

## Jean Maurice PECCOUD, Ph.D.

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[www.peccoud.net](http://www.peccoud.net)

Strong leader with the ability to set long-term objectives and design short-term work plans to achieve them. Outstanding ability to apply complex mathematical models to solve biological problems. Results-driven manager who not only plans execution, but also anticipates and circumvents road blocks. Flexible and adaptable to changing work environments. Leverage written and oral communications to maximize program impact. Reach out to new people to seize new opportunities.

Recognized as a fast learner who continually maximizes and stretches his knowledge; enjoys using his energy to lead; has the decision-making skills to make difficult decisions.

- 15 years of post-doctoral experience in computational biology gained in academia, Fortune 500 and emerging companies – 5 years of experimental molecular biology experience.
- Extensive experience successfully managing multidisciplinary cross-departmental R&D programs by identifying and securing the financial and human resources critical to the program development.
- Gained the respect of the academic community through a consistent record of high-impact peer-reviewed publications and a network of international collaborations.
- Experienced maximizing the impact of constrained budgets.
- Good working knowledge of patenting and licensing strategies. Identified and successfully negotiated technology licensing agreements in corporate and academic environments.

### Experience

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April 2003 to Present

Collaborator with rank of Associate Professor, Department of Genetics, Development, and Cell Biology, Iowa State University (Ames, IA).

Advisor to graduate students enrolled in the ISU Bioinformatics program. Occasionally taught graduate-level classes on gene network modeling.

January 2002 to Present

Computational Biologist, E.I. du Pont de Nemours (Johnston, IA)

With annual revenue exceeding \$2billion and more than 6,000 employees around the world, Pioneer Hi-Bred International, a fully owned subsidiary of DuPont, is the world leader of the crop genetics industry. Within the bioinformatics group, member of the leadership team of Crop Genetics Modeling, an initiative to explore and deploy computer modeling methods to increase the productivity of Pioneer R&D investment. In charge of the research program focusing on modeling molecular data. This program has three components:

- *Gene and regulatory network discovery*: In collaboration with trait groups, design functional genomics experiments (Lynx MPSS and Agilent micro-arrays, real-time PCR assays, metabolomics).
- *Design of transformation vectors*: Initiated and lead a project to develop software and experimental protocols to design transformation vectors using quantitative methods. This research project was awarded a Discovery Research grant, an internal competitive funding mechanism used to support high impact / high risk projects outside the scope of Pioneer main research initiatives. The project received \$404,000 over three years in direct funding. After only 18 months, the results of this project already have a visible impact on various research programs at Pioneer.

- *Genetics*: Inventor of a method to analyze the genetic properties of gene networks. This method led to a patent application and to a publication in the journal *Genetics*.

Conducted the development of these projects by assembling and managing teams of scientists across the Pioneer R&D organization. Identified, hired, and supervised research scientists and technical staff.

Identified strategic external partners and vendors. After gaining the support of the scientific leadership, worked with the Technology Licensing group to formalize the collaboration framework. Currently overseeing these collaborations by ensuring a timely delivery of results and developing the appropriate communication channels to bring these results back into the organization. The combined budget of these collaborations exceeds \$500,000.

Leading a collective effort aimed at defining Pioneer intellectual property strategy in Bioinformatics.

January 2000 to December 2001

Founder & President of e-NoteBooks, Inc. (Seattle, WA)

e-NoteBooks' mission was to provide targeted marketing, publishing, value-added reselling, and distribution channels to the technical computing industry. Thousands of developers write add-ons for *MATLAB*, *LabVIEW*, *AutoCAD*, and other technical software. Due to the specialization of their products, these developers need vertical channels to reach their market segments.

The business plan involved raising seed-level capital from private investors and maximizing the ROI of this budget in a critical phase of the company life; identifying and negotiating strategic partnerships and intellectual property licensing agreements with individuals, academic institutions, and corporate partners; managing direct sales and distributor accounts, pre- and post-sale support to customers; managing 2 software products through all the steps of their life cycle; developing, marketing, and operating multiple web sites.

Customers included Fortune 500 companies, government and academic institutions along with smaller companies and individuals. Approximately 25% of the customers lived outside of North America. Independent traffic assessments demonstrated that the traffic on e-NoteBooks' web sites was comparable to the traffic recorded by the largest web sites in this industry.

The company assets were sold to The MathWorks, Inc. (Natick, MA) and to BetterVIEW Consulting (Vancouver, BC) which still sells *Mathematica Link for LabVIEW*.

January 1994 to December 1999

Charge de Recherche INSERM

INSERM is the French Institute of Health and Medical Research. Charge de Recherche is a full time research position. Hired as Charge de Recherche de Seconde Classe (equivalent to Assistant Professor). Promoted to Charge de Recherche Premiere Classe (equivalent to Associate Professor) and tenured in 1998. "Charge de Recherche" are considered extremely desirable positions since they have no teaching obligation and the scientist works in the department of his choice.

January 1998 to December 1999 University of Washington (Seattle, WA).

Invited by the Genomation Laboratory to contribute to the development of a high-throughput gene quantification instrument. Assembled a multidisciplinary research team by setting up a collaboration between clinicians, biologists, and engineers. Actively contributed to the writing of a research proposal that was funded in March 2000 by the National Cancer Institute for a total amount of \$2.3 million.

Explored the possibility of creating a gene quantification company operating on a fee-for-service basis. The project combined the engineering expertise of Seattle-based ORCA Photonics (an industrial partner of the Genomation Laboratory), the Genomation Laboratory itself, and the biomedical expertise of a University of Paris research team. Presented the project to a business plan competition managed by Ernst & Young. Among 2,000 submissions, the project was one of the 70 winners eligible for a €150,000 grant.

January 94 to December 97: Universite Joseph Fourier School of Medicine (Grenoble, FR)

Three years before the first commercial real-time PCR instrument was released by Applied Biosystem, initiated a collaboration with a statistician to develop a new statistical method to analyze the data generated by this new generation of instruments. Results were published in the *Biophysical Journal* (1996) and in the *Journal of Applied Probability* (1998).

Established that a formalism used in computer science for quantitative analysis of computer architectures, could be applied to the modeling of complex genetic networks. This work was published in the *Proceedings of the National Academy of Sciences USA* in 1998. This project was a collaboration with a graduate student in Prof. Richard Lewontin's group (Harvard University).

In 1995, invited by Wolfram Research to prototype a software interfacing *Mathematica* with scientific instruments and data acquisition hardware. In 1996 and 1997, designed, developed, and documented *Mathematica Link for LabVIEW* in close association with Wolfram Research software engineers, technical writers, and Software Quality Assurance specialists. This application is still distributed by Wolfram Research.

August 92 to December 93

Research Associate, University Louis Pasteur (Strasbourg, FR)

Designed protein expression vectors and protein purification processes to crystallize a retinoic acid receptor under the supervision of Dr. Dino Moras and Prof. Pierre Chambon (US Academy of Science). A group of molecular biologists was in charge of producing the protein and a group of crystallographers was responsible for making crystals. Acted as an interface between the two groups.

February 91 to June 92

Plant Breeding Program Manager, IRHO (Vanuatu, South Pacific)

During national service, assigned to IRHO, a research organization for the improvement of tropical oil-producing crops. Managed the day-to-day operations of a genetic research programs. Supervised a Melanesian staff of 30 technicians. Developed hiring and compensation policies to attract and retain the most educated technicians.

November 87 to January 91

Research Assistant, Universites Louis Pasteur/Joseph Fourier (France)

Using site-directed mutagenesis, build a series of 30 cell lines with modified residues in the antigen-binding site of a MHC class II molecule. This molecular dissection contributed to confirm a model of the antigen presentation to the T cell receptor, which led to an article in the *EMBO Journal*. It also demonstrated that superantigens such as staphylococcal enterotoxins bind the MHC Class II molecule outside the antigen presentation groove as peptides do. These findings were published in a *Cell* article that keeps being cited 15 years totaling more than 360 citations as of 11/2005. This work was conducted under the supervision of Diane Mathis and Christophe Benoist who moved their group to the Joslin Diabetes Center at Harvard Medical School in 1999.

## Scientific Achievements & Awards

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### Publications

A Science Citation Index research conducted in December 2004, led to 614 articles citing at least one of the references below. Reprint of most articles can be downloaded from [www.peccoud.net](http://www.peccoud.net).

Griffith, M. ; Courtney,T. ; Peccoud,J. ; Sanders,W.H. (submitted) A dynamic partitioning scheme for hybrid simulation of biochemical systems

Peccoud, J. and Vander Velden, K. (2005) Parameterization of a non-linear genotype to phenotype map using molecular network. *Pac.Symp.Biocomput.*, 284-95

Peccoud, J., Velden, K.V., Podlich, D.W., Winkler, C.R., Arthur, W.L., and Cooper, M. (2004). The Selective Values of Alleles in a Molecular Network Model Are Context Dependent. *Genetics* 166, 1715-1725.

Vander Velden, K. and Peccoud, J. Modeling networks of molecular interactions in the living cell: structure, dynamics, and applications. Sanders, W. H. and Ciardo, G. 10, 2-10. 2003. Los Alamitos, CA, IEEE Computer Society. **International Workshop on Petri Nets and Performance Models**.

Goss, P.J. and Peccoud, J. (1999). Analysis of the stabilizing effect of ROM on the genetic network controlling ColE1 plasmid replication. In **Pacific Symposium on Biocomputing '99**. R.B Altam, A.K. Dunker, L. Hunter, T.E. Klein, and K. Lauderdale, eds. (Singapore New Jersey London Hong-Kong: World Scientific), pp. 65-76.

Goss, P.J. and Peccoud, J. (1998). Quantitative modeling of stochastic systems in molecular biology using stochastic Petri nets. *Proc. Natl. Acad. Sci. U. S. A.* 95, 6750-6755.

Jacob, C. and Peccoud, J. (1998). Estimation of the parameters of a branching process from migrating binomial observations. *Adv. Appl. Prob.* 30, 948-967.

Peccoud, J. and Jacob, C. (1998). Statistical estimation of PCR amplification rates. In **Gene Quantification**. F. Ferré, ed. (New-York: Birkhauser), pp. 111-128.

Peccoud, J. (1998). Stochastic Petri nets for genetic networks. *M S-Medecine Sciences* 14, 991-993.

Jacob, C., Breton, N., Daegelen, P., and Peccoud, J. (1997). Probability distribution of the chemical states of a closed system and thermodynamic law of mass action from kinetics: The RNA example. *J Chem. Phys.* 107, 2913-29 19.

Peccoud, J. and Damour, D. (1997). MathLink for LabVIEW: a new environment to control and interact with instruments; application to robotics. In **Proceedings of the Second International Mathematica Symposium**. P. Mitic and V. Keranen, eds. (Southampton: Computational Mechanics Publications),

Jacob, C. and Peccoud, J. (1996). Inference on the initial size of a supercritical branching process from partial and migrating observations. *C. R. Acad. Sci. Paris Série I* 322, 875-880.

Jacob, C. and Peccoud, J. (1996). Estimation of the offspring mean for a supercritical branching process from partial and migrating observations. *C. R. Acad. Sci. Paris Série I* 322, 736-768.

Peccoud, J. and Jacob, C. (1996). Theoretical uncertainty of measurements using quantitative polymerase chain reaction. *Biophys. J* 71, 101-108.

Peccoud, J. (1995). Automating molecular biology: A question of communication. *Bio/Technology* 13, 741-745.

Peccoud, J. and Ycart, B. (1995). Markovian modelling of gene products synthesis. *Theor. Pop. Biol.* 48, 222-234.

Peccoud, J. and Ycart, B. (1995). Analytical results related to the statistics of gene product synthesis. *J. Cell. Biochem.* S19A, 341.(Abstract)

Peccoud, J. (1995). Intricate loops: a pragmatic approach. *Bioessays* 17, 183.

Peccoud, J. and Viville, S. (1994). Aspects aléatoires de la dynamique de la différenciation cellulaire. *MS-Med. Sci.* 10, 877-883.

Peccoud, J. (1994). Valeur heuristique de la modélisation en biologie. *MS-Med. Sci.* 10, 606.

Peccoud, J. (1993). Quantitative PCR - A New Tool for Clinical Investigations. *MS-Med. Sci.* 9, 1378-1385.

Roucher, F. and Peccoud, J. (1992). Combined management plan for forests and roe deer *Carporeolus-Carporeolus* L.: eight years experience on a 4500 hectare area of the northern Vosges woodlands Part II. Methods and results. *Rev. For. Fr.* 44, 141-152.

Dellabona, P., Peccoud, J., Kappler, J., Marrack, P., Benoist, C., and Mathis, D. (1990). Superantigens interact with MHC class II molecules outside of the antigen groove. *Cell* 62, 1115-1121.

Peccoud, J., Dellabona, P., Allen, P., Benoist, C., and Mathis, D. (1990). Delineation of antigen contact residues on an MHC class II molecule. *EMBO J.* 9, 4215-4223.

Warren, A.P., Paschedag, I., Benoist, C., Peccoud, J., Mathis, D., and Thomas, D.B. (1990). Defects in antigen presentation of mutant influenza haemagglutinins are reversed by mutations in the MHC class II molecule. *EMBO J.* 9, 3849-3856.

Dellabona, P., Peccoud, J., Benoist, C., and Mathis, D. (1989). T-cell recognition of superantigens: inside or outside the groove? *Cold. Spring. Harb. Symp. Quant. Biol.* 54 Pt 1, 375-381.

Pierres, M., Marchetto, S., Naquet, P., Landais, D., Peccoud, J., Benoist, C., and Mathis, D. (1989). I-A alpha polymorphic residues that determine alloreactive T cell recognition. *J Exp. Med.* 169, 1655-1668.

Reske Kunz, A.B., Landais, D., Peccoud, J., Benoist, C., and Mathis, D. (1989). Functional sites on the A alpha-chain. Polymorphic residues involved in antigen presentation to insulin-specific, Ab alpha: Ak beta-restricted T cells. *J Immunol.* 143, 1472-1481.

## U.S. Patent Applications

Peccoud, J. and Vander Velden, K. (2005) Computer System for Genotype to Phenotype Mapping Using Molecular Network Models. #20050086035

## Recent Communications

01/05: Pacific Symposium on Biocomputing

09/03: Keynote lecture International Workshop on Petri Net and Performance Modeling

03/03: Coordinated Science Laboratory, University of Illinois

02/03: Bioinformatics Seminar, Iowa State University

## Honors and Awards

2003: Recipient of a Discovery Research grant internal to Pioneer.

1999: Winner of a business plan competition sponsored by the French agency for technology transfer.

1998: Recipient of a NATO "Advanced Scientist Fellowship".

1997: Invited as visiting professor in the Department of Electrical Engineering, University of Washington.

1995: Invited as visiting scholar by Wolfram Research Inc. (Champaign, IL)

1987-1991: Roussel-UCLAF/CNRS Graduate Student Fellowship

## Education

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January 1991	Ph.D. in Molecular Biology/Bioinformatics (University Joseph Fourier, France)
October 1987	DEA (graduate degree) in Quantitative Genetics (University of Paris Orsay, France)
October 1984 to October 1987	Student at "Institut National Agronomique de Paris-Grignon", one of the leading "Grandes Ecoles" in France. Graduated in October 87 (equivalent to a MSc.).
September 1982 to June 1984	Preparation for the competitive entrance to "Grandes Ecoles". Ranked 60th out of 2,000 on examination.

## References

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William H. Sanders	217 333 0345	<a href="mailto:whs@crhc.uiuc.edu">whs@crhc.uiuc.edu</a>
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Richard Lewontin	617 495 5667	<a href="mailto:lewontin@oeb.harvard.edu">lewontin@oeb.harvard.edu</a>

## Personal

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Citizen of France – Permanent resident of the United States.