Pauline C. Ng, PhD

pauline.c.ng@gmail.com
Skype: pauline.ng1

SKILLS

- 15+ years of experience in biotech (genomics, sequencing, and medical software). 30+ publications with 12,000+ citations
- Pioneer in precision medicine (characterize first individual human genome, assess personalized genomics companies like 23andMe)
- Deliver industry-grade products on-time (Illumina genotyping products, POLARIS sequencing panels)
- Manage a group of IT professionals and bioinformaticists in a clinical setting
- Regulatory compliance for working with clinical data (licensed by CAP- College of American Pathologists)
- Data mining, statistical analysis, genomics, and natural language processing
- Ad hoc reviewer for Nature Genetics, Nature Methods, Bioinformatics, Genome Biology, Nucleic Acids Research, Human Mutation, Human Genetics, Gene, and Personalized Medicine
- Programming skills in Perl, Python, C, C++, R, HTML. Development in Unix and cloud

EXPERIENCE

Chief Informatics Officer, POLARIS (2013-2017) **Singapore**
Group Leader, Computational & Mathematical Biology (2010-2017)
Genome Institute of Singapore

- Establish bioinformatics/IT infrastructure 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 (POLARIS translational medicine program).
- Create impactful algorithms for detecting disease mutations and increasing public health awareness: 1) SIFT for prediction of coding mutations (2001- present), 2) Phen-Gen for mutations in rare disorders (2014), 3) FactPub for open-access platform to scientific publications (2016). SIFT is considered to be a standard algorithm and has more than 8,000 citations.
- Mine online social media: 1) predict drug performance based on online consumer reviews, 2) viral patterns and spread of memes.
- Lead genome data sharing between > 5 different health and research institutes via a federated database hosted on cloud.
- Manage team of 11 bioinformaticians that deploy clinical applications or conduct research.

Visiting Professor (2011-2017) **Tartu, Estonia**
Estonian Genome Center

- Return incidental findings to biobank donors and survey impact.

Adjunct Associate Professor (2015-2017) **Singapore**
National University of Singapore

- Discover genotype-phenotype relationships for cardiac disease from biobank samples.

Assistant Professor, Genomic Medicine (2009-2010) **San Diego, CA**
Senior Scientist (2006-2008)
J. Craig Venter Institute

- Innovate 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.
- Propose agenda for personalized medicine for direct-to-consumer companies like 23andMe. Published in Nature.
- Develop and assess variant analysis from next-generation sequencing technologies from Roche, Illumina, and Complete Genomics. 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.

Bioinformatics Senior Scientist (2005-2006) **San Diego, CA**
Scientist I, Scientist II (2002-2005)
Illumina, Inc.

- Design and develop the content of the Human Infinium Beadchips by managing a team of 7 cross-functional leads. BeadChips are used in over half of genome-wide association studies (GWAS).

Bioinformatics Graduate Student (1998-2002) **Seattle, WA**
Fred Hutchinson Cancer Research Center

- 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 used by more than 100 companies.

EDUCATION

Ph.D., Bioengineering (GPA 3.9) **Seattle, WA**
University of Washington

B.S. with Honors, Biology (GPA 3.9) **Pasadena, CA**
California Institute of Technology (Caltech)

PUBLICATIONS

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

AWARDS AND MEMBERSHIPS

- Illumina Values Award for building successful teams, satisfying customers, and contributing to shareholders.
- Scholarship winner, Keystone Symposia: Human Genetics and Genomics
- Department of Energy Computational Science Graduate Fellowship. Awarded to 20 graduate students in the U.S.
- National Science Foundation Fellowship
- Tau Beta Pi Engineering Honor Society
- Member of American Society of Human Genetics
- Expert Review on Archon Genomics X-Prize

SEMINARS (partial list)

- Sharing and giving genomic information: Lessons learned from the CHORUS database and incidental findings. Duke-NUS Symposium on Population Health & Precision Medicine, Singapore (2017)
- Genomic findings. Conference on Research Ethics 2017, Singapore (2017)
- Breaking down paywalls for online health. Open Data Science Conference East, Boston (2016)

- Breaking down paywalls for online health. Data by the Bay, San Francisco (2016)
- Drug Decisions from Genomics and Online Data. Big Data World Show, Singapore (2015).
- A Journey through Genotype and Phenotype Relationships. Enabling Genomic Technologies, Singapore (2014).
- An Asian Approach to Genotyping Patients. Practical Biobanking Workshop, Tartu, Estonia (2013).
- Investigating Drug Effectiveness using Consumer-generated Reviews. Medicine 2.0, London, UK (2013).
- Caveats of Personalized Medicine. BioIT World Asia, Singapore (2013).
- The Responsibility of Personalized Medicine. HGM 2013 & 21rst ICG, Singapore (2013).
- Applications in Medical Genetics. NGS Asia Congress (2011).
- Assessment of CAGI Predictions. ISMB/ECCB, Vienna, Austria (2011).
- Future of Individual Genomes. ICG-VI, Shenzhen, China (2011).
- Bioinformatic tools and analyses for understanding genetic variation. FAOBMB, Singapore (2011).
- Characterizing Individual Genomes. HUGO 2011, Dubai (2011).
- Sequencing the Human Exome: Approaches, Methodologies, and Challenges. Science Webinar series, Washington, D.C. (2009).
- Understanding Individual Human Variation (Speaker and Organizer). UCSD Institute for Genomic Medicine and J. Craig Venter Institute Joint Symposium, San Diego, CA (2009).
- Next generation sequencing of humans. CHI: Next Gen Sequencing Technologies, San Diego, CA (2009).
- Individualized Genomics. UCSD Bioinformatics Expo, San Diego, CA (2009).
- Individual Genomes and Personalized Medicine. 5th La Jolla Biotech Day, La Jolla, CA (2008).
- Variation in the Human Exome. Human Genome Variation Meeting, Toronto, Canada (2008).
- Personalized Genomics: Benefits and Risks. ETech Emerging Technology Conference, San Diego, CA (2008).
- Genome-wide association studies: Infinite possibilities with Infinium Whole-Genome Genotyping. Illumina Workshop. American Society of Human Genetics, Salt Lake City, UT (2005).
- Capturing all common variation on a human SNP chip. Genomes, Medicine & Environment, Hilton Head, SC (2005).
- Ng, P.C. and Henikoff, S. SIFTing the human genome for polymorphisms predicted to affect protein function. Computational Biology Seminar Series, University of Washington (2002).