché-Buc, PI, Université Evry-Val d'Essonne, France); Development of double-channel radioactive microarray technology (1 article; Hélène Salin, PI).

Skills

Bioinformatics techniques Transcriptomics data analysis (selection of statistical tests, functional analysis of ranked lists or subset of genes using graph theory and gene set enrichment analysis, identification of best predictors or biomarkers of quantitative or qualitative phenotypes using machine learning and statistics), Next generation sequencing data analysis (reads processing —denoising and dereplication—and quality control, genome assembly, *de novo* and *ab initio* RNA–seq, ChIP–seq peak calling), Metagenomics data analysis (evaluation of community membership and comparison of communities membership—alpha and beta diversity, relationship between community membership and environment), Network–based data analysis (representation of biological systems as networks, characterization of the organization of these networks using graph theory, characterization of the dynamic of these networks using Petri nets, cellular automata or flux models), Development of ad–hoc analysis pipelines (programming, data parsing and format conversion, identifier mapping, data visualization, database development).

Bioinformatics toolkits Use and administration of BioJava, BioPython, Taverna, BioMoby, Cytoscape, EMBOSS, Galaxy.

Knowledge representation and inference Machine learning (Weka, Orange toolkits), statistics (R, JMP), rules engines (CLIPS, Jess).

Knowledge representation Population and query of relational databases (MySQL, PostgreSQL), document–oriented databases (MongoDB) and graph databases (Neo4j). Query and parsing of XML documents (XPath, XSLT) and RDF/OWL ontologies (SparQL).

Software development in Python, Java (J2SE), PHP, Perl, C/C++. Use of the Git distributed revision control system.

Web development HTML4, CSS3, JavaScript, RPC (SOAP), REST, CGI (Python and Perl).

Grid computing Amazon Web Services platform (EC2, EBS, S3). OpenPBS (Portable Batch System) and SGE (Sun Grid Engine) schedulers, on local hardware and on EC2 using StarCluster.

Operating systems administration Windows (95 to XP), Linux, MacOS X (FreeBSD).

Examples of bioinformatics tools developed at http://github.com/ajmazurie

Publications

(Legend: published as `PI` principal investigator, `Co-PI` co–principal investigator, or `Consultant` consultant)

Papers (7, plus 1 submitted) in refereed international journals:

○ **SREBP coordinates iron and ergosterol homeostasis to mediate triazole drug and hypoxia responses in the human fungal pathogen *Aspergillus fumigatus***
Blatzer M, Barker BM, Willger SD, Beckmann N, Blosser SJ, Cornish EJ, **Mazurie A**, Grahl N, Haas H, Cramer RA `Consultant`
PLoS Genetics (in press)

○ **Physiology of *Pseudomonas aeruginosa* in biofilms as revealed by transcriptome analysis**
Folsom JP, Richards L, Pitts B, Roe F, Ehrlich GD, Parker A, **Mazurie A**, Stewart PS `Consultant`
BMC Microbiology, Nov 2010; 10:294 — Impact Factor: 2.96. Tagged as 'Highly accessed' with 3008 accesses as of June 2011.

○ **Evolution of metabolic network organization**
Mazurie A, Bonchev D, Schwikowski B, Buck GA `PI`
BMC Systems Biology, May 2010; 4(1):59 — Impact Factor: 3.57. Cites by two publications* and tagged as 'Highly accessed' with 2670 accesses as of June 2011.

- **Phylogenetic distances are encoded in networks of interacting pathways**
  Mazurie A, Bonchev D, Schwikowski B, Buck GA [PI]
  *Bioinformatics, Nov 2008; 24(22):2579–2585 — Impact Factor: 4.926. Cited by 16 publications**
  and accessed 1698 times as of June 2011.

- **An evolutionary and functional assessment of regulatory network motifs**
  Mazurie A, Bottani S, Vergassola M [PI]
  Genome Biology, Mar 2005; 6(4):R35 — Impact Factor: 6.89. Rated as 'Must Read' (Factor 6.4)
  *by the Faculty of 1000 Biology. Cited by 16 publications** and accessed 6961 times as of June*
  2011.

- **Gene networks inference using dynamic Bayesian networks**
  Perrin BE, Ralaivola L, **Mazurie A**, Bottani S, Mallet J, d'Alché–Buc F [Co-PI]
  *Bioinformatics, Oct 2003; 19(2):II138–II148 — Impact Factor: 4.926. Cited by 128 publications**
  as of June 2011.

- **A novel sensitive microarray approach for differential screening using probes labeled with two different radio–elements**
  Salin H, Vujasinovic T, **Mazurie A**, Maitrejean S, Menini C, Mallet J, Dumas S [Co-PI]
  *Nucleic Acids Research, Feb 2002; 30(4):e17 — Impact Factor: 7.836. Cited by 22 publications**
  as of June 2011.

- **Transcriptomic and proteomic analyses of the *Aspergillus fumigatus* hypoxia response using an oxygen–controlled fermenter**
  Barker BM, Kroll K, Vödisch M, **Mazurie A**, Kniemeyer O, Cramer RA [Consultant]
  Submitted

Reviews (1) in refereed international journals:
- **Integrating genome–scale data for gene essentiality prediction**
  Roberts SB, **Mazurie A**, Buck GA [Co-PI]
  Chemistry and Biodiversity, 2007; 4(11):2618–2630 — Impact Factor: 1.926
  *Cited by 2 publications** as of June 2011.*

Papers (2) in refereed international conferences:
- **Understanding metabolic network evolution with stochastic simulations**
  Jolley CC, **Mazurie A**, Young M, Douglas T [Consultant]
  Biophysical Society 54th Annual Meeting, San Francisco CA, Feb 2010

- **Path–a–Way: a strategy for network analysis of microarray data**
  Arasappan D, **Mazurie A**, Alves J, Bonchev D, Buck GA [Co-PI]
  International Conference on BioMedical Engineering and Informatics, p. 432–436 (2008)

Book chapters (5) :
- **Metabolic networks and the phylogeny of species**
  Mazurie A, Bonchev D, Buck GA [PI]
  In 'Analysis of biomolecular structures and interaction networks', Kuznetsov VA editor, CRC/Taylor & Francis (2008)

- **Genetic networks: between theory and experimentation**
  Bottani S, **Mazurie A** [Co-PI]
  In 'Complex population dynamics: nonlinear modeling in ecology, epidemiology and genetics', Blasius B, Kurths J, and Stone L editors, World Scientific, pp. 215–236 (2007)

- **Genomes to networks, pathways and function**
  Buck GA, **Mazurie A**, Roberts SB, Alves J, Arassapan D, Serrano M, Manque P [Co-PI]
  In 'Recent progress in computational sciences and engineering: Lecture series on computer and computational sciences', Volume 7, Simos T and Maroulis G editors, Brill Academics, pp. 758–763 (2006)

- **A dynamic model of gene regulatory networks based on inertia principle**
  d'Alché–Buc F, Lahaye PJ, Perrin BE, Ralaivola L, Vujasinovic T, **Mazurie A**, Bottani S Co-PI
  In 'Bioinformatics using Computational Intelligence Paradigms', Seiffert U editor, Springer, pp. 93–118 (2005)

- **Réseaux bayésiens dynamiques pour l'inférence de structure de réseaux de régulation**
  Ralaivola L, Perrin BE, d'Alché–Buc F, **Mazurie A**, Bottani S Co-PI
  In 'Informatique pour l'analyse du transcriptome', Boulicaut JF and Gandrillon O editors, Lavoisier, pp. 291–319 (2004)

Invited talks (7) :

- **Evolution of metabolic networks organization**
  Applied Mathematics Seminar Series, Dept. of Mathematics, Montana State University, Bozeman MT (Mar 3, 2011)
  Seminar at the Center for the Study of Biological Complexity, Virginia Commonwealth University, Richmond VA (Mar 2, 2010)

- **Statistical challenges in bioinformatics and systems biology**
  Annual meeting of the Montana Chapter of the American Statistical Association, Montana State University, Bozeman MT (Sep 14, 2010)

- **Interaction networks**
  Guest lecturer for the Introductory Bioinformatics Laboratory 535 course (Marcie McClure, lecturer), Montana State University, Bozeman MT (Nov 17–19, 2010)

- **An evolutionary perspective on functional modules in metabolic networks**
  Workshop on Systems Biology & Networks, Institut Pasteur, Paris (Sep 22, 2008)

- **Modularity in intracellular systems**
  3ème Journée de Biologie Systémique, Paris V (Descartes) University, Paris (Apr 16, 2008)

- **Functional modules in intracellular systems: where are we?**
  Modularity in Synthetic Biology, Genopole, Evry (Mar 21, 2008)

- **An evolutionary and functional assessment of regulatory network motifs**
  Modularité, Compositionalité et Abstraction dans les réseaux géniques et protéiques, Institut Henry Poincaré, Paris (Nov 21, 2007)

- **Identification of biologically relevant modules in cells**
  Journées départementales de l'Institut Pasteur, Institut Pasteur, Paris (Jun 14, 2007)

Reviewer for Bioinformatics, BMC Systems Biology, PLoS Computational Biology, PLoS ONE, Nature Protocols, Cancer Informatics, Critical Reviews in Biotechnology, and Interface.

*sources: Google Scholar, PubMed and ISI Web of Knowledge

Grants

- **Complete systems biology study of a carbon fixing and recycling phototrophic mat community**
  Ward D (PI, MSU), **Mazurie A** `Co-PI`
  Gordon & Betty Moore Foundation; Pending

- **Determining residue defense across classes of endemic wheat pathogens**
  Dyer A (PI, MSU), **Mazurie A** `Co-PI`
  US Department of Agriculture; Pending

- **Modulation of amino acid networks for controlled tuning of chemosensory receptors**
  MacAllister IE (PI, ERDC–CERL), Grimme S (co-PI, ERDC–CERL), Wanner K (contractor, MSU), **Mazurie A** `Consultant`
  US Army Engineer Research and Development Center (#W9132T–11–2–0004); Mar. 2011 – Mar. 2014; $744,000

- **Integrated analysis of extremophile biology from genes to metabolites**
  Bothner B (PI, MSU), Young M (co-PI, MSU), McDermott T (co-PI, MSU), **Mazurie A** `Co-PI`
  National Science Foundation (#1022481); Jan. 2011 – Dec. 2014; $354,000

Reviewer for the NIH grant evaluation panel 'SBIR (small business innovative research)', NSF grant evaluation panel 'Advancing theory in biology', and French National Research Agency (ANR) panel 'Genomics, genetics, bioinformatics and systems biology'.

Teaching

- **Instructor of record**   Jan. 2010 – April 2010
  Montana State University
  IGERT DGED 614, 'Introduction to programming' (5 registered graduate students)

- **Lecturer (french "Vacataire")**   Jan. 2005 – Apr. 2005
  Paris XIII University. Bobigny, France
  Courses (100h): Introduction to Bioinformatics. Audience: biology undergraduate students.

- **Lecturer (french "Moniteur")**   Oct. 2001 – Jun. 2004
  Paris XIII University. Bobigny, France
  Courses (120h): Cellular Biology, Genetics, Embryology. Audience: biology undergrads and medschool students.

- **Tutor**
  Private courses in mathematics. Audience: high school students.

Other

Community involvement Secretary of the french BioDocs association in 2003, helping contacts between private research companies and PhDs. Co-organizer of the Paris, France edition of BioTechno2002 and BioTechno2003 forums.

Memberships AAAS (American Association for the Advancement of Science), ISCB (International Society for Computational Biology).