

**BIOGRAPHICAL SKETCH**

NAME <b>Gavin Sherlock</b>		POSITION TITLE <b>Assistant Professor (Research)</b>	
EDUCATION/TRAINING ( <i>Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.</i> )			
INSTITUTION AND LOCATION	DEGREE	YEAR(S)	FIELD OF STUDY
Manchester University, Manchester, U.K.	B.S.	1991	Genetics
Manchester University, Manchester, U.K.	Ph.D.	1994	Molecular Biology
Cold Spring Harbor Laboratory, NY, USA		1995-1998	Molecular Biology
Stanford University, Stanford, USA		1998-1999	Bioinformatics

**A. Positions and Honors.**

1990: **Summer Research Assistant:** Amersham International Plc..  
 1990-91: **Undergraduate Research Assistant:** Regional Molecular Genetics Laboratories, Manchester, U.K..  
 1995-1998: Postdoctoral Fellow in Bruce Futcher's laboratory, Cold Spring Harbor Laboratory.  
 1998-1999: Postdoctoral Fellow in David Botstein's laboratory, Stanford University.  
 1999-2000: Head, Microarray Informatics, Department of Genetics, Stanford University.  
 2000-2003: Director, Stanford Microarray Database.  
 2004-: Assistant Professor (Research) in Genetics, Stanford University.

**Other Experience and Professional Memberships**

2001- MGED (Microarray Gene Expression Data Society) steering committee ([www.mged.org](http://www.mged.org)).  
 2001- MGED chairman of normalization working group.  
 2002-present TAIR (The Arabidopsis Information Resource) Advisory board ([www.arabidopsis.org](http://www.arabidopsis.org)).  
 2002-present MGED board of Directors.  
 2003-present NINDS/NIMH Microarray Consortium Steering Committee (<http://arrayconsortium.cncresearch.org/>)  
 2003-present Guest Lecturer at Cold Spring Harbor Laboratory Microarray course.  
 2003-present Scientific Advisor on NSF plant genome proposal: "A rice oligonucleotide array and identification of genes expressed during the rice defense response."  
 2003-present PharmGKB Scientific Advisory Board (<http://www.pharmgkb.org/>)  
 2004-present Member of the American Society for Microbiology (ASM).

**Honors and Awards**

1988-1991 John Buckley Entrance Scholarship for Science.  
 1991-1994 Wellcome Trust Prize Studentship.  
 1996-1997 Cold Spring Harbor Fellowship.  
 1997-1998 Army Breast Cancer Research Fellowship.

**B. Selected peer-reviewed publications (in chronological order) (30 of 33).**

1. Spellman, P.T., **Sherlock, G.\***, Zhang, M.Q., Iyer, V.R., Anders, K., Eisen, M.B., Brown, P.O., Botstein, D., and B. Futcher (1998). Comprehensive Identification of Cell Cycle-regulated Genes of the Yeast *Saccharomyces cerevisiae* by Microarray Hybridization. *Molecular Biology of the Cell* **9**, 3273-3297. \* = **joint first author**.
2. Chervitz, SA, Hester, ET, Ball, CA, Dolinski, K, Dwight, SS, Harris, MA, Juvik, G, Malekian, A, Roberts, S, Roe, T, Scafe, C, Schroeder, M, **Sherlock, G**, Zhu, SWY, Cherry, JM, and Botstein, D (1999). Using the *Saccharomyces* Genome Database (SGD) for analysis of protein similarities and structure. *Nucleic Acids Research* **27**, 74-78.
3. **Sherlock, G.** (2000). Analysis of large-scale expression data. *Current Opinion in Immunology* **12** (2), 201-205.
4. Alizadeh, A.A, Eisen, M.B., Davis, R.E, Ma, C., Lossos, I.S., Rosenwald, A., Boldrick, J.C., Sabet, H., Tran, T., Yu, X., Powell, J.I., Yang, L., Marti, G.E., Moore, T., Hudson, J., Lu, L., Lewis, D.B., Tibshirani, R., **Sherlock, G.**, Chan, W.C., Greiner, T.C., Weisenburger, D.D., Armitage, J.O., Warnke, R., Levy, R., Wilson, W., Grever, M.R., Byrd, J.C., Botstein, D., Brown, P.O., and Staudt, L.M. (2000). Distinct types of diffuse large B-cell lymphoma identified by gene expression profiling. *Nature* **403**, 503-511.
5. Ball, C.A., Dolinski, K., Dwight, S.S., Harris, M.A., Issel-Tarver, L., Kasarskis, A., Scafe, C.R., **Sherlock, G.**, Binkley, G., Jin, H., Kaloper, M., Orr, S.D., Schroeder, M., Weng, S., Zhu, Y., Botstein, D., and Cherry, J.M. (2000). Integrating functional genomic information into the *Saccharomyces* Genome Database. *Nucleic Acids Research* **28**, 77-80.
6. The Gene Ontology Consortium (2000). Gene Ontology: tool for the unification of biology. *Nature Genetics* **25**, 25-29.
7. Salama, N., Guillemin, K., McDaniel, T.K., **Sherlock, G.**, Tompkins, L. and Falkow, S. (2000). A Whole Genome Microarray Reveals Genetic Diversity Among *Helicobacter Pylori* Strains. *Proceedings of the National Academy of Science USA* **97**, 14668-14673.

8. Ball, C.A., Jin, H., **Sherlock, G.**, Weng, S., Matese, J.C., Andrada, R. Binkley, G., Dolinski, K., Dwight S.S, Harris, M.A., Issel-Tarver, L., Schroeder, M., Botstein, D. and Cherry, J.M. (2001). *Saccharomyces* Genome Database provides tools to survey gene expression and functional analysis data. *Nucleic Acids Research* **29**, 80-81.
9. **Sherlock G.**, Hernandez-Boussard, T., Kasarskis, A., Binkley, G., Matese, J.C., Dwight, S.S., Kaloper, M., Weng, S., Jin, H., Ball, C.A., Eisen, M.B., Spellman, P.T., Brown, P.O., Botstein, D. and Cherry, J.M. (2001). The Stanford Microarray Database. *Nucleic Acids Research* **29**, 152-155.
10. Troyanskaya O., Cantor, M., **Sherlock G.**, Brown P.O., Hastie T., Tibshirani R., Botstein B., and Altman, R.B. (2001). Missing value estimation methods for DNA microarrays. *Bioinformatics* **17**, 520-525.
11. The Gene Ontology Consortium (2001). Creating the Gene Ontology Resource: Design and Implementation. *Genome Research* **11**, 1425-1433.
12. **Sherlock G.** (2001). Analysis of Large Scale Gene Expression Data. *Briefings in Bioinformatics* **2**, 350-362.
13. Brazma, A., Hingamp, P., Quackenbush, Q., **Sherlock, G.**, Spellman, P., Stoeckert, C., Ansorge, W., Ball, C.A., Causton, H., Glenison, P., Holstege, F., Kim, I.F., Markowitz, V., Matese, J.C., Robinson, A., Stewart, J., Taylor, R. and Vingron, M. (2001). Minimum Information About a Microarray Experiment – MIAME – towards Standards for Microarray Data. *Nature Genetics* **29**, 365-371.
14. Dwight, SS, Harris, MA, Dolinski, K., Ball, C.A., Binkley, G., Christie, K.R., Fisk, D.G., Issel-Tarver, L., Schroeder, M., **Sherlock, G.**, Sethuraman, A., Weng, S., Botstein, D., and Cherry, J.M. (2002). *Saccharomyces* Genome Database (SGD) provides secondary gene annotation using the Gene Ontology (GO). *Nucleic Acids Research* **30**, 69-72.
15. Tibshirani, R., Hastie, T., Narashimhan, B., Eisen, M., **Sherlock, G.**, Brown, P. and Botstein, D. (2002). Exploratory screening of genes and clusters from microarray experiments. *Statistica Sinica*, **12**, 47-49.
16. Whitfield, M.L., **Sherlock, G.**, Saldanha, A., Murray, J.I., Ball, C.A., Alexander, K.E., Matese, J.C., Perou, C.M., Hurt, M.M., Brown, P.O., and Botstein, D. (2002). Identification of Genes Periodically Expressed in the Human Cell Cycle and Their Expression in Tumors. *Molecular Biology of the Cell*, **13**, 1977-2000.
17. Nielsen, T.O., West, R.B., Linn, S.C., Alter, O., Knowling, M.A., J.X., Zhu, S., Fero, M., **Sherlock, G.**, Pollack, J.R., Brown, P.O., Botstein, D., and van de Rijn, M. (2002). Molecular characterisation of soft tissue tumours: a gene expression study. *The Lancet* **359**, 1301-07.
18. Spellman, PT, Miller, M, Stewart, J, Troup, C, Sarkans, U, Chervitz, C, Bernhart, D, **Sherlock, G.**, Ball, C, Lepage, M, Swiatek, M, Marks, WL, Goncalves, J, Markel, S, Iordan, D, Shojatalab, M, Pizzaro, A, White, J, Hubley, R, Deutsch, E, Senger, M, Arnow, BJ, Robinson, A, Bassett, D, Stoeckert, C., and Brazma, A. (2002). Design and Implementation of Microarray Gene Expression Markup Language (MAGE-ML). *Genome Biology* **3**, research0046.1-0046.9.
19. Diehn, M., **Sherlock, G.**, Binkley, G., Jin, H., Matese, J.C., Hernandez-Boussard, T., Rees, C.A., Cherry, J.M., Botstein, D., Brown, P.O., and Alizadeh, A.A. (2003). SOURCE: A Unified Genomic Resource of Functional Annotations, Ontologies, and Gene Expression Data. *Nucleic Acids Research*, **31**, 219-23.
20. Gollub J., Ball C.A., Binkley G., Demeter J., Finkelstein D.B., Hebert J.M., Hernandez-Boussard T., Jin H., Kaloper M., Matese J.C., Schroeder M., Brown P.O., Botstein D., and **Sherlock G.** (2003). The Stanford Microarray Database: data access and quality assessment tools. *Nucleic Acids Research* **31**, 94-6.
21. Killion, P., **Sherlock, G.**, and Iyer, V.R. (2003). The Longhorn Array Database (LAD): An Open-Source, MIAME compliant implementation of the Stanford Microarray Database (SMD). *BMC Bioinformatics* **4**:32.
22. Spellman, P.T. and **Sherlock, G.** (2004). Reply: Whole-Culture Synchronization - Effective Tools for Cell Cycle Studies. *Trends in Biotechnology* **22**, 270-3.
23. Spellman, P.T. and **Sherlock, G.** (2004). Final Words: Cell Age and Cell Cycle are Unlinked. *Trends in Biotechnology* **22**, 277-8.
24. **Sherlock, G.** (2004). STARTing to recycle. *Nature Genetics* **36**, 795-796.
25. Ball, C.A., **Sherlock, G.** and Brazma, A. (2004). Funding high-throughput data sharing. *Nature Biotechnology* **22**, 1179-1183.
26. Boyle, E.I., Weng, S., Gollub, J., Jin, H., Botstein, D., Cherry, J.M. and **Sherlock, G.** (2004). GO::TermFinder – open source software for accessing Gene Ontology information and finding significantly enriched Gene Ontology terms associated with a list of genes. *Bioinformatics*, in press.
27. Rees, C.A., Demeter, J., Matese, J.C., Botstein, D. and **Sherlock, G.** (2004). GeneXplorer: an interactive web application for microarray data visualization and analysis. *BMC Bioinformatics* **5**:41.
28. Awad, I.A.B, Rees, C.A., Hernandez-Boussard, T., Ball, C.A. and **Sherlock, G.** (2004). Caryoscope: An Open Source Java Application for Viewing Microarray Data in a Genomic Context. *BMC Bioinformatics*, in press.
29. Ball, C.A., Awad, I.A.B, Demeter, J., Gollub, J., Hebert, J., Hernandez-Boussard, T., Jin, H., Matese, J.C., Nitzberg, M., Wymore, F., Zachariah, Z., Brown, P.O. and **Sherlock, G.** (2005). The Stanford Microarray Database accommodates additional microarray platforms and data formats. *Nucleic Acids Research* **33**, in press.
30. Arnaud, M.B., Costanzo, M.C., Skrzypek, M.S., Binkley, G., Lane, C., Miyasoto, S.R. and **Sherlock, G.** (2005). The *Candida* Genome Database (CGD), a community resource for *Candida albicans* gene and protein information. *Nucleic Acids Research* **33**, in press.

**C. Research Support.**

**Ongoing Research Support**

RO1 HG02732-01 Sherlock (PI) 09/01/02->08/31/05 (final year is a no cost extension)  
NIH

Generic Software Modules for Microarray Data

This grant funds the creation of generic software modules that can be easily reused by Model Organism Databases to deal with microarray data.

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Role: PI

R01 DE015873 Sherlock (PI) 04/01/04->02/31/09

Genomic Database for *Candida albicans*

The grant funds the creation and maintenance of a genomic database for *Candida albicans*, and subsequent curation of *C. albicans* gene products.

Role: PI

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S10 RR019375 Sherlock (PI) 09/1/04 – 08/31/07

System for the Stanford Microarray Database

The major goal of this project is to deploy a new hardware system to serve as the production server for the Stanford Microarray Database.

Role: PI

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OTL Research Incentive Fund Award Sherlock (PI) 06/01/04-08/31/06

Genome Plasticity and Evolution in De Novo Yeast Species

This grant funds the design of a two species microarray, and the genomic characterization of hybrid yeast species.

Role: PI