Pauline C. Ng, PhD

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SKILLS

- 15+ years of experience in biotech and medical software (genomics, algorithm development and personalized medicine)
- Pioneer in personalized genomics: characterize first individual human genome (Craig Venter) and companies like 23andMe
- Deliver products on-time in startup environments: e.g. Illumina genotyping microarrays and clinical next-gen sequencing panels
- Clinical experience: Establish CAP lab and validation of clinical and FDA tests
- Manage bioinformaticists and IT professionals in clinical, industry and research settings
- Data mining, statistical analysis, genomics, and natural language processing
- h-index 25; 30+ publications with over 16,000 citations

EXPERIENCE

2017 - Present **Bioinformatics Consultant** **Singapore**

- Genetic risk scores for prenatal diagnosis (NIPT). Client: MyOme
- Conduct validation for FDA companion diagnostics. Advise scientific and market analysis for various projects (e.g. cancer, skin expression, consumer exome). Client: Genome Institute of Singapore
- Establish clinical-grade cancer panel for distribution in Southeast Asia by estimating market opportunity, creating workflow with China-based laboratory, and forming local business partnerships. Client: NovogeneAIT
- Save company licensing fees by directing bioinformatics team to implement in-house pipeline. Obtained patent on proprietary software. Client: Asia Genomics
- Provide technical advice for investment companies. Clients: Temasek, GFK, VinaCapital

2013 – 2017 **Chief Informatics Officer, POLARIS**

2010 – 2017 **Group Leader, Computational & Mathematical Biology**

Genome Institute of Singapore **Singapore**

- Established and managed bioinformatics/IT for the first lab in Southeast Asia to be certified by CAP (College of American Pathologists) for the specific purpose of next-generation sequencing clinical assays.
- Created impactful algorithms for detecting disease mutations:
  1. SIFT for prediction on coding mutations. SIFT is considered to be a standard algorithm and has more than 8,000 citations.
  2. Phen-Gen for mutations in rare disorders.
- Other projects: evolution of Facebook memes, drug performance based on online ratings, an open-access platform for scientific publications.
- Led omics data sharing between > 5 different health and research institutes via a federated database hosted on cloud.
- Managed team of 11 bioinformaticians that deploy clinical applications or conduct research.

2009 – 2010 **Assistant Professor, Genomic Medicine**

2006 – 2008 **Senior Scientist**

J. Craig Venter Institute **San Diego, CA**

- Innovated research on individual human genomes. A lead author on the first published individual human genome (Craig Venter's). Led the first analysis of a single human individual's exome.
- Proposed agenda for personalized medicine for direct-to-consumer companies like 23andMe. Published in Nature.
- Developed and assessed variant analysis from next-generation sequencing technologies. Co-first author on a paper comparing sequencing technologies, #2 most accessed article in Genome Biology for 2009.
- Awarded NHGRI R01 grant to further develop SIFT algorithm. Tripled traffic to new SIFT website in a span 6 months, and published in Nature Protocols.

2005 – 2006 **Bioinformatics Senior Scientist**
2002 – 2005 **Scientist I, Scientist II**

Illumina, Inc. — San Diego, CA

- Designed and developed the content of the Human Infinium Beadchips by managing a team of 7 cross-functional leads. BeadChips account for almost half of genome-wide association studies.

1998 – 2002 **Bioinformatics Graduate Student**

Fred Hutchinson Cancer Research Center — Seattle, WA

- Created SIFT (Sorting Intolerant From Tolerant), one of the first algorithms and a gold standard for predicting nonsynonymous mutations implicated in disease. Cited by more than 8,000 publications and licensed by more than 100 companies.

EDUCATION

2002 **University of Washington** — **Seattle, WA**
Ph.D., Bioengineering

1997 **California Institute of Technology (Caltech)** — **Pasadena, CA**
B.S. with Honors, Biology

PUBLICATIONS

ChronQC: A Quality Control Monitoring System for Clinical Next Generation Sequencing
N.R. Tawari, J.J.W. Seow, D. Perumal, J.L. Ow, S. Ang, A.G. Devasia, P.C. Ng (2018) *Bioinformatics* 34:1799

Reporting Incidental Findings of Genomic Disorder-Associated Copy Number Variants to Unselected Biobank Participants
L. Leitsalu, <8 authors>, P.C. Ng, A. Metspalu (2016) *Personalized Medicine* 13:303

Enabling Public Access to Non-Open Biomedical Literature via Idea-Expression Dichotomy and Fact Extraction
X. Huang and P.C. Ng (2016) *Association for the Advancement of Artificial Intelligence Workshop on Scholarly Big Data*

Information Evolution in Social Networks
L.A. Adamic, T.M. Lento, E. Adar, P.C. Ng (2016) *The 9th ACM International Conference on Web Search and Data Mining*

Assessment of Web-Based Consumer Reviews as a Resource for Drug Performance
S. Adusumalli, H. Lee, Q. Hoi, S.L. Koo, I.B. Tan, P.C. Ng (2015) *Journal of Medical Internet Research* 17:e211

SIFT Missense Predictions for Genomes
R. Vaser, S. Adusumalli, S.N. Leng, M. Sikic, P.C. Ng (2015) *Nature Protocols* 11:1-9

Phen-Gen: Combining Phenotype and Genotype to Predict Causal Variants in Rare Disorders
A. Javed, S. Agrawal, P.C. Ng (2014) *Nature Methods* 11:935

Whole Genome Sequencing Of Asian Lung Cancers: Second Hand Smoke Unlikely To Be Responsible for Higher Incidence Of Lung Cancer Among Asian Never-Smokers
V.G. Krishnan, P. J. Ebert, <13 authors>, P. Tan, A.M. Hillmer, P.C. Ng (2014) *Cancer Research* 74:6071

MOLECULAR FINGERPRINTING CATCHES RESPONDERS TO THERAPEUTIC AGENTS
S. Malik, P. Tan, P.C. Ng. (2013) *Genome biology* 14.10: 135

SIFT INDEL: PREDICTIONS FOR THE FUNCTIONAL EFFECTS OF AMINO ACID INSERTIONS/DELETIONS IN PROTEINS
J. Hu and P.C. Ng. PLoS One. (2013) 8:e77940

PREDICTING CANCER DRIVERS: ARE WE THERE YET?
V.G. Krishnan and P.C. Ng. (2012) *Genome Med*. 4:88

SIFT WEB SERVER: PREDICTING EFFECTS OF AMINO ACID SUBSTITUTIONS ON PROTEINS
N.L. Sim, P. Kumar, J. Hu, S. Henikoff, G. Schneider, P.C. Ng. (2012) *Nucleic Acids Res*. 40:W452-7

PREDICTING THE EFFECTS OF FRAMESHIFTING INDELS
J. Hu and P.C. Ng (2012) Genome Biol. 13:R9

THE HUMAN GENOME, MICROBIOME, AND DISEASE
J.H. Badger*, P.C. Ng*, Venter, J.C. In Metagenomics of the Human Body. 2011. pp. 1-14.

AN AGENDA FOR PERSONALIZED MEDICINE
P.C. Ng, S.S. Murray, S. Levy, J.C. Venter. (2009) *Nature* 46:724-726.

PREDICTING THE EFFECTS OF CODING NONSYNONYMOUS VARIANTS ON PROTEIN FUNCTION USING THE SIFT ALGORITHM
P. Kumar, S. Henikoff, P.C. Ng (2009) *Nature Protocols* 4:1073-81.

EVALUATION OF NEXT GENERATION SEQUENCING PLATFORMS FOR POPULATION TARGETED SEQUENCING STUDIES
O. Harismendy*, P.C.Ng*, R.L. Strausberg, X. Wang, T.B. Stockwell, et al. (2009) *Genome Biology* 10: R32. #2 most accessed article in Genome Biology for 2009.

THE HUREF BROWSER: A WEB RESOURCE FOR INDIVIDUAL HUMAN GENOMICS
N. Axelrod, Y. Lin, P.C. Ng, T.B. Stockwell, J. Crabtree, et al. (2009) *Nucleic Acids Research* 37:D1018

INDIVIDUAL GENOMES INSTEAD OF RACE FOR PERSONALIZED MEDICINE
P.C. Ng, Q. Zhao, S. Levy, R.L. Strausberg, J.C. Venter (2008) *Clinical and Pharmacology and Therapeutics* 84:306

GENETIC VARIATION IN AN INDIVIDUAL HUMAN EXOME
P.C. Ng, S. Levy, J. Huang, T.B. Stockwell, B.P. Walenz, et al. (2008) *PLoS Genetics* 4:e1000160.

POWER TO DETECT RISK ALLELES USING GENOME-WIDE TAG SNP PANELS
M.A. Eberle*, P.C. Ng*, K. Kuhn, L. Zhou, D.A. Peiffer, et al. (2007) *PLoS Genetics* **3**:e170

THE DIPLOID GENOME SEQUENCE OF AN INDIVIDUAL HUMAN
S. Levy, G. Sutton, P.C. Ng, L. Feuk, A.L. Halpern, et al. (2007) *PLoS Biology* **5**:e254

PREDICTING THE EFFECTS OF AMINO ACID SUBSTITUTIONS ON PROTEIN FUNCTION
P.C. Ng and S. Henikoff (2006) *Annual Review of Genomics and Genetics* **7**:61-80

WHOLE-GENOME GENOTYPING OF HAPLOTYPE TAG SINGLE NUCLEOTIDE POLYMORPHISMS
K.L. Gunderson, K.M. Kuhn, F.J. Steemers, P. Ng, S.S. Murray, R.Shen (2006) *Pharmacogenomics* **7**:641-648

WHOLE-GENOME GENOTYPING.
K.L. Gunderson, F.J. Steemers, H. Ren, P. Ng, L. Zhou, C. Tsan, W. Chang, D. Bullis, J. Musmacker, C. King, et al. *Methods Enzymology* **410**:359-376

WHOLE GENOME GENOTYPING ON BEADCHIPS WITH ILLUMINA'S INFINIUM ASSAY
K.L. Gunderson, F.J. Steemers, K. Kuhn, H. Ren, L. Zhou, P. Ng, C. King, G. Lee, C. Tsan, et al. (2006) Genetic Variance Detection-Technologies for Pharmacogenomics (pp. 221-236). DNA Press.

SIFT: PREDICTING AMINO ACID CHANGES THAT AFFECT PROTEIN FUNCTION
P.C. Ng and S. Henikoff (2003) *Nucleic Acids Research* **13**:3812-3814

ACCOUNTING FOR HUMAN POLYMORPHISMS PREDICTED TO AFFECT PROTEIN FUNCTION
P.C. Ng and S. Henikoff (2002) *Genome Research* **12**:436-446

PREDICTING DELETERIOUS AMINO ACID SUBSTITUTIONS
P.C. Ng and S. Henikoff (2001) *Genome Research* **11**:863-74

PHAT: A TRANSMEMBRANE-SPECIFIC SUBSTITUTION MATRIX
P.C. Ng, J.G. Henikoff and S. Henikoff (2000) *Bioinformatics* **16**: 760-6

*Equal author contribution