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Career Summary

A scientist (Principal Investigator/Full Professor) with an interdisciplinary background in: critical thinking, problem-solving, innovative discoveries, training scientists, and leading and working within collaborative relationships. I have published numerous peer-reviewed articles in microbiology, engineering, transcriptomics, genomes, DNA microarrays, Next-Gen Sequencing, statistics, and Artificial Intelligence [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 and preprints: <http://peteranoble.com/publications.html>

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

Press articles: <http://peteranoble.com/press.html>

Work Experience

Chief Science Officer, BuddyEngineer, 07/2023 to now.

Duties:

- Built Convolutional Neural Network (CNN) software for classifying Dog Emotions (images and sounds) in PyTorch. Sound wave files were converted to spectrograms, MFCCs, pitch tracking, and waveforms to serve as inputs to the model. The accuracy matched the best on the internet (see <http://peteranoble.com/software>).
- Built CNN software for classifying sugarcane leaf disease images in PyTorch. The accuracy matched the best on the internet (see <http://peteranoble.com/software>).
- Wrote a manuscript entitled "Unraveling the Enigma of Organismal Death: Insights, Implications and Unexplored Frontiers" based on an NIH-sponsored workshop. Published: <https://pubmed.ncbi.nlm.nih.gov/38624244/>
- Built a Stone Decision Engine web interface predicting kidney stone removal success and treatment complications for shock wave lithotripsy and laser ureteroscopy patients: <http://peteranoble.com/webapps.html>

- Published: <https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0301812>
- Published: <https://www.preprints.org/manuscript/202405.2160/v1>
- Wrote a NIH SBIR grant proposal entitled "An Automated Ethanol Vapor Generating System for Alcohol Use Disorder (AUD) Animal Studies.

Chief Science Officer, Translation and Analytical Statistics, Arizona 09/2021 to 07/2023.

Duties:

- Developed calibrated models for monitoring the fragmentation of kidney stones during shock wave lithotripsy. Developed AI models to predict lithotripsy parameters (power level, shock rate, and shock counts) using machine learning techniques like random forests and support vector machines.
- Developed a kidney stone decision engine (SDE) using statistical modeling and machine learning algorithms. The SDE aids physicians to make informed choices on the most suitable procedure for stone fragmentation (laser or shock wave lithotripsy) based on factors such as stone composition, size, location, and patient demographics.

Principal Investigator, Visualization of Gene/Protein Expression System Networks. Sabbatical leave, Tucson Arizona 03/2020 to 09/2021.

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>) determined 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 (<http://peteranoble.com/Current.html>).

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

Duties:

- Developed predictive analytics to anticipate future medical expenses, resource management, and assess patient needs (see 'Analytics to predict future ICD codes based on Bayesian probabilities and network analyses' on peteranoble.com/software.html) using Bayesian probabilities and R. The database was based on multiple visits of 91000+ patients and enables prediction of disease progression/risk.
- Identified patients at risk of readmission 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).

- Developed Natural Language Processing (NLP) pipeline in C++. 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>

System Data Scientist, Prokarma/Union Pacific Railway/Omaha NE, 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.

Affiliate Professor Periodontics, University of Washington, Seattle. 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 [44] to increase computational efficiency. Mined the data for patterns using Machine Learning tools [28] 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 [4].
- 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 [6].
- 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 [8,13,20].
- Co-PI on two projects: (i) a potential cure for periodontitis by oral microbiome transplant [16] and (ii) preventing microbial corrosion of Ti dental implants [17].

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).

Professor of Microbiology, University of Alabama, Birmingham, AL, 06/2010 – (current) and Alabama State University, Montgomery, AL., 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.
- Managed, maintained and operated high throughput DNA microarray and NGS laboratories (Whole genome sequencing, amplicon sequencing, RNA-seq) for 6+ years.
- Taught 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 from National Science Foundation (NSF), National Institute of Health (NIH), National Institute of Justice (NIJ)).
- 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/>) [20].
- 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 [7].

- Primary author on invited research and review articles. Designed the tables and figures and wrote peer-reviewed articles: [9, 10, 12]. Article 12 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 [15].
- 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 [19].
- 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 [18].

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 [21,27,28,37,42]. Extracted equations from the software for integrated software programs (i.e., Deep Learning) [38]. 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: [23 to 42].
- 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 the high impact journal ‘Nucleic Acids Research’ [20,23,31,34]. Developed and tested various methods to mitigate noise problems (e.g., fingerprint approach) [23,26,31]. Discovered a solution to the ‘noise problem’: calibrated DNA microarrays (i.e., Gene Meters) [11, 18].
- Designed machine-learning software for biologists [28] 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 Next-Generation DNA Sequencing (NGS). Developed calibrated DNA microarrays to solve ‘noise problems’.

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

Career Expertise

Molecular biology (hands-on): 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, Next-Generation DNA Sequencing, SNP and CNV typing.

Bioinformatics and AI modeling: 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; Jupyter Notebooks), 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. Web interfaces between C++ programs and user input/output (<http://peteranoble.com/webapps.html>).

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

Leadership: 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.

Teaching and Communication Skills: Taught graduate 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 100’s of university students, 5+ graduates, 2 post-doctoral students, 1 junior faculty member and 1 visiting professor.

Writing: designed, organized and published many peer-reviewed papers.

Appendix 1. Peer-Reviewed Publications and Preprints (*primary author).

2024

1. Noble, PA*. Smart Computer Program to Assist Healthcare Providers in Selecting the Best Treatment for Patients with Urinary Stones. Preprints 2024, 2024052160. <https://doi.org/10.20944/preprints202405.2160.v1>
2. Noble PA*, Pozhitkov A, Singh K, Woods E., Liu CY, Levin M, Javan G, Wan J, Abouhashem AA, Mathew-Steiner SS, Sen CK (2024) Unraveling the enigma of organismal death: insights, implications and frontiers, *APS Physiology* (<https://pubmed.ncbi.nlm.nih.gov/38624244/>).
3. Noble PA*, Hamilton BD., Gerber G (2024) Stone Decision Engine accurately predicts kidney stone removal and treatment complications for shock wave lithotripsy and laser ureterorenoscopy patients, *PlosOne* (<https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0301812>)

2018

4. Noble PA*, Pozhitkov A. (2018) Cryptic sequencing features in the active postmortem transcriptome, *BMC Genomics* 19:675, Cited by: 3. doi: 10.1186/s12864-018-5042-x. PMID: 30217147
5. Bagwell CE, Noble PA, Milliken CE, Li D, and Kaplan DI. (2018) Amplicon sequencing reveals microbiological signatures in spent nuclear fuel storage basins. *Frontiers of Microbiology*, 9:377, Cited by: 12. doi: 10.3389/fmicb.2018.00377. PMID: 29593667

2017

6. 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: 67. doi: 10.1098/rsob.160267. PMID: 28123054
7. 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: 14. doi: 10.1016/j.forsciint.2017.02.027 PMID: 28329724
8. 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 Cited by: 1. PMID: 28123054
9. Noble PA*, Pozhitkov A. (2017) What happens to our genes in the twilight of death? *TheScienceBreaker*, <https://goo.gl/ijq3sm>
10. 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>
11. Pozhitkov A. Noble PA*. (2017b) Gene Meter: accurate abundance calculations of gene expression. *Communicative and Integrative Biology* 10: e1329785. Cited by: 3. PMID: 28919937 Youtube video: <https://youtu.be/neb907CQHJc>
12. Pozhitkov AE, Noble PA*. (2017a) Gene expression in the twilight of death. *BioEssays* 39 (9): 1700066, Cited by: 7. PMID: 28787088 Recommended in

F1000PRIME (see DOI: 10.3410/F.727965647.793538051) Youtube video:
https://youtu.be/NV1TYz_SbkU.

2016

13. 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: 14. PMID: 27717873
14. 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: 18. PMID: 27148205
15. 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: 7. PMID: 27294381

2015

16. 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: 44. PMID: 26468081
17. 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: 19. PMID: 26461491

2014

18. 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
19. 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: 113. PMID: 25091187

2013

20. 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: 48.

2012

21. 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: 8. Impact factor of: 3.20.

2011

22. 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: 31. PMID: 21134229

2010

23. 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: 23. PMID: 19969547

2009

24. 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: 5. PMID: 19007823

2008

25. 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: 8. PMID: 18471911
26. 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: 7. PMID: 18579240
27. 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: 11.

2007

28. 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.
29. 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: 8. PMID: 17396676
30. Pozhitkov A, Noble PA*. (2007) High variability in melting profiles from gel pad arrays. *Environmental Microbiology* 9:1865. Cited by: 4. PMID: 17564621
31. 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: 28. PMID: 17430966

32. 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: 11. PMID: 17553581
33. Pozhitkov A, Tautz D, Noble PA*. (2007) Oligonucleotide arrays: widely applied -- poorly understood. *Briefings in Functional Genomics and Proteomics* 6:141-148. Cited by: 55. PMID: 17644526

2006

34. Pozhitkov A, Noble PA*, Domazet-Loso 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: 96. PMID: 16707658

2005

35. Lewitus, AJ, White DL, Tymowski RG, Geesey ME, Hymel SN, Noble PA*. (2005) Adapting the CHEMTAX method for assessing phytoplankton taxonomic composition in southeastern U.S. estuaries. *Estuaries* 28:160-172. Cited by: 97.
36. Kelly JJ, Siripong S, McCormack J, Janus LR, Urakawa H., ElFantroussi 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: 73. PMID: 16009395
37. 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: 113.
38. 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. PMID: 16332861

2003

39. 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: 126. PMID: 12732557
40. 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: 98. PMID: 12676724
41. 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: 29. PMID: 12839791

2002

42. 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: 101. PMID: 11772632
43. Ogunseitan OA, LeBlanc J, Noble PA. (2002) Ecological dimensions of microbial proteomics. *Recent Research Developments in Microbiology* 6:487-501.

2001

44. 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: 179. PMID: 11331237

2000

45. 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: 38. PMID: 10653738
46. Almeida JS, Noble PA*. (2000) Neural computing in microbiology. *Journal of Microbiological Methods* 43:1-2. Cited by: 10. PMID: 11084224

1990-1999

47. Noble PA*. (1999) Minireview: a hypothetical model for monitoring microbial growth by using capacitance measurements. *Journal of Microbiological Methods* 37:45-49. Cited by: 32. PMID: 10395463
48. 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: 31. PMID: 10395464
49. 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: 71.
50. Noble, PA, R.W. Citek, D.A. Ogunseitan. (1998) Tetranucleotide frequencies in microbial genomes. *Electrophoresis* 19:528-535. Cited by: 31.
51. Noble, PA, K.D. Bidle, 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 51.
52. Noble, PA, D.L. Clark, 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 18.
53. Albritton, WL, Noble PA, Webster KD. (1994) Clarification of the plasmid RSF0885 in *Haemophilus influenzae* serotype b. *Canadian Journal of Microbiology* 40:154-157. Cited by 1.
54. Dasgupta, MK, Ward K, Noble PA, Larabie M, Costerton JW. (1994) Development of bacterial biofilms on silastic catheter materials in peritoneal dialysis fluids. *American Journal of Kidney Diseases* 23:709-716. Cited by 32.

55. Dziuba, M, Noble PA, and Albritton WL. (1993) A study of the nutritional requirements of a selected *Haemophilus ducreyi* strain by impedance and conventional methods. *Current Microbiology* 27:109-113. Cited by 6.
56. Noble PA, Ashton E, Davidson CA, and Albritton WL. (1991) Heterotrophic plate counts of surface water samples by using impedance methods, *Applied and Environmental Microbiology* 57:3287-3291. Cited by 22.
57. Noble PA, Dabinett PE, Gow JA. (1990) Numerical taxonomic study of pelagic and benthic surface-layer bacteria in seasonally-cold coastal waters. *Systematic and Applied Microbiology* 13:77-85. Cited by 8.