# 2011 Genome Assembly Workshop

## Agenda

### MONDAY, MARCH 14, 2011

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
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<tbody>
<tr>
<td>4:00 pm to 10:00 pm</td>
<td>Registration&lt;br&gt;Seacliff Terrace&lt;br&gt;Reception (appetizers and beverages)&lt;br&gt;Annonce workshop goals and agenda</td>
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### TUESDAY, MARCH 15, 2011

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
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<tr>
<td>7:00 am to 8:00 am</td>
<td>Breakfast in Sunset Room&lt;br&gt;Registration</td>
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<td>8:00 am to 9:45 am</td>
<td>Opening comments&lt;br&gt;Session 1 presentations:&lt;br&gt;&lt;br&gt;<strong>A generic sequence graph exchange format for assembly and population variation</strong>&lt;br&gt;Richard Durbin, Wellcome Trust Sanger Institute&lt;br&gt;&lt;br&gt;<strong>Results of the Assemblathon</strong>&lt;br&gt;Ian Korf, University of California, Davis&lt;br&gt;Dent Earl, University of California, Santa Cruz</td>
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<td>9:45 am to 10:00 am</td>
<td>Break</td>
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<td>10:00 am to 12:00 pm</td>
<td>Session 2 presentations:&lt;br&gt;&lt;br&gt;<strong>High-quality draft assemblies of a dozen vertebrate genomes from massively parallel sequence data</strong>&lt;br&gt;David Jaffe, Broad Institute&lt;br&gt;&lt;br&gt;<strong>ALLPATH-LG algorithms for large genome assembly</strong>&lt;br&gt;Sante Gnerre, Broad Institute&lt;br&gt;&lt;br&gt;<strong>Columbus: Templated assembly of partially mapped reads</strong>&lt;br&gt;Daniel Zerbino, University of California, Santa Cruz&lt;br&gt;&lt;br&gt;<strong>NGS de novo assembly: Progresses and challenges</strong>&lt;br&gt;Yingrui Li, BGI-Shenzhen</td>
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<td>12:00 pm to 1:00 pm</td>
<td>Lunch in the Sunset Room</td>
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1:00 pm to 2:00 pm
Santa Cruz Room

Session 3 presentations:

De novo assembly of *Vibrio cholerae* using Pacific Biosciences SMRT™ DNA sequencing technology
Aaron Klammer, Pacific Biosciences

Efficient assembly algorithms using the FM-index
Jared Simpson, Wellcome Trust Sanger Institute

2:00 pm to 3:00 pm
New Brighton Room
Santa Cruz Room
La Selva Room

Break-out groups:

Genome Assembly and Assemblathon 2
Framework Physical Maps
Data Policy, Targets, and Standards

3:00 pm to 3:15 pm
Break

3:15 pm to 5:00 pm
New Brighton Room
Santa Cruz Room
La Selva Room

Break-out groups:

Genome Assembly and Assemblathon 2
Framework Physical Maps
Data Policy, Targets, and Standards

5:00 pm to 6:10 pm
Group plenary reports

6:10 pm
Group photo

6:30 pm to 9:00 pm
Dinner in the Sunset Room (no host bar)

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**WEDNESDAY, MARCH 16, 2011**

7:00 am to 8:00 am
Breakfast in Sunset Room

8:00 am to 10:00 am
Santa Cruz Room

Session 1 presentations:

HMP assembly analysis at JCVI
Jason Miller, J Craig Venter Institute

Experimental approaches to massively parallel contiguity mapping
Jay Shendure, University of Washington

Newbler and large genome assembly
Jim Knight, University of Washington

De novo genome assembly from metagenomic mixtures using PRICE
Graham Ruby, University of California, San Francisco

10:00 am to 10:15 am
Break
Session 2 presentations:

**Assembly and validation of large genomes from short reads**
Michael Schatz, Cold Spring Harbor Laboratory

**A call for standardization of physical markers for use in the analysis of genome assemblies**
Joan Pontius, National Cancer Institute

**Optical mapping and nanocoding systems for genome assembly and analysis**
David Schwartz, University of Wisconsin

"**Dark side" of genomes: What’s missing in current sequence assemblies?**
Can Alkan, University of Washington

Lunch

Session 3 presentations:

**Modernizing and managing genome assembly data**
Deanna Church, NIH/NLM/NCBI

**What quality do we need to achieve for Genome 10K genomes?**
Federica Di Palma, Broad Institute

**Announcement**
Laurie Goodman, BGI-Shenzhen

Break

Break-out groups:

**Genome Assembly and Assemblathon 2**
**Framework Physical Maps**
**Data Policy, Targets, and Standards**

Final group plenary reports

Closing remarks

Genome Assembly Workshop closes