# Peter Anthony Noble PhD

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## Career Statement

Senior scientist (Full Professor) with an interdisciplinary background in critical thinking, solving problems, and making innovative discoveries, with experience in training scientists. I have managed and worked on national and international projects, all of which have been peer-reviewed and published across diverse fields, including artificial intelligence, microbiology, engineering, transcriptomics, genomics, and statistics (see Appendix 1). My goal is to leverage my expertise and skills to solve problems in medicine and industry, such as building intelligent machines to address healthcare challenges (see Refs. 1 to 7).

## Education

Postdoctoral fellow in Bioinformatics, University of Maryland Baltimore
Postdoctoral fellow 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

## Accomplishments

Peer-reviewed articles and preprints: http://peteranoble.com/publications.html
Discoveries: http://peteranoble.com/discoveries.pdf
Software and tutorial programs: http://peteranoble.com/software.html
Popular Press articles: http://peteranoble.com/press.html

## Work Experience

### Chief Scientist, Sabbatical Leave, 07/2023 to now.

**Duties:**

- Filed US patents: 63/796,696 and 19/192,086.
- Pending Publication: AI-Driven Solutions to Fragment Urinary Stones During Deep Space Missions and Beyond. The Conversation, Youtube: https://youtu.be/ej2jaY5_bAI
- Publication: Real-time Monitoring of Urinary Stone Status During Shockwave Lithotripsy. Urology, http://dx.doi.org/10.2139/ssrn.5226785 Youtube: https://youtu.be/42aP4Eq8qPw
- Published: https://arxiv.org/abs/2502.07860
- Built Convolutional Neural Networks (CNNs) to detect urinary tract stones in 11,000 C-arm X-ray images. The optimized software consists of 4 CNN layers, built using Python in Jupyter Notebooks. The weights and biases were extracted and incorporated into User-interface app using C++ and OpenCV. Developed traffic light signaling to assist operators in appropriate delivery that maximizes shockwaves while minimizing

treatment complications. Wrote paper on the automated shockwave delivery system for treatment of urinary tract stones (above).

- Built CNN software to classify Dog Emotions (images and sounds) in PyTorch. Sound wave files converted to spectrograms, MFCCs, pitch tracking, and waveforms served as inputs to the model. The accuracy matched the best on the Web (see http://peteranoble.com/software).
- Built CNN software for classifying sugarcane leaf disease images. The accuracy matches those on Kaggle (see http://peteranoble.com/software).
- Built Stone Decision Engine web interface: http://peteranoble.com/webapps.html
- Published: https://pubmed.ncbi.nlm.nih.gov/38696418/
- Published: https://www.opastpublishers.com/citation/a-smart-computer-program-to-assist-healthcare-providers-in-selecting-the-best-treatment-for-patients-with-urinary-stones-7768.html
- Published: https://pubmed.ncbi.nlm.nih.gov/38624244/
- Published: https://theconversation.com/biobots-arise-from-the-cells-of-dead-organisms-pushing-the-boundaries-of-life-death-and-medicine-238176?fbclid=IwY2xjawFP6-NleHRuA2FlbQIxMAABHazPuYGxWrSi5XoSeSTzIQCPFQV__NTlYu-4PT9F_7QUG2zZSH2wZpA1yw_aem_i6L5v1JkwLN7QEFDL1Akig
- Published: https://onlinelibrary.wiley.com/doi/10.1002/bies.202400158
- Wrote NIH SBIR grant proposal: "An Automated Ethanol Vapor Generating System for Alcohol Use Disorder (AUD) Animal Studies".

**Chief Scientist, NextMed, Tucson, Arizona 09/2021 to 07/2023.**
**Duties:**

- Developed calibrated models for monitoring the fragmentation of urinary stones.
- Developed AI stone decision engine (SDE) that helps physicians make informed decisions on the optimal procedure for stone fragmentation (laser or shock wave lithotripsy) based on stone composition, size, location, and patient metrics.

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

- ANOVA of the mouse protein/transcript abundances for 1331 mandible proteins, 37364 brain gene transcripts and 37364 liver transcripts. STRING software (https://version-11-0b.string-db.org) determined the relationships among the proteins/transcripts.
- Custom C++ program 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. 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:**

- Predictive analytics to anticipate future medical expenses, resource management, and assess patient needs using Bayesian probabilities and R. The database was based on multiple visits of 91000+ patients and enables prediction of disease progression/risk.
- Calculator for 'Predictive Re-Admission of Patients at Risk' using AI and 31,885 electronic patient records. See "*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" on publication web page.

- Natural Language Processing (NLP) pipeline to identify smokers from non-smokers in thousands of unstructured electronic medical records. Programs, tutorials and a Powerpoint presentations are 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.

**Professor Periodontics, University of Washington, Seattle. 06/2009 – 06/2017.**
**Duties**:

- Examined microbial signatures (biomarkers of disease and health) in the human oral microbiome. Calibrated DNA microarrays (Gene Meters) measured microbial abundances in patients with edentulism, periodontitis, caries and health. Conducted statistical analyses of the data in SAS/JMP and R.
- Published: (i) a potential cure for periodontitis by oral microbiome transplant and (ii) a method to prevent microbial corrosion of Ti dental implants.
- Post-transcriptional regulation in stressed zebrafish and mice. Designed massively paralleled C++ programs (with Unix scripts) to manipulate transcript data. Converted transcriptomic sequences to *x*- and *y*- coordinates 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. Published in BMC Genomics.
- 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.

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

- Supervised 30 undergraduate, 5 graduate students and 1 faculty member in molecular biology techniques (e.g., nucleic acid extraction, cell culture, PCR, emulsion PCR, qPCR, electrophoresis, 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 and operated high throughput DNA microarray and sequencing laboratories (Whole genome sequencing, amplicon sequencing, RNA-seq) for 6+ years.

- Taught graduate-level courses in biotechnology, bioinformatics, biostatistics, biochemistry, and microbial physiology.
- Chaired State-wide College Research Symposia in 2013, 2014, and 2015 for undergraduate/graduates and faculty science presentations.
- Chair for administrative committees (e.g., curriculum development, faculty recruitment/hires).
- Awarded research proposals from National Science Foundation (NSF), National Institute of Health (NIH), and National Institute of Justice (NIJ).
- Served as Editorial Board Member 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 for NIH, NSF, and USDA national funding committees.
- 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/).
- 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 a new method to 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.
- Biofilms on wastewater treatment aeration diffusers. Sequenced raw DNA and 16S rRNA gene amplicons collected by University of California Irvine collaborators.
- Examined microbiome associated with solid organs of cadavers.
- Co-Investigator on project that calibrated DNA microarrays using Langmuir and Freundlich models for accurate and precise measurements of gene transcripts.

**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 predict experimental outcomes. Built, tested and used machine intelligence software to analyze biological data. Extracted equations from the software for integrated software programs (i.e., Deep Learning). Developed pipelines to link C++/Java analysis software programs to user-friendly web interfaces. Wrote research proposals to: NSF, EPA, NIH.
- Panelist on national funding committees for National Institute of Health (NIH), National Science Foundation (NSF), and Environmental Protection Agency (EPA)..
- Studied 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'. Tested methods to mitigate noise problems (e.g., fingerprint approach). Discovered a solution to the 'noise problem': calibrated DNA microarrays (i.e., Gene Meters).
- Designed machine-learning software (Neuroet) 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. Cross-validation approaches were used to validate Neuroet.

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

## 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. Built Web interfaces: 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 below). Converting and transforming image files (Magick) and arrays. Detecting target patterns in arrays and images.

Leadership: Principal Investigator/collaborator on 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 four 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).

### 2025

1. Noble, PA*. (2025) AI-Driven Solutions to Fragment Urinary Stones During Deep Space Missions and Beyond. TBD. Youtube: https://youtu.be/ej2jaY5_bAI

2. Noble, PA*. (2025) Real-time Monitoring of Urinary Stone Status During Shockwave Lithotripsy. Urology (in review); http://dx.doi.org/10.2139/ssrn.5226785 ; Youtube https://youtu.be/42aP4Eq8qPw

3. Pozhitkov A., Noble P.A. (2025) Design of an Automated Ethanol Vapor Generating System for Alcohol Use Disorder (AUD) Animal Studies. Arxiv 2502.07860 [https://arxiv.org/abs/2502.07860].

### 2024

4. Noble, PA* and Pozhitkov A. (2024) Perspective on death: a gateway to a new biology. BioEssays 47(3) https://doi.org/10.1002/bies.202400158.

5. Noble, PA*. (2024) A Smart Computer Program to Assist Healthcare Providers in Selecting the Best Treatment for Patients with Urinary Stones. Adv J Uro Nephro, 6(1), 01-05.
6. 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, Physiology (https://pubmed.ncbi.nlm.nih.gov/38624244/).
7. 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

8. 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
9. 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

10. 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
11. 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
12. 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. PMCID: PMC5137327

13. Noble PA*, Pozhitkov A. (2017) What happens to our genes in the twilight of death? TheScienceBreaker, https://goo.gl/iqj3sm

14. 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

15. 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

16. 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**

17. 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

18. 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

19. 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**

20. 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

21. 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**

22. 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

23. 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**

24. 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**

25. 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**

26. 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**

27. 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**

28. 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**

29. 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
30. 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
31. 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**

32. 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
33. 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
34. Pozhitkov A, Noble PA*. (2007) High variability in melting profiles from gel pad arrays. Environmental Microbiology 9:1865. Cited by: 4. PMID: 17564621
35. 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
36. 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

37. 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**

38. 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**

39. 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.
40. 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
41. 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.
42. 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**

43. 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
44. 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
45. 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**

46. 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
47. Ogunseitan OA, LeBlanc J, Noble PA. (2002) Ecological dimensions of microbial proteomics. Recent Research Developments in Microbiology 6:487-501.

**2001**

48. 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: 179. PMID: 11331237

## 2000

49. 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
50. Almeida JS, Noble PA*. (2000) Neural computing in microbiology. Journal of Microbiological Methods 43:1-2. Cited by: 10. PMID: 11084224

## 1990-1999

51. 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
52. 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
53. 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.
54. Noble, PA, R.W. Citek, D.A. Ogunseitan. (1998) Tetranucleotide frequencies in microbial genomes. Electrophoresis 19:528-535. Cited by: 31.
55. 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.
56. 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.
57. 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.
58. 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.
59. 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.
60. 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.
61. 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.