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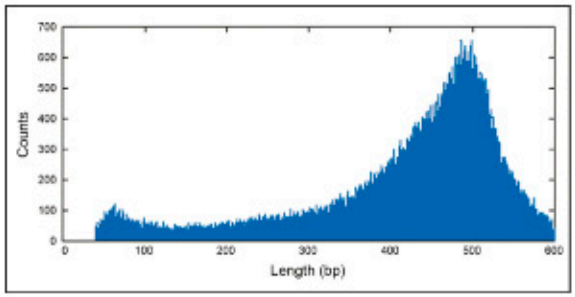

Figure 1: Example Read Length Distribution of 100,000 reads from *E. coli* K-12 (genome size approximately 4.5 Mb), from a single GS Junior System run.

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System	Genome Sequencer FLX System	GS Junior Sequencing System
Throughput	400-600 million high-quality, filter-passed bases per run†	>35 million high-quality, filter-passed bases per run†
Run Time	10 hours sequencing time, 2 hours data processing†	10 hours sequencing time, 2 hours data processing†
Read Length	Modal length = 500 bases, Average length = 400 bases† ***Coming later this year: read lengths of up to 1,000 bases***	Modal length = 500 bases, Average length = 400 bases†
Accuracy	Q20 read length at 400 bases (99% accuracy at 400 bases)	Q20 read length at 400 bases (99% accuracy at 400 bases)
Reads per Run	>1 million reads	100,000 reads (on average)
Software Included	GS *De Novo* Assembler, GS Reference Mapper, GS Amplicon Variant Analyzer	GS *De Novo* Assembler, GS Reference Mapper, GS Amplicon Variant Analyzer
Computing Requirements	Cluster recommended (Roche GS FLX Titanium Cluster available)	Linux-based OS on HP desktop computer, included
Sample Input Requirements	Purified gDNA, amplicons, cDNA, or RNA, depending on the application	Purified gDNA, amplicons, cDNA, or RNA, depending on the application
Physical Dimensions	Upper assembly: 74.3 cm W × 69.8 cm D × 36.1 cm H including monitor 82.5 cm H Permanently affixed lower assembly: 75.2 cm W × 90.8 cm D × 92.7 cm H Weight: 532 lb.	Benchtop sequencer: 40 cm W x 60 cm D x 40 cm H Weight: 55 lb.

† Typical results using GS FLX Titanium Series chemistry. Average read length and number of reads depend on specific sample and genome characteristics.

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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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Generation and Interpretation of Morphogen Gradients

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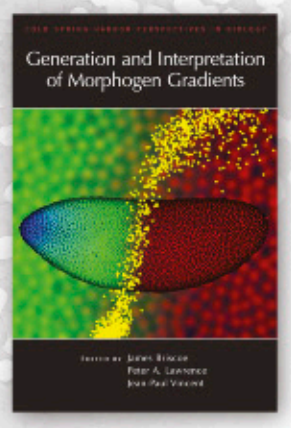

Edited by James Briscoe, *MRC National Institute for Medical Research,* Peter A. Lawrence, *University of Cambridge, and MRC Laboratory of Molecular Biology,* and Jean-Paul Vincent, *MRC National Institute for Medical Research*

Signaling by diffusible morphogens, such as Hedgehog, Wingless, TGF-β, and various growth factors, is essential during embryogenesis. The establishment of concentration gradients of these morphogens is vital for developmental patterning, ensuring that distinct differentiated cell types appear in the right place and at the right time in forming tissues.

Written and edited by experts in the field, this volume explores how morphogen gradients are generated and interpreted during development. The contributors examine the regulation of morphogen synthesis, trafficking, and diffusion, as well as the complex webs of signaling mechanisms and transcriptional responses in recipient cells — whose fates are dictated by these morphogens. Including discussion of the roles of morphogen gradients in various tissues in organisms from yeast to humans, the volume is a vital reference for developmental biologists and cell biologists wishing to know how cell fate is determined during embryogenesis.

2010, 308 pp., illus., index
Hardcover $135
ISBN 978-087969881-2

Contents

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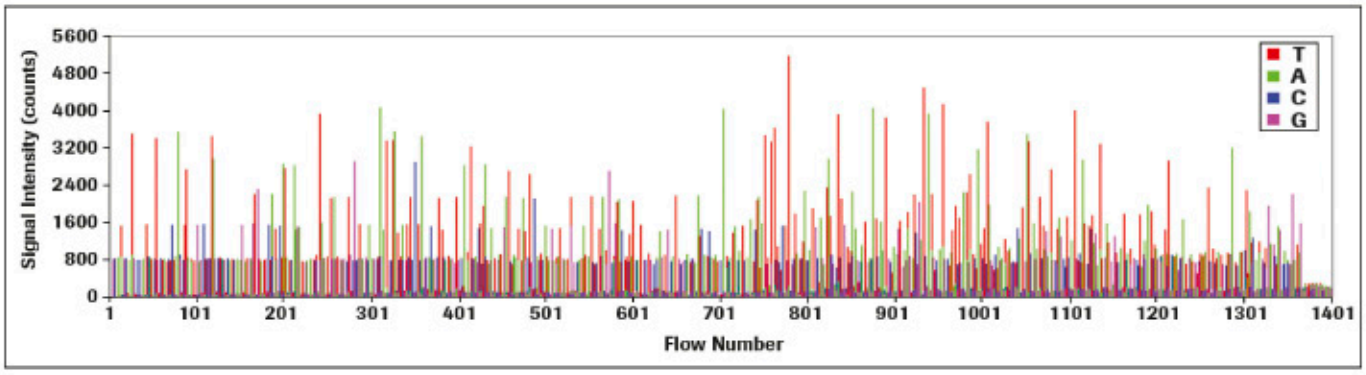
Genome Sequencer FLX System

Less ~~Some~~ assembly required



DNA Sequencing Flowgram: Each bar within the flowgram represents a discrete nucleotide (A, T, C, or G) and the height of the bar corresponds to the number of nucleotides detected. The flowgram above represents a 1008-base-pair sequencing read from *E. coli* K-12.

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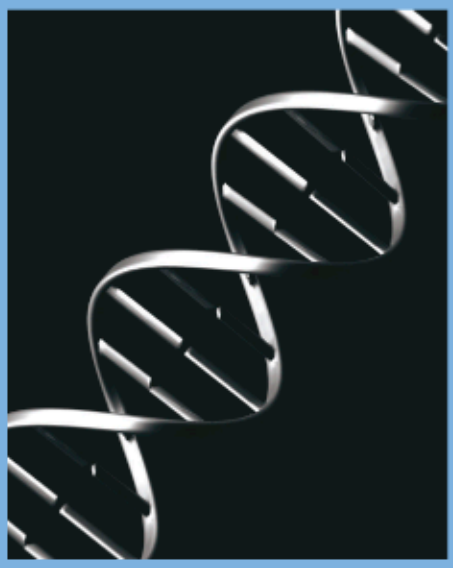


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University of Maryland, School of Medicine
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The newly created Institute for Genome Sciences (IGS) at the University of Maryland, School of Medicine is in a period of rapid expansion. The Institute is led by Claire M. Fraser-Liggett, Ph.D., one of the world's preeminent genome scientists, and encompasses an inter-disciplinary, multi-departmental team of collaborative investigators with a broad research program related to the genomics of infectious disease agents, human microbial metagenomics, functional genomics and bioinformatics. The impact of the members of IGS on the field of genomics has been substantial, with more than 500 publications during the past 15 years which have been cited more than 30,000 times.

The Institute is currently seeking a postdoctoral fellow with experience in bioinformatics to study human genetic variation. Our main goal is to study "alternative" (non-SNP) forms of genetic variation such as small insertions and deletions (INDELs) and transposon insertions in diverse humans (Mills et al. 2006, Genome Res.16, 1182-1190; Mills et al.2007, Trends Genet. 23, 183-91, 2007; Bennett et al. 2008, Genome Res. 18, 1875-83). A future goal is to develop innovative approaches to study the impact of INDELs and transposon insertions on human traits and diseases, including cancers. The candidate should have advanced informatics skills (ideally, a working knowledge of Java, PERL, Python, MySQL, and web development) and a Ph.D. in a relevant field (Genetics, Biochemistry or Bioinformatics). Experience with data modeling is desirable. Molecular Biology or Biochemistry wet lab skills, a plus. The candidate must be eligible to apply for an NIH postdoctoral fellowship.

Please send your C.V. electronically to:
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University of Maryland, School of Medicine
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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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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.

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9–15 May

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16–25 June

Molecular Neurology and Neuropathology
19–26 June

Practical Aspects of Small Molecule Drug Discovery
4–9 July

Next Generation Sequencing
18–24 July

Human Genome Analysis: Genetic Analysis of Multifactorial Diseases
21–27 July

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23–27 August

WORKSHOPS

Working with the Human Genome Sequence
10–12 May

Proteomics Bioinformatics
12–18 December

OVERSEAS COURSES

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1–3 March

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Training workshop 17-18 March
Conference 18-19 March

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24–27 March

The Evolutionary Biology of Caenorhabditis and Other Nematodes
6–9 June

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9–13 June

EBI-Wellcome Trust Bioinformatics Summer School
14–18 June

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11–15 August

Wellcome Trust School of Human Genomics
22–26 August

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4–7 September

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8–11 September

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Adam Eyre-Walker
University of Sussex, UK

Kateryna Makova
Penn State University, US

Gil McVean
University of Oxford, UK

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Howard Hughes Medical Institute at UT Southwestern, US

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Uppsala University, SE
Broad Institute of MIT and Harvard, US

Steven McCarroll
Harvard Medical School, US

Mark McCarthy
Oxford Centre for Diabetes, Endocrinology & Metabolism, UK

Mike Stratton
Wellcome Trust Sanger Institute, UK

John Trowsdale
Cambridge Institute for Medical Research, UK

KEYNOTE SPEAKERS

Svante Pääbo
Max Planck Institute for Evolutionary Anthropology, DE

Kári Stefánsson
deCODE genetics, IS

SESSION | Functional Variation

CHAIR | **Ewan Birney**
European Bioinformatics Institute, UK

Stephan Beck
University College London, UK

Søren Brunak
University of Denmark, DK

Vivian Cheung
University of Pennsylvania, US

Manolis Dermitzakis
University of Geneva Medical School, CH

Jorge Ferrer
Institut d'Investigacions Biomediques August Pi i Sunyer, ES

SESSION | Population Genetics

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Carlos D. Bustamante
Cornell University, US

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Additional speakers will be selected from abstracts.

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15 January 2010	Call for Tutorials Deadline
15 January 2010	Call for Workshops Deadline
3 May 2010	Call for Papers Deadline
2 June 2010	Early Registration Deadline
4 June 2010	Notification of Acceptance
1 October 2010	Pre-Registration Deadline
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