

## Dr Dawn Field, Centre for Ecology & Hydrology

### Publications (73) – June 2010: 4 in review, 7 in preparation

1. Mitra S, Gilbert JA, Field D, Huson DH. (2010) Comparison of multiple metagenomes using phylogenetic networks based on ecological indices. *ISME J.* 2010 Apr 29. [Epub ahead of print]
2. Sterk P, Hirschman L, Field D, Wooley J. (2010) Genomic standards consortium workshop: metagenomics, metadata and metaanalysis (m3). *Pac Symp Biocomput.* :481-4.
3. Field D, Sansone SA, Collis A, Booth T, Dukes P, Gregurick SK, Kennedy K, Kolar P, Kolker E, Maxon M, Millard S, Mugabushaka AM, Perrin N, Remacle JE, Remington K, Rocca-Serra P, Taylor CF, Thorley M, Tiwari B, Wilbanks J. (2009) 'Omics data sharing. *Science* 326:234-6
4. Chain PS, Grafham DV, Fulton RS, Fitzgerald MG, Hostetler J, Muzny D, Ali J, Birren B, Bruce DC, Buhay C, Cole JR, Ding Y, Dugan S, Field D, Garrity GM, Gibbs R, Graves T, Han CS, Harrison SH, Highlander S, Hugenholtz P, Khouri HM, Kodira CD, Kolker E, Kyrpides NC, Lang D, Lapidus A, Malfatti SA, Markowitz V, Metha T, Nelson KE, Parkhill J, Pitluck S, Qin X, Read TD, Schmutz J, Sozhamannan S, Sterk P, Strausberg RL, Sutton G, Thomson NR, Tiedje JM, Weinstock G, Wollam A; Genomic Standards Consortium Human Microbiome Project Jumpstart Consortium, Detter JC. (2009) Genome project standards in a new era of sequencing. *Science* 326:236-7.
5. Schofield PN, Bubela T, Weaver T, Portilla L, Brown SD, Hancock JM, Einhorn D, Tocchini-Valentini G, Hrabe de Angelis M, Rosenthal N; CASIMIR Rome Meeting participants (including Dawn Field) (2009) Post-publication sharing of data and tools. *Nature.* 461:171-3.
6. Jack A. Gilbert, Dawn Field, Paul Swift, Lindsay Newbold, Anna Oliver, Tim Smyth, Paul J. Somerfield, Sue Huse and Ian Joint (2009) Seasonal succession of microbial communities in the Western English Channel using 16S rRNA-tag pyrosequencing of the V6 region. *Environ Microbiology* 2009 Jul 31. [Epub ahead of print]
7. Chervitz, S, Parkinson, H, Fostel, JM, Causton, HC, Sansone, S-A, Deutsch, E.W., Field, D, Taylor, C.F., Rocca-Serra, P, White, J, Stoeckert, CJ (2009) *Bioinformatics: Tools and Applications* (book chapter, in press).
8. Garrity, G, Field D, Kyrpides N (2009) Editorial: Standards in Genomic Sciences. *Standards in Genomic Sciences* 1: 1-2.
9. Field D, Sterk P, Kyrpides N, Kottmann, R, Glockner F, Hirschman L, Garrity G, Wooley, J, Gilna P (2009) Meeting Report from the Genomic Standards Consortium (GSC) Workshops 6 and 7 *Standards in Genomic Sciences* 1: 68-71.
10. Wooley, J, Field D, Glockner F (2009) Extending standards for genomic and metagenomic data: A Research Co-ordination Network for the Genomic Standards Consortium (*RCN4GSC*) *Standards in Genomic Sciences* 1: 87-90.
11. Ben Temperton, Anna Oliver, Dawn Field, Bela Tiwari, Martin Mühlhng, Ian Joint and Jack A. Gilbert (2009) Bias in culture-independent assessments of microbial biodiversity in the global ocean. *ISME* 2009 3(7):792-6.
12. Gilbert JA, Thomas S, Cooley NA, Kulakova A, Field D, Booth T, McGrath JW, Quinn JP, Joint I. (2008) Potential for phosphonoacetate utilization by marine bacteria. *Environ Microbiol.* 11:111-25
13. Gilbert JA, Field D, Huang Y, Edwards R, Li W, Gilna P, Joint I. (2008) Detection of large numbers of novel sequences in the metatranscriptomes of complex marine microbial communities. *PLoS ONE.* Aug 22;3(8):e3042.
14. Taylor, C. D Field, S-A. Sansone et al with 30 authors. MIBBI: A Minimum Information Checklist Resource. *Nature Biotechnology* 26(8):889-96.
15. Field D (2008) Working together to put molecules on the map. *Nature.* 19;453(7198):978

16. Allen, M, Cossins, AR, Hall N, Blaxter M and D Field. "Use of arrays with non model organisms: a UK perspective" Editor Frank Columbus, In *Oligonucleotide Array Sequence Analysis*. Nova Publishers. (in press, **Book Chapter**)
17. Kottmann R, Gray T, Murphy S, Kagan L, Kravitz S, Lombardot T, Field D, Glöckner FO; Genomic Standards Consortium. (2008) A standard MIGS/MIMS compliant XML Schema: toward the development of the Genomic Contextual Data Markup Language (GCDML). *OMICS*. 12(2):115-21.
18. Van Brabant B, Gray T, Verslyppe B, Kyrpides N, Dietrich K, Glöckner FO, Cole J, Farris R, Schriml LM, De Vos P, De Baets B, Field D, Dawyndt P; Genomic Standards Consortium. (2008) Laying the foundation for a Genomic Rosetta Stone: creating information hubs through the use of consensus identifiers. *OMICS*. 12(2):123-7.
19. Hirschman L, Clark C, Cohen KB, Mardis S, Luciano J, Kottmann R, Cole J, Markowitz V, Kyrpides N, Morrison N, Schriml LM, Field D (2008) Habitat-Lite: a GSC case study based on free text terms for environmental metadata. *OMICS*.12(2):129-36.
20. San Gil, I, Sheldon W, Schmidt T, Servilla M, Aguilar R, Gries C, Gray T, Field D, Cole J, Pan JY, Palanisamy G, Henshaw D, O'Brien M, Kinkel L, McMahan K, Kottmann R, Amaral-Zettler L, Hobbie J, Goldstein P, Guralnick RP, Brunt J, Michener WK.(2008) Defining linkages between the GSC and NSF's LTER program: how the Ecological Metadata Language (EML) relates to GCDML and other outcomes. *OMICS*.12(2):151-6.
21. Garrity GM, Field D, Kyrpides N, Hirschman L, Sansone SA, Angiuoli S, Cole JR, Glöckner FO, Kolker E, Kowalchuk G, Moran MA, Ussery D, White O. (2008) Toward a standards-compliant genomic and metagenomic publication record. *OMICS*. 12(2):157-60.
22. Angiuoli SV, Gussman A, Klimke W, Cochrane G, Field D, Garrity G, Kodira CD, Kyrpides N, Madupu R, Markowitz V, Tatusova T, Thomson N, White O. (2008) Toward an online repository of Standard Operating Procedures (SOPs) for (meta)genomic annotation. *OMICS*. 2008 12:137-41
23. Sansone SA, Rocca-Serra P, Brandizi M, Brazma A, Field D, Fostel J, Garrow AG, Gilbert J, Goodsaid F, Hardy N, Jones P, Lister A, Miller M, Morrison N, Rayner T, Sklyar N, Taylor C, Tong W, Warner G, Wiemann S; Members of the RSBI Working Group. (2008) The first RSBI (ISA-TAB) workshop: "can a simple format work for complex studies?". *OMICS*. 12(2):143-9.
24. Field D, Garrity GM, Sansone SA, Sterk P, Gray T, Kyrpides N, Hirschman L, Glöckner FO, Kottmann R, Angiuoli S, White O, Dawyndt P, Thomson N, Gil IS, Morrison N, Tatusova T, Mizrahi I, Vaughan R, Cochrane G, Kagan L, Murphy S, Schriml L; Genomic Standards Consortium.(2008) Meeting report: the fifth Genomic Standards Consortium (GSC) workshop. *OMICS*. 12(2):109-13.
25. Field D, Glöckner FO, Garrity GM, Gray T, Sterk P, Cochrane G, Vaughan R, Kolker E, Kottmann R, Kyrpides N, Angiuoli S, Dawyndt P, Guralnick R, Goldstein P, Hall N, Hirschman L, Kravitz S, Lister AL, Markowitz V, Thomson N, Whetzel T. (2008) Meeting report: the fourth Genomic Standards Consortium (GSC) workshop. *OMICS*. 12(2):101-8.
26. Field D, Sansone SA, Garrity GM.(2008) Foreword to the special issue on the Fifth Genomic Standards consortium workshop. *OMICS*. 12(2):99.
27. Field D et al with 66 authors (2008) The "Minimum Information about a Genome Sequence" (MIGS) specification. *Nature Biotechnology* 26(5):541-7
28. Wall PK, Leebens-Mack J, Müller KF, Field D, Altman NS, Depamphilis CW (2007) PlantTribes: a gene and gene family resource for comparative genomics in plants. *Nucleic Acids Res*. 7:22–31
29. Smith, B et al with the OBI Working Group (including Field D). (2006) The OBO Foundry: Remoulding Ontology to Support Data Integration. *Nature Biotechnology* 25(11):1251-5.
30. Wilson GA, Feil EJ, Lilley AK, Field D. Large-scale comparative genomic ranking of taxonomically restricted genes (TRGs) in bacterial and archaeal genomes. *PLoS ONE*. 2007 28;2(3):e324.

31. Tett A, Spiers AJ, Crossman LC, Ager D, Ciric L, Dow JM, Fry JC, Harris D, Lilley A, Oliver A, Parkhill J, Quail MA, Rainey PB, Saunders NJ, Seeger K, Snyder LA, Squares R, Thomas CM, Turner SL, Zhang XX, Field D, Bailey MJ. Sequence-based analysis of pQBR103; a representative of a unique, transfer-proficient mega plasmid resident in the microbial community of sugar beet. *ISME J.* 2007 1:331-40.
32. Field D, Garrity G, Gray T, Selengut J, Sterk P, Thomson N, Tatusova T, Cochrane G, Glockner F.O, Kottmann R, Lister A.L, Tateno Y and Vaughan R. Meeting Report: eGenomics: Cataloguing Our Complete Genome Collection III *Comparative and Functional Genomics* (2007) 47304: 1-7.
33. Morrison N, Bearden D, Bundy J.G, Collette T, Currie F, Davey M.P, Haigh N.S, Hancock D, Jones O.A.H, Rochfort S, Sansone S-A, Dalibor S, Teng Q, Field D, Viant M. Standard reporting requirements for biological samples in metabolomics experiments: Environmental context *Metabolomics* (2007) 3, 203-210
34. Booth T, Gilbert J, Neufeld JD, Ball J, Thurston M, Chipman K, Joint I, and Field D. Handlebar: a flexible, web-based inventory manager for handling barcoded samples *BioTechniques* (2007) 42:300-02.
35. Field D and Kyripides N. Facilitating eco-genomic studies. *Microbial Ecology* (2006) 53:507-11.
36. Field D., Wilson G. Swift P and E Feil (2006) Analyzing the evolution of infectious bacteria. *Bioinformatics: From Genomes to Therapies* Chapter 41 p 655-698.
37. Field D, Wilson G, van der Gast C. (2006) How do we compare hundreds of bacterial genomes? *Curr Opin Microbiol.* 9:499-504.
38. Carlson JE, Leebens-Mack JH, Wall PK, Zahn LM, Mueller LA, Landherr LL, Hu Y, Ilut DC, Arrington JM, Choirean S, Becker A, Field D, Tanksley SD, Ma H, Depamphilis CW. EST database for early flower development in California poppy (*Eschscholzia californica* Cham., Papaveraceae) tags over 6000 genes from a basal eudicot. *Plant Mol Biol.* (2006) 62:351-69
39. Field D, Sansone S-A. A special issue on Omic data standards *OMICS: A journal of integrative biology* (2006) June, Vol. 10, No. 2: 84 -93
40. Field D, Morrison N, Selengut J, Sterk P. Meeting Report: eGenomics: Cataloguing Our Complete Genome Collection II *OMICS: A journal of integrative biology* (2006) June, Vol. 10, No. 2: 100 -104
41. Whetzl P.L, Brinkman R.R, Causton H.C, Fan L, Field D, Fostel J, Frago G, Gray T, Heiskanen M, Hernandez-Boussard T, Morrison N, Parkinson H, Rocca-Serra P, Sansone S-A, Schober D, Smith B, Stevens R, Stoeckert Jnr C.J, Taylor C, White J, Wood A, and the FuGO Working Group Development of FuGO: An Ontology for Functional Genomics Investigations *OMICS: A journal of integrative biology* (2006) June, Vol. 10, No. 2: 199 -204
42. Morrison N, Cochrane G, Faruque N, Tatusova T, Tateno Y, Hancock D, and Field D. The concept of Sample in Omics Technology *OMICS: A journal of integrative biology* (2006) June, Vol. 10, No. 2: 127 -137
43. Morrison N, Wood JA, Hancock D, Shah S, Hakes L, Gray T, Tiwari B, Kille P, Cossins A, Hegarty M, Allen MJ, Wilson WH, Olive P, Last K, Kramer C, Bailhache T, Reeves J, Pallett D, Warne J, Nashar K, Parkinson H, Sansone S-A, Rocca-Serra P, Stevens R, Snape J, Brass A., Field D Standard annotation of environmental 'omic data - Application to the transcriptomics domain *OMICS: A journal of integrative biology* (2006) June, Vol. 10, No. 2: 172 -178
44. Field D, Garrity G, Morrison N, Selengut J, Sterk P, Thomson N, Tatusova T. Meeting Report: eGenomics: Cataloguing our Complete Genome Collection. *Comparative and Functional Genomics* (2006) 6: 363-368
45. Field D, Tiwari B, Booth T, Houten S, Swan D, Bertrand N, and Thurston M. Bioinformatics for Biologists: from Famine to Feast *Nature Biotechnology* (2006) 24, 801 – 803
46. Orchard S, Apweiler R, Barkovich R, Field D, Garavelli JS, Horn D, Jones A, Jones P, Julian R, McNally R, Nerothin J, Paton N, Pizarro A, Seymour S, Taylor C, Wiemann S, Hermjakob H.

- Proteomics and Beyond. A report on the 3rd Annual Spring Workshop of the HUPO-PSI 21-23 April 2006, San Francisco, CA, USA *Proteomics* 2006 Aug 8;6(16):4439-4443
47. Tiwari B, Field D, Snape J. Public repositories need serious funding *Nature* (2006) 439, 912  
Field D, Tiwari B, Snape J. Meeting Report: eGenomics: Genomes and the environment. *Comparative and Functional Genomics* (2006) 6: 357-362
  48. Field D, & Hughes J (2005). Cataloguing our current genome collection. *Microbiology*. 151: 1016-1019.
  49. Wilson, G., N. Bertrand, Y. Patel, J. Hughes, E. Feil, and D. Field. (2005). "Orphans as taxonomically restricted and ecologically important genes." *Microbiology* 151: 2499-2501.
  50. Field D., & Feil E, and Wilson G. (2005) Databases and software for the comparative genomic study of collections of prokaryotic genomes. *Microbiology* 151:2125-32.
  51. Martiny J. & Field D. (2005) Ecological Perspectives on our complete genome collection. *Ecology Letters* 8: 1334-1345
  52. Tiwari B. and Field D. (2005) A Bioinformatics Playground. LinuxUser and Developer. 46: 110-115.
  53. Field D, Tiwari B, Snape J. Bioinformatics and Data Management Support for Environmental Genomics. *PLoS Biology* (2005) Vol 3. Issue 8. e297.
  54. Dawn Field, Richard Moxon, and Jennifer Hughes (2003) *Using the genome to understand pathogenicity*. In: *Genomics, Proteomics, and Clinical Bacteriology*, Editor Neil Woodford p 221-235.
  55. Molbak, L., D. Ussery, A. Tett, S. Turner, K. Wall, M. Bailey and D. Field. (2003) "The Plasmid Genome Database". *Microbiology*. 149:3043-5
  56. Alison J. Cody, Dawn Field, Edward J. Feil, Suzanna Stringer, Mary Deadman, Anthony Tsolaki, Brett Gratz, Valérie Bouchet, Richard Goldstein, Derek W. Hood & E. Richard Moxon (2003) High rates of recombination in otitis media isolates of non-typeable *Haemophilus influenzae*. *Infect Genet Evol.* 3:57-66.
  57. Udalova, I., R. Mott, D. Field, & D. Kwiatkowski (2002) Quantitative prediction of NF- $\kappa$ B DNA-protein interactions *Proc Natl Acad Sci U S A*. 2002 Jun 11;99(12):8167-72.
  58. Bayliss, C. D., D. Field, & E.R. Moxon. 2001. The simple sequence contingency loci of *Haemophilus influenzae* and *Neisseria meningitidis*. *J. Clin Invest.* 107:657-62
  59. Spiers, A.J., D. Field, M. Bailey, & P. Rainey. 2001. Notes on Designing a Partial Genomic Database: The PfSBW25 Encyclopaedia, a sequence database for *Pseudomonas fluorescens* SBW25. *Microbiol.* 147:247-249.
  60. Metzgar D., E Thomas, C. Davis, D Field & C Wills. 2001. The microsatellites of *Escherichia coli*: rapidly evolving repetitive DNAs in a non-pathogenic prokaryote. *Mol Microbiol.* 39:183-90.
  61. Bayliss, C. D., D. Field, X. de Bolle & E.R. Moxon. 2000. The generation of diversity by *Haemophilus influenzae*. *Trends in Microbiology* 8:435-6.
  62. X. De Bolle, C.D. Bayliss, D. Field, T. van de Ven, N.J. Saunders, D.W. Hood, and E.R. Moxon. 2000. The length of a tetranucleotide repeat tract in *Haemophilus influenzae* determines the phase variation rate of a gene with homology to type III DNA methyltransferases. *Mol Microbiol.* 35:211-22.
  63. Field, D., D. Hood, & R.E. Moxon. 1999. Contribution of genomics to bacterial pathogenesis. *Current Opinion in Genetics and Development.* 9:700-3.
  64. Davis, C., D. Field, D. Metzgar, R. Saiz, P. Morin, I. L. Smith, S. A. Spector, & C. Wills. 1999. Numerous Length Polymorphisms at Short Tandem Repeats in Human Cytomegalovirus. *Journal of Virology*, 73:6265-70.
  65. Field D, M. O. Magnasco, E. R. Moxon, D. Metzgar, M. Tanaka, C. Wills, & D. S. Thaler. 1998. Contingency loci, mutator alleles and their interactions: synergistic strategies for microbial evolution and adaptation in pathogenesis. *Annals of the New York Academy of Sciences*, 870:378-382.

66. Field, D & C. Wills. 1998. Abundant microsatellite polymorphism in *S. cerevisiae*, and the different distributions of microsatellites in prokaryotes and eukaryotes, result from strong mutation pressures and a variety of selective forces. ***Proceedings of the National Academy of Sciences of the United States of America***, 95:1647-52
67. Metzgar, D., Field, D. Haubrich, R., & C. Wills. 1998 Sequence analysis of a compound coding-region microsatellite in *Candida albicans* resolves homoplasies and provides a high resolution tool for genotyping. ***Fems Immunology and Medical Microbiology***, Feb, 20:103-9.
68. Metzgar D; A. van Belkum, D. Field, R. Haubrich, & C. Wills. 1998. Random amplification of polymorphic DNA and microsatellite genotyping of pre- and posttreatment isolates of *Candida* spp. from human immunodeficiency virus-infected patients on different fluconazole regimens. ***Journal of Clinical Microbiology*** 36:2308-13.
69. Field, D., L. Chemnick & O. Ryder. 1998. Microsatellite-based paternity determination in captive gorillas and orangutans. ***Primates***. 39:199-209.
70. Field, D., L. Eggert, D. Metzgar, R. Rose & C. Wills. 1996. Use of polymorphic short and clustered coding-region microsatellites to distinguish strains of *Candida albicans*. ***Fems Immunology and Medical Microbiology***, 15:73-9.
71. Field, D. & C. Wills. 1996. Long, polymorphic microsatellites in simple organisms. ***Proc. Roy. Soc. London B*** 263: 209-215.
72. Srikwan, S., D. Field & D.S. Woodruff. 1996. Noninvasive genotyping of free-ranging rodents with heterologous PCR primer pairs for hypervariable nuclear microsatellite loci. ***J. Science Society of Thailand*** 22: 267-274
73. Broadwater, S, J. Scott, D. Field and B. Saunders. 1993. An ultrastructural study of cell division in the coralline red alga *Bosienella orbigniance*. ***Canadian Journal of Botany*** 71:434-446.