Friday 20 April

18:00	20:00	**REGISTRATION OPENS in Fira Palace**
20:00	21:30	**WELCOME RECEPTION in CaixaForum (access map)**

Saturday 21 April

8:00	8:50		**REGISTRATION**
8:50	9:00		**Opening Remarks (Roderic GUIGÓ and Benny CHOR)**
Session 1. Chair: Roderic GUIGÓ (CRG, Barcelona ES)			
9:00	10:00		**Richard DURBIN** *The Wellcome Trust Sanger Institute, Hinxton UK* **"Computational analysis of population genome sequencing data"**
10:00	10:20	44	Yaw-Ling Lin, Charles Ward and Steven Skiena Synthetic Sequence Design for Signal Location Search
10:20	10:40	62	Kai Song, Jie Ren, Zhiyuan Zhai, Xuemei Liu, Minghua Deng and Fengzhu Sun Alignment-Free Sequence Comparison Based on Next Generation Sequencing Reads
10:40	11:00	178	Yang Li, Hong-Mei Li, Paul Burns, Mark Borodovsky, Gene Robinson and Jian Ma TrueSight: Self-training Algorithm for Splice Junction Detection using RNA-seq
11:00	11:30		*coffee break*
Session 2. Chair: Bonnie BERGER (MIT, Cambrige US)			
11:30	11:50	139	Son Pham, Dmitry Antipov, Alexander Sirotkin, Glenn Tesler, Pavel Pevzner and Max Alekseyev PATH-SETS: A Novel Approach for Comprehensive Utilization of Mate-Pairs in Genome Assembly
11:50	12:10	171	Yan Huang, Yin Hu and Jinze Liu A Robust Method for Transcript Quantification with RNA-seq Data
12:10	12:30	120	Zhanyong Wang, Farhad Hormozdiari, Wen-Yun Yang, Eran Halperin and Eleazar Eskin CNVeM: Copy Number Variation detection Using Uncertainty of Read Mapping
12:30	12:50	205	Dmitri Pervouchine Evidence for widespread association of mammalian splicing and conserved long range RNA structures
12:50	13:10	169	Melissa Gymrek, David Golan, Saharon Rosset and Yaniv Erlich lobSTR: A Novel Pipeline for Short Tandem Repeats Profiling in Personal Genomes
13:10	13:30	217	Rory Stark Differential oestrogen receptor binding is associated with clinical outcome in breast cancer
13:30	15:00		*lunch break*
Session 3. NSF Sponsored Special Session on Challenges in Computational Biology. **Chairs: Mona SINGH** (Princeton University, Princeton US) and **Mitra BASU** (The National Science Foundation)			
15:00	15:20		Laxmi Parida (IBM Research) "Combinatorics: an underdog in the tool-box?"
15:20	15:40		Dirk Evers (New York Genome Center) "The Effect of Ubiquitous DNA Sequencing"
15:40	16:00		Teresa Przytycka (NIH/NLM/NCBI) "From genotype to phenotype: exploiting molecular structure, networks and dynamics"
16:00	16:20		Christina Leslie (Memorial Sloan-Kettering Cancer Center) "New insights into regulatory transcriptomics from next-generation sequencing"
16:20	16:40		Amos Tanay (Weizmann Institute of Science) "Being average is not cool anymore - computational biology in the era of single-cell experiments"
16:40	17:30		*coffee break*

17:30	18:30		Business Meeting
			    RECOMB2012 / RECOMB-Seq Statistics: Roderic Guigó, Benny Chor
			    RECOMB2013 Presentation: Xuegong Zhang
			    ISCB/ISMB Presentation: Michal Linial
			    RECOMB Satellites Presentation:
			    - RECOMB Computational Proteomics (Vineet Bafna)
			    - RECOMB Comparative Genomics (David Sankoff)
			    - RECOMB Algorithmic Biology and RECOMB Bioinformatics Education (Pavel Pevzner)
			    - RECOMB Regulatory Genomics and RECOMB Systems Biology (Miguel Ángel Pujana)
			    - RECOMB Computational Cancer Biology (TBA)
			    Open Discussion

18:30	20:00		**Saturday Poster Session**

Sunday 22 April

Session 4. Chair: Benny CHOR (Tel-Aviv University, Tel-Aviv, IL)			
9:00	10:00		**Ada E. YONATH** *Weizmann Institute of Science, Rehovot IL* **"A vestige of a prebiotic RNA bonding apparatus is embedded and functions within the modern ribosome"**
10:00	10:20	142	Stefan Canzar, Mohammed El-Kebir, Rene Pool, Khaled Elbassioni, Alpesh Malde, Alan Mark, Daan Geerke, Leen Stougie and Gunnar W. Klau Charge Group Partitioning in Biomolecular Simulation
10:20	10:40	71	Lu He, Fabio Vandin, Gopal Pandurangan and Chris Bailey-Kellogg Ballast: A Ball-based Algorithm for Structural Motifs
10:40	11:00	45	Raheleh Salari, Chava Kimchi-Sarfaty, Michael Gottesman and Teresa Przytycka Detecting SNP-induced structural changes in RNA: application to disease studies
11:00	11:40		*coffee break*
Session 5. Chair: Martin VINGRON (MPI, Berlin DE)			
11:40	12:00	185	Sivan Bercovici, Jesse Rodriguez, Megan Elmore and Serafim Batzoglou Ancestry inference in complex admixtures via variable-length Markov chain linkage models
12:00	12:20	160	Dan He, Buhm Han and Eleazar Eskin Optimal Algorithm for Haplotype Phasing with Imputation using Sequencing Data
12:20	12:40	100	Osvaldo Zagordi, Armin Toepfer, Sandhya Prabhakaran, Volker Roth, Eran Halperin and Niko Beerenwinkel Probabilistic inference of viral quasispecies subject to recombination
12:40	13:00	33	Imran Rauf, Florian Rasche, Francois Nicolas and Sebastian Bocker Finding Maximum Colorful Subtrees in practice
13:00	14:30		*lunch break*
Session 6. "A memorial to one of the first Genomicist: Roy Britten" **Chair: Temple F. SMITH**			
14:30	14:40		Introductory words by **Temple F. SMITH**
14:40	15:00	206	David Sankoff A model for biased fractionation after whole genome duplication
15:00	15:20	2	Babak Alipanahi Ramandi, Nathan Krislock, Henry Wolkowicz, Ali Ghodsi, Logan Donaldson and Ming Li Protein Structure by Semidefinite Facial Reduction
15:20	15:40	119	Christina Schmiedl, Mathias Mohl, Steffen Heyne, Mika Amit, Gad M. Landau, Sebastian Will and Rolf Backofen Exact Pattern Matchings for RNA Structure Ensembles
15:40	16:00	38	Zhizhuo Zhang, Cheng Wei Chang, Willy Hugo, Edwin Cheung and Wing-Kin Sung Simultaneously Learning DNA Motif along with Its Position and Sequence Rank Preferences through EM Algorithm
16:00	16:30		*coffee break*
16:30	17:50		**NFS Panel "Emerging Areas and Challenges in Computational Biology"** Moderator: Benny Chor Participants: **Dirk Evers** (New York Genome Center), **Christina Leslie** (Memorial Sloan-Kettering Cancer Center), **Laxmi Parida** (IBM Research), **Teresa Przytycka** (NIH/NLM/NCBI), **Richard Durbin** (The Wellcome Trust Sanger Institute), **Thomas Gingeras** (Cold Spring Harbor Laboratory).
17:50	19:20		**Sunday Poster Session**

Monday 23 April

Session 7. PRACE Sponsored Session. Chair: Modesto OROZCO (IRB, BSC, UB)		
9:00	9:05	Introductory words by **Modesto OROZCO**
9:05	10:00	**Alfonso VALENCIA** *Spanish National Cancer Research Centre (CNIO) and Spanish National Bioinformatics Institute (INAB), Madrid ES* **"Protein Networks in the Analysis of Cancer Genome Data"**
10:00	10:20	58 Roded Sharan and Richard Karp Reconstructing Boolean models of Signaling
10:20	10:40	83 Sayed Mohammad, Ebrahim Sahraeian and Byung-Jun Yoon RESQUE: Network reduction using semi-Markov random walk scores for efficient querying of biological networks
10:40	11:00	103 Nurcan Tuncbag, Alfredo Braunstein, Andrea Pagnani, Shao-Shan Carol Huang, Jennifer Chayes, Christian Borgs, Riccardo Zecchina and Ernest Fraenkel Simultaneous reconstruction of multiple signaling pathways via the prize-collecting Steiner forest problem
11:00	11:40	*coffee break*
Session 8. Chair: Vineet BAFNA (University of California, San Diego)		
11:40	12:00	184 Hua Wang, Heng Huang and Chris Ding Function-Function Correlated Multi-Label Protein Function Prediction over Interaction Networks
12:00	12:20	164 Hua Wang, Heng Huang and Chris Ding Predicting Protein-Protein Interactions from Multimodal Biological Data Sources via Nonnegative Matrix Factorization
12:20	12:40	242 T. M. Murali Network-Based Prediction and Analysis of HIV Dependency Factors
12:40	13:00	1 Matthew Francis and Elana Fertig Quantifying the dynamics of coupled networks of switches and oscillators
13:00	14:30	*lunch break*
Session 9. Chair: Michal Ziv-Ukelson (Ben Gurion University of the Negev)		
14:30	14:50	166 Sebastien Roch and Sagi Snir Recovering a tree-like trend of evolution despite extensive lateral genetic transfer: A probabilistic analysis
14:50	15:10	236 Hector Corrada Bravo Increased methylation variation in epigenetic domains across cancer types
15:10	16:10	**Eileen FURLONG** *Genome Biology Unit, EMBL Heidelberg, Heidelberg DE* **"Understanding and predicting cis-regulatory activity"**
16:10	20:30	Free afternoon. We invite you to visit the activities related to Saint Georges festivity in Barcelona. More info in the book of abstracts.
20:30	23:00	Gala Dinner

Session 10. Chair: Cenk SAHINALP (Simon Fraser University, Burnaby CA)		
9:00	10:00	**Thomas GINGERAS** *Cold Spring Harbor Laboratory (CSHL), Cold Spring Harbor US* **"High resolution landscape of transcription in human cells"**
10:00	10:20	113 Andrew Parker, Karl Griswold and Chris Bailey-Kellogg Structure-Guided Deimmunization of Therapeutic Proteins
10:20	10:40	145 Sebastian Will, Michael Yu and Bonnie Berger Structure-based Whole Genome Realignment Reveals Many Novel Non-coding RNAs
10:40	11:00	141 Daniel Holtby, Shuai Cheng Li and Ming Li LoopWeaver - Loop Modeling by the Weighted Scaling of Verified Proteins
11:00	11:30	*coffee break*
Session 11. Chair: Cedric NOTREDAME (CRG, Barcelona ES)		
11:30	11:50	198 Dan DeBlasio, Travis Wheeler and John Kececioglu Estimating the Accuracy of Multiple Alignments and Its Use in Parameter Advising
11:50	12:10	16 Marcus Kinsella and Vineet Bafna Modeling the Breakage-Fusion-Bridge Mechanism: Combinatorics and Cancer Genomics
12:10	12:30	151 Andrew Mcpherson, Chunxiao Wu, Alexander Wyatt, Sohrab Shah, Colin Collins and Cenk Sahinalp Discovery of complex genomic rearrangements in cancer using high-throughput sequencing
12:30	12:50	207 Marc A. Marti-Renom The Three-Dimensional Architecture of a Bacterial Genome and Its Alteration by Genetic Perturbation
12:50	13:10	131 Patrick Holloway, Krister Swenson, David Ardell and Nadia El-Mabrouk Evolution of Genome Organization by Duplication and Loss: a Linear Programming approach
13:10	13:30	Best Paper, Best Poster and Test-of-Time AWARDS
13:30	15:00	*Goodbye Cocktail*
15:00		Departure