

PETER ANTHONY NOBLE

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Career Summary

A scientist (Principal Investigator/Full Professor) with an interdisciplinary background in: critical thinking, solving problems, innovative discoveries, training scientists, and leading (and working within) collaborative relationships. I have published 50+ peer-reviewed articles in microbiology, engineering, transcriptomics, genomes, DNA microarrays, Next-Gen-Sequencing, statistics and bioinformatics [see Appendix 1].

Education

Postdoctoral training in Bioinformatics, University of Maryland Center of Marine Biotechnology

Postdoctoral training in Molecular Biology, University of California Irvine

Ph.D. in Applied Microbiology, University of Saskatchewan

Teaching Diploma in Science Education, University of British Columbia

M.Sc. and B.Sc. Honors degrees in Biology, Memorial University of Newfoundland

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

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

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

Work Experience

Visualization of Gene/Protein Expression System Networks. Sabbatical leave, Tucson Arizona 03/2020 to present.

Duties:

- ANOVAs of the mouse protein/transcript abundances (7 sampling times, each with 2 to 4 replicates) were conducted on 1331 mandible proteins, 37364 brain gene transcripts and 37364 liver transcripts. Protein/transcripts not significantly changing in abundance (FDR of 0.05) were excluded. STRING software (<https://version-11-0b.string-db.org>) was used to determine the relationships among the proteins/transcripts. The STRING database contains known and predicted protein-protein interactions determined from computational prediction and from interactions aggregated from other (primary) databases. A custom designed C++ program was built to modify the STRING output (SVG) files so that transcripts/proteins that increased or decreased in abundance relative to baseline were colored red or blue, respectively. The transcript/protein system networks were visualized by bundling the modified files as a movie (Krita software) that shows how gene/protein abundances change through postmortem time (videos at <http://peteranoble.com/Current.html>). I am currently writing a peer-reviewed publication on this research. The novel approach can be used to study system dynamics associated with disease and cancer.

Prokarma/Health Care Analytics, Denver CO, 11/2018 to 03/2020.

Duties:

- Predictive analytics anticipate future medical expenses, resource management, and assess patient needs. To address these issues, I developed novel software and databases (see ‘Analytics to predict future ICD codes based on Bayesian probabilities and network analyses’ on peteranoble.com/software.html) to map ICD10 (International Statistical Classification of Diseases) networks of patients using Bayesian probabilities and R. The database was based on multiple visits of 91000+ patients and enables prediction of disease progression/risk.
- Patient readmissions are a substantial financial burden to healthcare systems. One challenge is to identify patients at risk of readmission. I solved this problem by building a Predictive Re-Admission Calculator using artificial intelligence (AI) and 31,885 electronic patient records. The Calculator provided superior predictive power to existing methods in terms of the number of false negative and false positives as documented here: “*How to Use AI to Circumvent Hospital Readmissions and Improve Patient and Business Outcomes*”, Healthcare Business Today, April 25, 2019 and “Predicting Hospital Readmissions Using AI” (publication web page).

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- Developed Natural Language Processing (NLP) pipeline in C++ because the popular SpaCy was too slow. The program identified smokers from non-smokers in thousands of unstructured electronic medical records with a performance AUC of 0.94. Programs, tutorials and a Powerpoint presentations are available here: <http://peteranoble.com/software.html>
- Developed NLP approach using SpaCy in Jupyter notebooks for extracting information (patient age, gender, diagnosis, procedures and drugs) from autopsy reports and physician transcripts.

Prokarma/Union Pacific Railway/Omaha NE, System Data Scientist, 06/2018-11/2018.**Duties:**

- Estimated “final arrival times” of ~20,000 cargo trains passing through more than 12,849+ ping 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 my software web site under Azure Cloud computing). 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. The research is an example of BIG data analysis since there were millions of rows and thousands of columns of data.

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 the 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 Full 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 a Unix environment to manipulate transcript data (see sample programs at <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].
- 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 National Institute of Health (NIH) and various agencies for research funding. Some 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 of Microbiology, 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,

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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.

- Managed, maintained and operated high throughput DNA microarray and NGS laboratories (Whole genome sequencing, amplicon sequencing, RNA-seq) for 6+ years.
- Taught 10 graduate-level 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 (National Science Foundation (NSF), National Institute of Health (NIH), National Institute of Justice (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 to 9]. Article 9 was recommended in F1000Prime.
- 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 analyses. 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 manuscript [15].

Research Professor, Civil and Environmental 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 National Institute of Health (NIH), National Science Foundation (NSF), and Environmental Protection Agency (EPA). Designed figures and tables and wrote the following papers: [20 to 39].
- Designed experiments to study the physico-chemistry of DNA/RNA hybridization and washing. Discovered the major sources of noise in DNA microarrays output. Published 4 articles in the high impact journal 'Nucleic Acids Research'

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[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 used 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, 2010 and Spring 2011.

Duties:

- Learned fundamentals of Next-Generation DNA Sequencing (NGS). Developed the concept of calibrated DNA microarrays to solve the ‘noise problem’.

Visiting Scholar, Engineering, Northwestern University, Evanston, IL. Summer, 1999.

Expertise

Molecular biology: Next-Generation DNA Sequencing, polymerase chain reaction (PCR), RT-PCR, emulsion PCR, 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 and other bioinformatics (e.g., sequence alignment and mining).

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

<http://peteranoble.com/software.html>), multivariate data analyses, ROC-AUC analysis, big data analysis (Azure cloud), statistics (SAS, SPSS, R-Program, C++ custom-designed statistical software for faster iterative analyses, SkLearn, Pandas, Matplotlib, NumPy, R), matrix algebra, relational database construction (4th-Dimension, SQL). Visualization of transcript/protein system networks using STRING, custom-designed software to manipulate SVG files and Krita for making movies for publication and web sites.

Computer Programming: developed C++ standalone software and hundreds of other software programs (e.g., Neuroet, an artificial intelligence 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 expert panelist on national funding review boards: NSF, NIH, EPA, USDA. Served as Associate Editor and Board Member for 4 peer-reviewed journals and Editor-in-Chief of Death Research (Mary Ann Liebert, Inc.)

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 university students, several graduates, post-doctoral students, junior faculty members and visiting professors.

Writing: designed, organized and published 50+ peer-reviewed papers (my work has featured in 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: Publications 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, Cited by: 1; 1532 views, 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: 36. Altmetric Score: 344; Downloaded: 30,076 times. March 2018: Most read article in Open Biology with 30,000+ 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: 17. Altmetric Score: 14; 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 PMCID: PMC5137327
6. **Noble PA***, Pozhitkov A. (2017) What happens to our genes in the twilight of death? *TheScienceBreaker*, <https://goo.gl/iqj3sm>
7. **Noble PA***, Pozhitkov A. (2017) The postmortem microbiome and gene expression in vertebrates. *The Biochemist* 39:14-17. Cited by: 1. <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: 4. 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: 6. Altmetric Score: 4, 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: 17. 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: 11. 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: 5. 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: 30. 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* 13: e0140393. DOI: 10.1371/journal.pone.0140393, Cited by: 13. 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: 22. 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: 68. 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: 55. 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: 5. 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: 37. 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: 32. 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: 14. 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: 15. 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: 37. 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: 4. 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: 5. 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: 33. 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: 83. 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: 119. 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: 127. 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: 108. 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: 116. 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: 36. 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: 189. 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: 141. 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: 35. 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: 143. 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, Maretzek A, **Noble PA**, Fletcher M. (2001) Analysis of genomic sequences by chaos game representation. *Bioinformatics* 17:429-437. Cited by: 221. 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: 61. 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: 8. 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: 38. 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: 38. 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: 103. Impact factor of: 2.912.
47. **Noble, P.A.**, R.W. Citek, and D.A. Ogunseitan. (1998) Tetranucleotide frequencies in microbial genomes. *Electrophoresis* 19:528-535. Cited by: 31.
48. **Noble, P.A.**, K.D. Bidle, and M. Fletcher (1997) Natural microbial community compositions compared by a back-propagating neural network and cluster analysis of 5S rRNA. *Applied and Environmental Microbiology* 63:1762-1770. Cited by 62.

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49. **Noble, P.A.**, D.L. Clark, and B.H. Olson (1996) Biological stability of ground water treated for organic carbon removal by conventional and membrane filtration methods. *Journal of the American Water Works Association* 88:87-96. Cited by 28.
50. Albritton, W.L., **P.A. Noble**, and K.D. Webster (1994) Clarification of the plasmid RSF0885 in *Haemophilus influenzae* serotype b. *Canadian Journal of Microbiology* 40:154-157. Cited by 1.
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