

**GSC19 – Agenda**  
**Stamford Plaza, Brisbane**  
**The River Room, Level 2**

Time	Monday, May 15th 2017	Tuesday, May 16th 2017	Wednesday, May 17th 2017	Time
	<b>Theme: Bioinformatic Workflows and Databases</b>	<b>Theme: Viral and Eukaryal Genome Standards</b>	<b>Theme: Single Cell and Fine-Scale Genomics</b>	
8:30	Doors open for check-in/name badge			
9:00-9:15	Meeting Kickoff <b>GSC President, Local Host</b>	Crete Island Sampling Day (ISD) <b>Lynn Schriml</b>	Advancement in Metagenomic Standards - <b>Scott Tighe</b>	9:00-9:15
9:15-10:00	<b>Keynote 1 - Aaron Darling</b> Topic: The Critical Assessment of Metagenome Interpretation (CAMI): results, challenges, and the future	<b>Keynote 2 - Nikos Kyrpides</b> Topic: Virus standards, mining from metagenomes	<b>Keynote 3 - Tanja Woyke</b> Topic: Single-cell sequencing: from standards to novel function-based approaches	9:15-10:00
10:00-10:30	MORNING TEA	MORNING TEA	MORNING TEA	10:00-10:30
10:30-12:30	Speaker session (20+5’): Chair: Folker Meyer <ul style="list-style-type: none"> <li>• <b>Michael Crusoe</b> - Comparable, portable, and reusable metagenomics workflows with the Common Workflow Language</li> <li>• <b>Donovan Parks</b> - Mining population genomes from public metagenomes</li> <li>• <b>Jodie Van de Kamp</b> - Australian Microbial Diversity (AMD database)</li> <li>• <b>Scott Tighe</b> - Genomic Investigations in Antarctica</li> </ul>	Speaker session (20+5’): Chair: Lynn Schriml <ul style="list-style-type: none"> <li>• <b>Thomas Rattei</b> - Viral Protein Families</li> <li>• <b>Jan Meier-Kolthoff</b> - Exploring the Virosphere - a Novel Bioinformatic Approach for the Genome-based Classification and Phylogeny of Viruses</li> <li>• <b>Pelin Yilmaz</b> - Towards a unified eukaryotic taxonomy</li> <li>• <b>Guy Cochrane</b> - Eukaryal genome standards</li> </ul>	Speaker session (20+5’): Chair: Guy Cochrane <ul style="list-style-type: none"> <li>• <b>Jian Xu</b> - Ramanome and metaramanome: label-free functional imaging of microbial population and consortium at single-cell resolution</li> <li>• <b>Howard Ochman</b> - Bacteria, Archaea and the Species Problem</li> <li>• <b>Maria Dzunkova</b> - Linking bacterial dark matter with viral dark matter</li> <li>• <b>Chris Rinke</b> - Lower input metagenomics and single cell QC</li> </ul>	10:30-12:30
12:30-14:00	LUNCH	LUNCH & <b>Group Photo</b>	LUNCH	12:30-14:00
14:00-15:00	General Discussion: Challenge/Problem Soapbox:  Topics: (short) – 5 slides max, challenges and how to deal with them in relation to “Bioinformatic Workflows and Databases”. For example: <i>how public is public data?</i>	General Discussion: Challenge/Problem Soapbox:  Topics: (short) - 5 slides max, challenges and how to deal with them in relation to “Viral and Eukaryal Genome Standards”. For example: <i>concatenated gene-based viral taxonomy.</i>	General Discussion: Challenge/Problem Soapbox:  Topics: (short) - 5 slides max, challenges and how to deal with them in relation to “Single Cell and Fine-Scale Genomics”. For example: <i>naming taxa without cultures.</i>	14:00-15:00
15:00-15:15	AFTERNOON TEA	AFTERNOON TEA	AFTERNOON TEA	15:00-15:15
15:15-16:30	Breakout sessions: working session towards a common QC <ul style="list-style-type: none"> <li>• GTDB demo and discussion</li> <li>• Data submission</li> </ul>	Breakout sessions: <ul style="list-style-type: none"> <li>• Viral taxonomy</li> <li>• Expanding Standards</li> </ul>	Breakout sessions: <ul style="list-style-type: none"> <li>• Outreach/grants/conferences/ future directions</li> </ul>	15:15-16:30
16:30-17:00			Handoff GSC 20 & Meeting Close	16:30-17:00
18:30		Dinner at “Brasserie Marquee” Ground Floor, Stamford Plaza		