

Michael C. Wendl

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Dr. Wendl is broadly interested in the mathematical theory underlying pressing problems in the biomedical and engineering sciences. He has participated in many of the pioneering “big-biology” efforts of our time, including the Human Genome Project (HGP), and is lately part of a research group at the Washington U. Genome Institute focusing on cancer genomics and biophysics. He is a leading expert in the industrial engineering aspects of DNA sequencing, having published several of the seminal papers in this area (see e.g. “DNA sequencing theory” on Wikipedia), is an enthusiastic instructor and mentor, a proponent of mathematical and scientific literacy for the general public, and is interested in policy issues related to research, science, technology, and education.

- BS *cum laude* ('89), MS ('90), and Doctorate ('94) all from Washington U. with a dissertation on the incompressible form of the Navier–Stokes equations under R. K. Agarwal, PhD
- Postdoc ('94–'97) Washington U. GSC: Phred base-calling algorithm and other bioinformatics infrastructure under R. H. Waterston, MD, PhD
- more than a decade of continuous teaching experience in the Washington U. School of Engineering and U. Missouri joint program with emphasis on undergraduate thermo–fluid science courses
- 39 research publications in high-impact journals plus various book chapters, op-ed pieces, and conference papers covering topics in molecular biology, mathematics, and physics & engineering science — Google Scholar reports >15,500 citations to this work, including HGP (~8,000) and mouse sequence papers (~2,600), and Phred paper (~3,500).
- referee for Bioinformatics, Genome Res., J. Appl. Probability, Nature journals, Phys. Rev. journals, PLoS journals, Science, *et al.*; NSF & NIH referee; thesis/dissertation and search committees; high-school career outreach and individual undergraduate summer mentoring

Representative Peer-Reviewed Publications

1. **Wendl, M. C.** *et al.* (2011) “PathScan: A Tool for Discerning Mutational Significance in Groups of Putative Cancer Genes”, *Bioinformatics*, **27** (12), 1595–1602.
2. **Wendl, M. C.** and Wilson, R. K. (2009) “Statistical Aspects of Discerning Indel-Type Structural Variation via DNA Sequence Alignment”, *BMC Genomics*, **10** (article number 359).
3. **Wendl, M. C.** (2008) “Random Covering of Multiple One-Dimensional Finite Domains with an Application to DNA Sequencing”, *SIAM Journal on Applied Mathematics*, **68** (3), 890–905.
4. **Wendl, M. C.** (2005) “Probabilistic Assessment of Clone Overlaps in DNA Fingerprint Mapping via *a priori* Models”, *Journal of Computational Biology*, **12** (3), 283–297.
5. **Wendl, M. C.** (2003) “Collision Probability Between Sets of Random Variables”, *Statistics & Probability Letters*, **64** (3), 249–254.
6. **Wendl, M. C.** (2001) “Mathematical Analysis of Coaxial Disk Cellular Shear Loading Devices”, *Review of Scientific Instruments*, **72** (11), 4212–4217.
7. **Wendl, M. C.** (1999) “General Solution for the Couette Flow Profile”, *Physical Review E*, **60** (5), 6192–6194.
8. Ewing, B., Hillier, L., **Wendl, M. C.**, and Green, P. (1998) “Base-calling of Automated Sequencer Traces Using PHRED. I. Accuracy Assessment”, *Genome Research*, **8** (3), 175–185.