

Greg Tyrelle, PhD.

A scientist who...

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Nationality: Australian (04/05/1975)

Enjoys working in industry
Internationally experienced
At the cutting edge of genomic level
data analysis and interpretation

Research Scientist • Product development and support

I am a computational biologist, with extensive experience in analysis and interpretation of genome level datasets. I have worked with microarrays for over 10 years, from optimization of laboratory protocols, data quality assessment, and biological interpretation of data. In addition, to data analysis and management, I have lead teams in microarray product development including whole genome probe design and annotation. I have implemented customer focused data management and services for microarrays.

Professional Profile:

- Australian citizen based in the Netherlands as a knowledge migrant
- Next-generation sequencing data analysis tools and file formats: Fastq files, SAM/BAM, pileup, UCSC bed file formats, UCSC genome browser, custom track displays, SNP calling tools VarScan, Samtools var filter
- Data analysis, data visualization, data management, statistics, computer programming, database development, website and on-line community development
- Product development and technical support (microarrays)
- Experience in management of R&D projects and collaborations
- Understanding of aging and its pathologies, such as neurodegeneration and osteoporosis

Career Development

DNage BV.

Leiden, the Netherlands

<http://www.dnage.nl/>

2009 May – Present

Research Scientist

DNage BV is a startup pharmaceutical company developing novel drug treatments for accelerated aging diseases. I am responsible for computational research strategies as part of the company's drug development and biomarker identification programs.

- Develop bioinformatics strategies to understand aging using microarrays and NGS
- Initiate leads on new targets and biomarkers for neurodegeneration and osteoporosis
- Presented research results at Systems Biology for Aging Meeting, Rostock German 2010

Phalanx Biotech Group Inc.

Hsinchu, Taiwan

<http://www.phalanxbiotech.com/>

2006 August – May 2009

Bioinformatics/IT Department Manager

Phalanx Biotech is a developer and manufacturer of microarray technology for use in fundamental research and diagnostics. I managed the bioinformatics team, which was responsible for new product development, and product technical support.

- Developed product annotation pipeline and database (gene-to-probe-mapping)
- Built up the bioinformatics team and hired key engineers
- Successfully implemented company wide LIMS and data management systems

- Experience working with international clients and doing business in Asia, US and Europe

Proteomics Center

Chung Gang Medical University
Tao-Yuan, Taiwan

2005 November – July 2006*Data Center Manager*

Responsible for data management and analysis for Proteomics Center.

Advanced Bioinformatics Core Lab

Yang Ming Medical University
Taipei, Taiwan

2004 November – 2005 September*Postdoctoral Researcher*

Develop tools to understand relationship between alternative splicing and disease.

Education

PhD in Bioinformatics (2000 - 2004)

School of Biotechnology and Biomolecular Sciences
The University of New South Wales, Sydney, Australia

Thesis title: A platform for secure data sharing and integration for personalized medicine.

Main topic: **Semantic Web for Personalized Medicine**

Sub topic: **Pixel-by-pixel analysis of two-color microarray images**

B Sc (Honours, 1st class) in Biochemistry (1995-1999)

School of Biotechnology and Biomolecular Sciences
The University of New South Wales, Sydney, Australia

Thesis title: Site directed mutagenesis of T7 RNA polymerase

Publications

- G.D. Tyrelle (2008) Whole Genome Microarray Probe Content Interoperability, *Phalanx Biotech TechNote*. http://www.phalanxbiotech.com/Support/TN_ANNO.pdf
 - G.C. King, S.M. Knox, B.B. Williams, J. Harris, D.M. Gupta, D.A. Di Giusto, E.R. Gabutero, G.D. Tyrelle, Y. Lai, M.T. Aung, S.T. McCutcheon, N. Voelcker and H.T.T. Le. (2005) Multivalent Circular Aptamers: Versatile Nanostructures for Biomedical Applications, *Proceedings of the 2005 NSTI Bio Nano Conference and Trade Show*.
 - G.C. King, D.A. Di Giusto, W.A. Wlassoff, S. Giesebrecht, E. Flening & G.D. Tyrelle (2004) Proofreading genotyping assays and electrochemical detection of SNPs, *Hum. Mutat.*, 23, 420-425.
 - Tyrelle, G. D. and King, G. C. (2003) A platform for the description, distribution and analysis of genetic polymorphism data. *Conferences on Research and Practice in Information Technology* 19, 173-180.
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Presentations

- A Systems Biology Approach to Translation of Aging Research into Medicine for Premature Aging Disease, Systems Biology of Aging, Rostock Germany, 5th May 2010
- A platform for the description, distribution and analysis of genetic polymorphism data, First Asia Pacific Bioinformatics Conference (APBC), Adelaide SA, February 4-7 2003.
- Biological Variation Markup Language (BVML), Bioinformatics Open Source Conference (BOSC), Brisbane QLD, June 27 – 28, 2003.

- Nodalpoint, a bioinformatics weblog Bioinformatics Open Source Conference (BOSC), Brisbane QLD, June 27 – 28, 2003.
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Posters

- Whole Genome Microarray Probe Content Interoperability, Intelligent Systems in Molecular Biology (ISMB), Vienna, July 21-25, 2007.
- SpliceML: an XML file format for alternative splicing data exchange, Intelligent Systems in Molecular Biology (ISMB), Detroit, June 25-29, 2005.
- A genetic polymorphism object model and XML implementation: Biological Variation Markup Language, Intelligent Systems in Molecular Biology (ISMB), Brisbane QLD, June 29 – July 3, 2003.
- Reliable feature extraction from mechanically spotted two color microarrays, Intelligent Systems in Molecular Biology (ISMB), Brisbane QLD, June 29 – July 3, 2003.
- Modeling SNPs in the Haemostasis Pathway: Towards a Network Interaction Approach, Lorne Proteins Conference, Lorne VIC, February, 2002.

Relevant technical knowledge

Bioinformatics: microarrays, next-generation sequencing (Illumina GA), Samtools, Varscan, Ensembl and UCSC genome databases, R and Bioconductor, Genespring, pathway analysis, Biopython (advanced knowledge), Bioperl, BLAST, ClustalW, protein structure modelling and visualization. Statistics, novel algorithm development, microarray statistics, GO-enrichment.

Computer Science Skills: Programming in Python (Advanced level), Perl, PHP, C, Ruby, Java, XML, RDF, RDF Schema, OWL, ontology development, PostgreSQL, MySQL, Oracle, schema design. HTML, XHTML, CSS, CMS systems. Linux, Mac OS X, Debian Linux, Ubuntu Linux, RedHat Enterprise Linux.

Molecular Biology: Cloning, PCR, site directed mutagenesis, protein expression and purification, molecular mechanics/dynamics simulations, differential scanning calorimetry (DSC), microarray sample preparation.

Scholarships

- Apple Australia Computer Scholarship, Apple Computer Inc., 2002 - 2003
- Australian Postgraduate Award (APA), DEST, 2000 - 2004

Personal Interests

- Anti-aging movement, health and fitness (jogging)
- Bioinformatics community (<http://www.nodalpoint.org>)

Press

- My analysis of an artificial meme featured in the New York Times:
 - <http://www.nytimes.com/2004/10/26/arts/26meme.html?ex=1256529600&en=30b7dc917b13f0d5&ei=5090&partner=rssuserland>
- Nodalpoint featured in The scientist Magazine:
 - The power of the blog: <http://www.the-scientist.com/2005/8/1/37/1>
- Nodalpoint featured in Nature News special on weblogs:
 - Science in the web age: <http://www.nature.com/nature/journal/v438/n7068/full/438548a.html>

References

Available upon request.