

PETER ANTHONY NOBLE
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Career Summary

A scientist (Principal Investigator) with an interdisciplinary background in: critical thinking, solving problems, making innovative discoveries, training scientists, and leading (and working within) collaborative relationships. I have published 50+ peer-reviewed articles in microbiology, transcriptomes, genomes, DNA microarrays, next-gen-sequencing, statistics and bioinformatics. My latest work deals with post-transcriptional regulation in stressed zebrafish and mouse cells/organs/tissues (<https://rdcu.be/6LMY>). My career goal is to combine my background in 'hands-on' molecular biology (eukaryotic/prokaryote genomes and transcriptomics) with high-end informatic/statistical analysis to model entire 'systems'. Understanding 'systems' will lead to breakthroughs in precision medicine, pharmaceutical and biological fields (e.g., cancer research).

Education

Postdoctoral training in Molecular Biology, University of California Irvine
Postdoctoral training in Bioinformatics, University of Maryland Center of Marine Biotechnology
Ph.D. in Applied Microbiology, University of Saskatchewan
M.Sc. and B.Sc. Honors degrees in Biology, Memorial University of Newfoundland

Peer-reviewed articles: <http://peteranoble.com/publications.html>

Press articles written on my research: <http://peteranoble.com/press.html>

Software programs: <http://peteranoble.com/software.html>

Work Experience

Prokarma/Health Care Analytics/Precision Medicine, 11/2018-current.

Duties:

- Developed exploratory analytic models examining disease progression by combining social network analysis (SNA) with machine learning approaches. The models were based on millions of diagnosis and procedure codes reported by a network of hospitals. The models were constructed in C++, Python, R, and Pytorch (4 GPUs, Nvidia-smi; tutorials available on software web site; Pandas, Numpy, Scipy, ggplot, network analysis; algorithm development), trained/optimized/tested/ validated/models in the Cloud. The research is an example of BIG data analysis since there were millions of rows and thousands of columns of data. Future research involves incorporating genomic/transcriptomic data into the models.

Prokarma/Union Pacific Railway, System Data Scientist, 06/2018-11/2018.

Duties:

- Estimated "time-travel" of ~20,000 cargo trains passing through more than 12,000+ locations using massive computer simulations and machine learning tools. The models were constructed in C++, Python, and Pytorch (4 GPUs, Nvidia-smi; tutorials available on software web site). The weights and biases of the models were extracted and incorporated into C++ programs for statistical analyses and deployment in the field. I conceived of the idea and built/optimized/validated the models.

Pacific Northwest National Laboratory, Bioinformatic Consultant. 06/2017 – 03/2018.

Duties:

- Data analyses of microbial communities (16S rRNA genes) from spent nuclear reactor water storage basin (Savannah River National Laboratory). Compared our data to existing rRNA databases (NCBI) using Principal Component and Hierarchical Clustering analyses in SAS and R-program. Made figures and tables and published a paper [2].

University of Washington, Seattle. Affiliate Professor Periodontics, 06/2009 – 06/2017.

Duties:

- Principal Investigator (PI) examining post-transcriptional regulation in stressed zebrafish and mice. Designed massively paralleled C++ programs (+scripts) in Unix environment to manipulate transcript data (see sample programs at

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<http://peteranoble.com/software.html>). Converted transcriptomic sequences to x- and y- coordinates [41] to increase computational efficiency. Mined the data for patterns using Machine Learning tools [25] and performed statistical and network analyses in SAS/JMP, R, Python, and Gephi 0.9. Assembled tables/figures and wrote the manuscript published in BMC Genomics [1].

- PI examining the effects of extreme stress on gene regulation in zebrafish and mice. Discovered 500+ gene transcripts increased in abundance up to 48 to 96 h postmortem. Annotated gene transcripts, assembled the databases, performed statistical analyses, made the figures and tables, wrote the manuscript, obtained consensus among university and institutional collaborators to submit the manuscript for publication [3]. The study is one of the most read (21,000+) in *Open Biology* (http://rsob.royalsocietypublishing.org/front.roysoc_most_read) and has been featured in science magazines including *Science* and *New Scientist* (see press articles written about my lab).
- PI on project examining microbial signatures (biomarkers of disease and health) in the human oral microbiome. Calibrated DNA microarrays (Gene Meters) were used to precisely measure microbial abundances in clinical patients with edentulism, periodontitis, caries and health. Made databases and compared results to those obtained by NGS of the same samples. Conducted statistical analyses of the data in SAS/JMP and R. Assembled the tables, datasets, figures and wrote manuscripts published in peer-reviewed journals [5,10,19].
- Co-PI on two projects: (i) a potential cure for periodontitis by oral microbiome transplant [13] and (ii) preventing microbial corrosion of Ti dental implants [14]. Determined the microbial community composition using NGS and performed bioinformatic and statistical analyses. Assembled tables and figures and co-authored the manuscripts.
- Wrote proposals and financial budgets to NIH and various agencies for research funding. Several proposals were awarded and funded (available on request).

University of Alabama, Birmingham, AL, Adjunct Professor of Microbiology, 06/2010 – (current) and Alabama State University, Montgomery, AL. Full Professor, 06/2009 – 05/2016.

Duties:

- Supervised and trained 30 undergraduate, 5 graduate students and one faculty member in molecular biology (e.g., nucleic acid extraction, cell culture, PCR, emulsion PCR, qPCR, electrophoresis, sequencing library preparation, DNA sequencing, bioinformatics). Analyzed DNA microarray and NGS data (coded in C++; SAS, R-project; R-Bioconductor, SQL; used software to *de novo* assemble bacterial genomes of *Streptococcus* sp. and plasmids). Developed massively paralleled C++ programs (Alabama Supercomputer) to search for patterns in Craig Venter's genome projects.
- Maintained and operated high throughput DNA microarray and NGS laboratories (Whole genome sequencing, amplicon sequencing, RNA-seq) for 6+ years.
- Taught graduate courses in biotechnology, bioinformatics, biostatistics, biochemistry, and microbial physiology.
- Organized and chaired State-wide College Research Symposia (2-day) in 2013, 2014, and 2015 for undergraduate/graduates and faculty science presentations. Served as chair for administrative committees (e.g., curriculum development, faculty recruitment/hires).
- Awarded research proposals and wrote final reports to funding agencies (NSF, NIH, NIJ) (available upon request).
- Served as Editorial Board Member and Associate Editor for peer-reviewed journals (e.g., *Journal for Microbiological Methods* and *Microarrays* (now *High Throughput*)) and *ad hoc* reviewer for high impact journals (e.g., *Nature* and *Nucleic Acids Research*). Served as expert panelist on NIH, NSF, and USDA national funding committees.
- Organized and co-chaired an international genetics meeting entitled "Physicochemical fundamentals of DNA hybridizations on surfaces as applied to microarrays and bead-based sequencing technologies" (<http://www.evolbio.mpg.de/ploenworkshop/>) [17].
- Maintained, organized and chaired meetings with collaborators at the University of California Irvine, the University of Washington Seattle, Max-Planck-Institute for Evolutionary Biology and Savannah River National Laboratory.
- Developed an innovated method to accurately and precisely determine the postmortem interval (i.e., time since death) using gene expression data sets and a massively paralleled matrix algebra algorithm. Tested the models using cross-validation methods and sensitivity analyses. Assembled tables, datasets, figures and wrote the manuscript [4].
- Primary author on invited research and review articles. Designed the tables and figures and wrote peer-reviewed articles: [6-9]. Article 9 was recommended in F1000Prime.

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- PI on project examining biofilms on wastewater treatment aeration diffusers. Sequenced raw DNA and 16S rRNA gene amplicons collected by University of California Irvine collaborators. Conducted bioinformatics analysis of the sequencing output. Assembled the databases and compared raw (metagenomic) sequences to rDNA amplicons. Designed all the tables and figures and wrote the manuscript. Obtained consensus from collaborators to publish [12].
- PI on project examining the microbiome associated with solid organs of cadavers. Designed the study, supervised the graduate student, and sequenced the 16S rRNA gene amplicons. Assembled the sequencing dataset and conducted bioinformatic analysis. Made figures and table and wrote the manuscript which is published [16].
- Co-PI on project that calibrated DNA microarrays using Langmuir and Freundlich models for accurate and precise measurements of gene and transcripts of biological samples. Analyzed the data (SAS) and made all the figures and tables. Wrote most of the manuscript [15].

Research Professor, Engineering, University of Washington, Seattle, 06/2001 – 06/2009.

Duties:

- Supervised 3 undergraduate, 4 graduate and 3 post-doctoral students. Designed experiments and analyzed datasets (C++ programs, SAS, MS Excel). Developed software programs in C++ to analyze nucleic acid sequences (melt temperatures; nearest neighbor model) to help molecular biologists predict experimental outcomes. Built, tested and used machine intelligence software to analyze biological data [18,24,25,34,39]. Extracted equations from the software for integrated software programs (i.e., Deep Learning) [35]. Developed pipelines that linked C++/Java analysis software programs to user-friendly web interfaces. Discovered the physicochemistry of DNA microarrays and wrote research proposals, some of which were award (e.g., NSF, EPA, NIH). Served as panelist on national funding committees for NIH, NSF, and EPA. Designed figures and tables and wrote the following papers: [20-39].
- Designed experiments to study the physicochemistry of DNA/RNA hybridization and washing. Discovered the major sources of noise in DNA microarrays output. Published 4 articles in high impact journal Nucleic Acids Research [17,20,28,31]. Developed and tested various methods to mitigate noise problems (e.g., fingerprint approach) [21,23,29]. Discovered a solution to the ‘noise problem’: calibrated DNA microarrays (i.e., Gene Meters) [15].
- Designed machine-learning software for biologists [25] that uses Levenberg-Marquardt, conjugate gradient and standard back-propagation algorithms and different activation functions (e.g., log sigmoid, hyperbolic tangent, exponential) to model training sets. Performed cross-validation approaches to test models.

Visiting Professor, Max-Planck-Institute for Evolutionary Biology, Ploen, Germany, Spring and Summer, 2010 and Spring 2011.

Duties:

- Learned fundamentals of NGS. Developed the concept of calibrated DNA microarrays to solve the ‘noise problem’.

Expertise

Molecular biology: NGS, polymerase chain reaction (PCR), RT-PCR, emPCR, quantitative RT-PCR, nucleic acid extraction and quantification/qualification (Nanodrop, BioAnalyzer), gene cloning, library preparation, electrophoresis, assay development, biochemistry, genetics/genomics/transcriptomics, pipetting, SNP and CNV typing

Bioinformatics: machine learning/artificial intelligence modeling (see Neuroet software here:

<http://peteranoble.com/software.html>), multivariate data analyses, AUC-ROC analysis, big data analysis (Azure cloud), statistics (SAS, SPSS, R-Program, Bioconductor, C++ custom-designed statistical software for faster iterative analyses, SkLearn, Pandas, Matplotlib), matrix algebra, relational database construction (4th-Dimension, SQL).

Computer Programming: developed C++ standalone software and hundreds of other software programs (e.g., Neuroet, an artificial neural network applications for biologists (see [25] below)).

Leadership: Lead Principal Investigator/collaborator on 7+ international and national science projects involving 50+ scientists; organized and chaired regional, national and international science conferences. Served as panelist expert on national funding review boards: NSF, NIH, EPA, USDA. Served as Associate Editor and Board Member for 4 peer-reviewed journals.

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Teaching and Communication Skills: taught graduate level university courses in Microbiology, Genomics, Biostatistics, Biotechniques, Microbial Physiology, and Instrumentation, laboratory experience; produced Youtube videos for two science publications (see <http://peteranoble/publications.html>).

Supervision/Management: trained/mentored and evaluated hundreds of students, several graduates, post-doctoral students, junior faculty members and visiting professors, troubleshooted their problems.

Writing: designed, organized and published 50+ peer-reviewed papers (my work has featured in many major science magazines including *Science* (twice) and *New Scientist* (twice), technical writing, Designed, organized and wrote about 100 research funding proposals to government agencies (including budgeting and timelines).

Appendix 1. Selected Journal Peer-Reviewed Publications (* indicates primary author). Note: Can be downloaded at <http://peteranoble.com/publications.html>; Not all publications are shown.

2018

1. **Noble P.A.***, Pozhitkov A. (2018) Cryptic sequencing features in the active postmortem transcriptome, *BMC Genomics* 19:675, doi: 10.1186/s12864-018-5042-x. PMID: 30217147
2. Bagwell C.E., **Noble P.A.**, Milliken C.E., Li D., and Kaplan D.I. (2018) Amplicon sequencing reveals microbiological signatures in spent nuclear fuel storage basins. *Frontiers of Microbiology*, 9:377, doi: 10.3389/fmicb.2018.00377. PMID: 29593667

2017

3. Pozhitkov A, Neme R, Domazet-Lošo T, Leroux BG, Soni S, Tautz, D, **Noble PA***. (2017) Tracing the dynamics of gene transcripts after organismal death. *Open Biology*. 7:160267. Cited by: 11. Impact factor of 5.303. March 2018: Most read article in Open Biology in March, 2018 with 18,000+ reads. doi: 10.1098/rsob.160267. PMID: 28123054
4. Hunter MC, Pozhitkov A, **Noble PA***. (2017) Accurate predictions of postmortem interval using linear regression analyses of gene meter expression data. *Forensic Science International*. 275:90–101. Cited by: 7. Impact factor of 2.140. doi: 10.1016/j.forsciint.2017.02.027 PMID: 28329724
5. Hunter MC, Pozhitkov A, **Noble PA***. (2017) Datasets used to discover the microbial signatures of oral dysbiosis, periodontitis and edentulism in humans. *Data in Brief* 10:30–32. doi: 10.1016/j.dib.2016.11.051 PMID: PMC5137327
6. **Noble PA***, Pozhitkov A. (2017) What happens to our genes in the twilight of death? *TheScienceBreaker*, <https://goo.gl/ijq3sm>
7. **Noble PA***, Pozhitkov A. (2017) The postmortem microbiome and gene expression in vertebrates. *The Biochemist* 39:14-17. <http://www.biochemist.org/bio/03902/0014/039020014.pdf>
8. Pozhitkov A. **Noble PA***. (2017b) Gene Meter: accurate abundance calculations of gene expression. *Communicative and Integrative Biology* 10: e1329785. Cited by: 2. Impact factor of 1.56. Youtube video: <https://youtu.be/neb907CQHJc> PMID: 28919937
9. Pozhitkov AE, **Noble PA***. (2017a) Gene expression in the twilight of death. *BioEssays* 39 (9): 1700066, Cited by: 0. Impact factor of 4.725 Youtube video: https://youtu.be/NV1TYz_SbkU PMID: 28787088 **Recommended in F1000PRIME (see DOI: 10.3410/F.727965647.793538051).**

2016

10. Hunter MC, Pozhitkov A, **Noble PA***. (2016) Microbial signatures of oral dysbiosis, periodontitis and edentulism revealed by Gene Meter methodology. *Journal of Microbiological Methods* 131:85-101 Cited by: 8. Impact factor of 2.544. PMID: 27717873
11. Bagwell CE, Abernathy A, Barnwell R, Milliken CE, **Noble PA**, Dale T, Beauchesne KR, Moeller PDR. (2016) Discovery of bioactive metabolites in biofuel microalgae that offer protection against predatory bacteria. *Frontiers in Microbiology* 7:516 Cited by: 1. Impact factor of 4.165. PMID: 27148205
12. **Noble, PA***, Park H-D, Olson BH, Asvapathanagul P, Hunter MC, Rosso D. (2016) A survey of biofilms on wastewater aeration diffusers suggests bacterial community composition and function varies by substrate type and time. *Applied Microbiology and Biotechnology* 100:6361-73. Cited by: 2. Impact factor of 3.3376. PMID: 27294381

2015

13. Pozhitkov A, Leroux B, Randolph TW, Beikler T, Flemmig TF, **Noble PA***. (2015) Towards microbiome transplant as a therapy for periodontitis: an exploratory study of periodontitis microbial signature contrasted by oral health, caries and edentulism. *BMC Oral Health* 15:125. Cited by: 18. Impact factor of: 1.3 PMID: 26468081
14. Pozhitkov A, Daubert D, BrochwiczDonimirski A, Goodgion D, Leroux B, Flemmig T, Hunter C, **Noble PA**, Bryers J.D. (2015) Interruption of electrical conductivity of titanium dental implants suggests a path towards elimination of the implant's corrosion. *PlosOne* 10: e0140393. DOI: 10.1371/journal.pone.0140393, Cited by: 3. Impact factor of 3.730. PMID: 26461491

2014

15. Pozhitkov A, **Noble PA**, Bryk J, Tautz D. (2014) A revised design for microarray experiments to account for experimental noise and the uncertainty of probe response. *PlosOne* 9:e91295. Cited by: 18. Impact factor of 3.730. PMID: 24618910
16. Can I, Javan GT, Pozhitkov AE, **Noble PA***. (2014) Distinctive thanatomicrobiome signatures found in the blood and internal organs of humans. *Journal of Microbiological Methods* 104:1-7. Cited by: 39. Impact factor of 2.544. PMID: 25091187

2013

17. Harrison A, Binder H, Buhot A, Burden C, Carlon E, Gibas C, Gamble L, Halperin A, Hooyberghs J, Kreil D, Levicky R, **Noble PA**, Ott A, Pettitt M, Tautz D, Pozhitkov AE. (2013) Physico-chemical foundations underpinning microarray and next generation sequencing experiments. *Nucleic Acids Research* 41:2779-96. Cited by: 46. Impact factor of: 9.112. PMID: 23307556

2012

18. Kang H-Y, Rule RA, **Noble PA***. (2012) Artificial neural network modeling of phytoplankton blooms using long-term ecological research data sets and its application to sampling sites within the same estuary. *Treatise on Coastal and Estuarine Science* 9.09:161-171. Cited by: 3. Impact factor of: 3.20.

2011

19. Pozhitkov AE., Beikler T, Flemmig T, **Noble PA***. (2011) High-throughput methods for the analysis of human oral microbiome. *Periodontology 2000* 55:70-86. Cited by: 29. Impact factor of: 4.012. PMID: 21134229

2010

20. Pozhitkov AE, Boubeb I, Brouwer MH, **Noble PA***. (2010) Beyond Affymetrix arrays: expanding the set of known hybridization isotherms and observing pre-wash signal intensities. *Nucleic Acids Research* 38:e28. Cited by: 29. Impact factor of: 9.112. PMID: 19969547

2009

21. Rule RA, Pozhitkov AE, **Noble PA***. (2009) Use of hidden correlations in short oligonucleotide array data is insufficient for accurate quantification of nucleic acid targets in complex target mixtures. *Journal of Microbiological Methods* 76:188-195. Cited by: 10. Impact factor of: 2.544. PMID: 19007823

2008

22. Pozhitkov A, Rule RA, Stedtfeld RG, Hashsham SA, **Noble PA***. (2008) Concentration-dependency of nonequilibrium thermal dissociation curves in complex target samples. *Journal of Microbiological Methods*. 74:82-88. Cited by: 10. Impact factor of: 2.544. PMID: 18471911

23. Pozhitkov AE, Nies G, Kleinhenz B, Tautz D, **Noble PA***. (2008). Simultaneous quantification of multiple nucleic acids in target mixtures using high density microarrays. *Journal of Microbiological Methods* 75: 92-102. Cited by: 12. Impact factor of: 2.544. PMID: 18579240
24. Gough, HL, Dahl AL, Tribou E, **Noble PA**, Gaillard J-F, Stahl DA. (2008). Elevated sulfate reduction in metal contaminated freshwater lake sediments. *Journal of Geophysical Research - Biosciences* 113:G04037. Cited by: 10. Impact factor of: 3.303.

2007

25. **Noble PA**, Tribou E. (2007) Neuroet: an easy-to-use artificial neural network for ecological and biological modelling. *Ecological Modelling* 203:87-98. Cited by: 29. Impact factor of: 2.399. Software download is here: <http://peteranoble.com/software.html>
26. Pozhitkov A, **Noble PA***. (2007) Comment on discrimination of shifts in soil microbial communities using nonequilibrium thermal dissociation and gel pad array technology. *Environmental Science and Technology*. 41:1797-1798. Cited by: 7. Impact factor of: 4.764. PMID: 17396676
27. Pozhitkov A, **Noble PA***. (2007) High variability in melting profiles from gel pad arrays. *Environmental Microbiology* 9:1865. Cited by: 4. Impact factor of: 5.843. PMID: 17564621
28. Pozhitkov A, Stedtfeld RG, Hashsham SA, **Noble PA***. (2007) Revision of the nonequilibrium dissociation and stringent washing approaches for identification of mixed nucleic acid targets by microarrays. *Nucleic Acids Research* 35:e70. Cited by: 34. Impact factor of: 9.112. PMID: 17430966
29. Pozhitkov A, Bailey KD, **Noble PA***. (2007) Development of a statistically robust quantification method for microorganisms in mixtures using oligonucleotide microarrays. *Journal of Microbiological Methods* 70:292-300. Cited by: 13. Impact factor of: 2.544. PMID: 17553581
30. Pozhitkov A, Tautz D, **Noble PA***. (2007) Oligonucleotide arrays: widely applied -- poorly understood. *Briefings in Functional Genomics and Proteomics* 6:141-148. Cited by: 76. Impact factor of: 4.210. PMID: 17644526

2006

31. Pozhitkov A, **Noble PA***, Domazet-Lozo T, Nolte A, Sonnenberg R, Staehler P, Beier M, Tautz D. (2006) Tests of rRNA hybridization to microarrays suggest that hybridization characteristics of oligonucleotide probes for species discrimination cannot be predicted. *Nucleic Acids Research* 34:e66. Cited by: 118. Impact factor of: 9.112. PMID: 16707658

2005

32. Lewitus, AJ, White DL, Tymowski RG, Geesey ME, Hymel SN, **P. A. Noble***. (2005) Adapting the CHEMTAX method for assessing phytoplankton taxonomic composition in southeastern U.S. estuaries. *Estuaries* 28:160-172. Cited by: 114. Impact factor of: 2.13.
33. Kelly JJ, Siripong S, McCormack J, Janus LR, Urakawa H., ElFanthroussi S., **Noble PA**, Sappelsa L, Rittmann BE, Stahl DA. (2005) DNA microarray detection of nitrifying bacterial 16S rRNA in wastewater treatment plant samples. *Water Research* 39:3229-3238. Cited by: 97. Impact factor of: 5.315. PMID: 16009395
34. Morris J, Porter D, Neet M, **Noble PA**, Schmidt L, Lapine LA, Jensen J. (2005) Salt and brackish marsh characterization at North Inlet, SC using LIDAR-derived elevation data and land cover extracted from multispectral imagery using a neural network. *International Journal of Remote Sensing* 26:5221-5234. Cited by: 100. Impact factor of: 1.138.
35. Pozhitkov A, Chernov B, Yershov G, **Noble PA***. (2005) Evaluation of gel-pad oligonucleotide microarray technology using artificial neural networks. *Applied and Environmental Microbiology* 71:8663-8676. Cited by: 34. Impact factor of: 4.486. PMID: 16332861

2003

36. Urakawa H, ElFantroussi S, Smidt H, Smoot JC, Tribou E, Kelly JJ, **Noble PA**, Stahl DA. (2003) Optimization of single-base-pair mismatch discrimination in oligonucleotide microarrays. *Applied and Environmental Microbiology* 69:2848-2856. Cited by: 180. Impact factor of: 4.453. PMID: 12732557
37. ElFantroussi S, Urakawa H, Bernhard AE, Kelly JJ, **Noble PA**, Smidt H, Yershov GM, Stahl DA. (2003) Direct profiling of environmental microbial populations by thermal dissociation analysis of native ribosomal rRNAs hybridized to oligonucleotide microarrays. *Applied and Environmental Microbiology* 69:2377-2382. Cited by: 139. Impact factor of: 4.486. PMID: 12676724
38. **Noble PA***, Tymowski RG, Morris JT, Fletcher M, Lewitus AJ. (2003) Contrasting patterns of phytoplankton community pigment composition in two salt marsh estuaries in Southeastern United States. *Applied and Environmental Microbiology* 69:4129-4143. Cited by: 30. Impact factor of: 4.486. PMID: 12839791

2002

39. Urakawa H, **Noble PA***, ElFantroussi S, Kelly JJ, Stahl DA. (2002) Single-base pair discrimination of terminal mismatches by using oligonucleotide microarrays and neural network analyses. *Applied and Environmental Microbiology* 68:235-244. Cited by: 142. Impact factor of: 4.486. PMID: 11772632
40. Ogunseitan OA, LeBlanc J, **Noble PA**. (2002) Ecological dimensions of microbial proteomics. *Recent Research Developments in Microbiology* 6:487-501.

2001

41. Almeida JS, Carrico JA, Marezek A, **Noble PA**, Fletcher M. (2001) Analysis of genomic sequences by chaos game representation. *Bioinformatics* 17:429-437. Cited by: 196. Impact factor of: 5.468. PMID: 11331237

2000

42. **Noble PA***, Almeida JS, Lovell CR. (2000) Application of neural computing methods for interpreting phospholipid fatty acid profiles from natural microbial communities. *Applied and Environmental Microbiology* 66:694-699. Cited by: 53. Impact factor of: 4.486. PMID: 10653738
43. Almeida JS, **Noble PA***. (2000) Neural computing in microbiology. *Journal of Microbiological Methods* 43:1-2. Cited by: 5. Impact factor of: 2.544. PMID: 11084224

1999

44. **Noble PA***. (1999) Minireview: a hypothetical model for monitoring microbial growth by using capacitance measurements. *Journal of Microbiological Methods* 37:45-49. Cited by: 33. Impact factor of: 2.544. PMID: 10395463
45. **Noble PA***, Dziuba M, Harrison DJ, Albritton WL. (1999) Factors influencing capacitance-based monitoring of microbial growth. *Journal of Microbiological Methods* 37, 51-64. Cited by: 36. Impact factor of: 2.544. PMID: 10395464
46. Piceno YM, **Noble PA**, Lovell CR. (1999) A comparison of diazotroph assemblages in two vegetated salt marsh zones using denaturing gradient gel electrophoresis (DGGE) analysis. *Microbial Ecology* 38:157-167. Cited by: 94. Impact factor of: 2.912.