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- Validated on Roche 454™ GS FLX Titanium™ and Illumina Solexa® GAI, GAII.

Summary data from Nextera libraries sequenced using GS FLX Titanium chemistry.

Sample	Total Reads	% Total Nucleotides Identified	Reference Sequence Length	X Coverage	% Mapped Reads
E. coli	472,007	99.95	4.64 Mb	33.21	88.74
Plasmid 1	10,657	99.93	19.7 Kb	151.38	93.74
Plasmid 2	6,291	99.89	6.3 Kb	284.17	86.73
Soy (W82)	572,162	99.90	973 Mb	0.16	87.64

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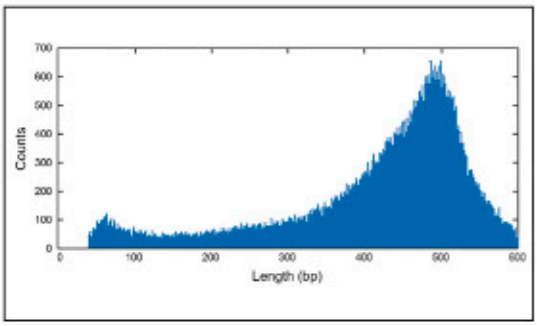

Figure 1: Example Read Length Distribution of 100,000 reads from *E. coli* K-12 (genome size approximately 4.5 Mb), from a single GS Junior System run.

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At the Helm
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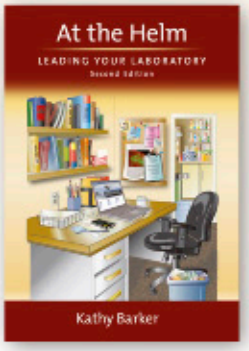

By Kathy Barker, *Seattle, Washington*

Since 2002, the first edition of this best-selling book has helped thousands of newly appointed principal investigators successfully transition to running their own labs. But changes in technology continue to transform the way science is done, affecting ways in which labs communicate and collaborate, organize data and supplies, and keep current on the latest developments. The culture of science has also evolved, as more scientists explore non-academic career paths, seek new ways to communicate information and ideas, and acquire skills and knowledge outside of their field. In the second edition of this book, Kathy Barker has substantially revised the text, offering PIs advice on adapting to the changes and challenges that the years have brought. New topics include collaboration contracts, performance evaluations, communicating with non-scientists, tips for succeeding on the tenure track, and professional development. With this book as a guide, any new or aspiring PI will be well-equipped to manage personnel, time, and institutional responsibilities with confidence.

About the author: Kathy Barker received her B.A. in Biology and English, and her M.A. and Ph.D. in Microbiology, from various branches of the University of Massachusetts. She did her postdoctoral work in the laboratory of Viral Oncology at Rockefeller University and was an Assistant Professor in the Laboratory of Cell Physiology and Immunology at Rockefeller University. She is now based in Seattle, where she writes and gives workshops on various aspects of running a lab.

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Mango Lab
http://www2.lsdiv.harvard.edu/mango_lab/

Liu Lab
http://liulab.dfci.harvard.edu/

Interested applicants should submit a letter of interest with a one-page proposal for a possible project, CV, and three references to Susan Mango: smango at mcb.harvard.edu.

Requirements:
Ideally, the applicant should have:
A. a PhD degree in a related field (physical sciences or biology)
B. strong programming skills: ((Python | Perl) & (C | C++ | Java) & R)
C. strong quantitative background (machine learning, Bayesian inference, etc.) or computational genomics experiences (DNA sequence analysis, microarray analysis, etc.)
D. at least two first-author papers in their previous area of research (not necessarily computational biology)

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ÉCOLE POLYTECHNIQUE
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Tenure-track Assistant Professorships in Statistical Genetics and Bioinformatics

at Ecole Polytechnique Fédérale de Lausanne (EPFL)

The Faculty of Life Science (http://sv.epfl.ch) of the Swiss Federal Institute of Technology Lausanne (EPFL) seeks **a tenure track Assistant Professor** in the field of Statistical Genetics and Bioinformatics.

The open faculty position is offered in an environment of translational biomedical research, rich for seeking deeper understanding of integrative (patho) physiological mechanisms contributing to the development of complex diseases, with as ultimate goal the development of novel preventive and therapeutic approaches. The Faculty of Life Sciences has recently opened the Center of PhenoGenomics, a state-of-the-art platform that combines the capacity to generate and analyze mouse models of disease in a high throughput fashion. The Faculty of Life Sciences furthermore fosters interactions with other relevant domains of the EPFL, such as the Faculty of Basic Sciences (mathematics, statistics) and of Information and Communication Technologies. In addition close ties exist with relevant clinical departments at the Centre Hospitalier Universitaire Vaudois (CHUV), with the Faculty of Biology and Medicine of the University of Lausanne, and with the Swiss Institute of Bioinformatics.

The candidate should be trained in statistical genetics and in bioinformatics. Skills in clinical genetics as applied to mouse or human disease models, biomedical informatics, and databases / programming would be a plus.

He/she is expected to develop an independent and creative research program that will improve the analysis of large data sets derived from clinical, genetic, genomic, proteomic, and phenomic analyses of genetically engineered mouse models, of mouse genetic reference populations, and of human populations. Successful candidates will participate in undergraduate and graduate teaching.

While the faculty search will be ongoing, we will begin considering applications in **September 2010.**

Applications should be uploaded at **http://biostatsearch.epfl.ch**

Inquiries and questions may be addressed to:
Professor Johan Auwerx
biostat.search@epfl.ch

For additional information on the School of Life Sciences and EPFL, please consult **http://sv.epfl.ch/ and http://www.epfl.ch,** respectively.

EPFL is committed to expanding the ranks of women on its faculty, and qualified women are strongly encouraged to apply.

Postdoctoral Positions at Cold Spring Harbor Laboratory

Cold Spring Harbor Laboratory is a world-renowned research and educational institution recognized internationally for its excellence in ground-breaking research and educational activities. We invite highly motivated individuals to visit our website at www.cshl.edu to review and apply for current postdoctoral opportunities in the following areas.

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Plant Biology: The CSHL Plant Biology program focuses primarily on development, stem cells, morphogenesis, plant genomics and epigenetics.

Genomics and Bioinformatics: The CSHL Genomics program uses state-of-the-art technologies including high-throughput sequencing, copy number variation analysis and transcriptome analysis. Efforts are ongoing to understand genomic variation associated with several human diseases as well as elucidating and characterizing new functional outputs of the genome.

Quantitative Biology: The CSHL Center for Quantitative Biology is comprised of scientists in the fields of physics, computer science, engineering, statistics and applied mathematics dedicated to applying quantitative methods to studies in human genetics, genomic, neurobiology, and signal and image processing.

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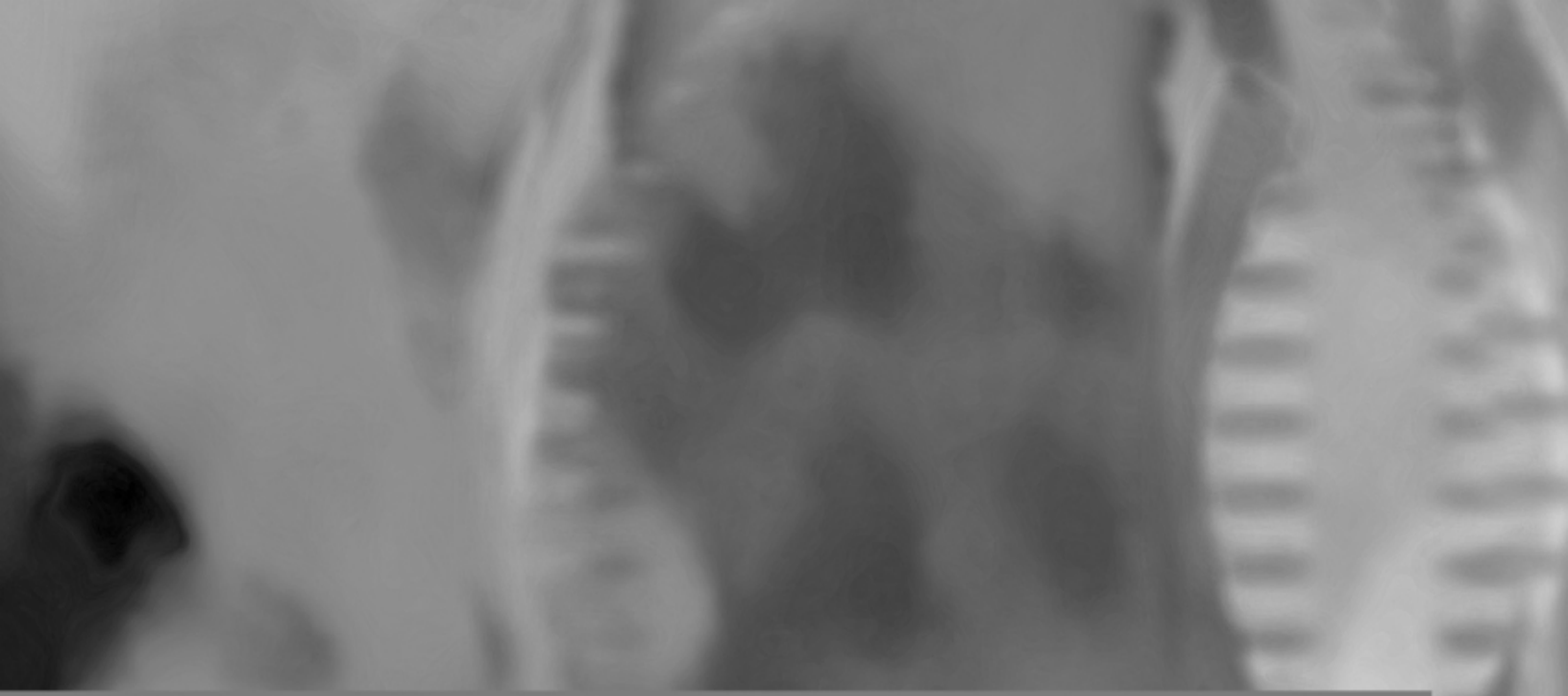

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4–9 July

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18–24 July

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21–27 July

Design and Analysis of Genetic-based Association Studies
23–27 August

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10–12 May

Proteomics Bioinformatics
12–18 December

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12–15 September

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