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Hatice Osmanbeyoglu and Xinghua Lu. Investigating Mechanisms of Estrogen-Mediated Repression of ERα Target Genes in Breast Cancer Cell Lines

Sean Chun-Chang Chen, Feng-Chi Chen and Wen-Hsiung Li. Distinct evolutionary rates of phosphorylated and nonphosphoryalted amino acid residues in mammals

David Sankoff, Chunfang Zheng and Baoyong Wang. A model for biased fractionation after whole genome duplication

Ana Paula Leite, Maxim N. Artyomov, Fadi Towfic and Aviv Regev. Systematic identification of topologically essential interactions in regulatory networks

David Knox and Robin Dowell. Automated Generation of Stochastic Model Rules for Single Cell Simulation of Transcriptional Regulation Mechanisms

Serghei Mangul, Adrian Caciula, Nicholas Mancuso, Ion Mandoiu and Alex Zelikovsky. Poster : An Integer Programming Approach to Novel Transcript Reconstruction from Paired-End RNA-Seq Reads

Noah Daniels, Raghavendra Hosur, Bonnie Berger and Lenore Cowen. SMURFLite: combining simplified Markov random fields with simulated evolution improves remote homology detection for beta-structural proteins

Andre E. Minoche, Juliane C. Dohm and Heinz Himmelbauer. Errors and biases in Illumina second generation sequencing data

Eva Maria Novoa, Mariana Pavon-Eternod, Tao Pan and Lluis Ribas de Pouplana. A role for tRNA modifications in genome structure and codon usage

Gwo-Yu Chuang, Jeffrey Boyington, Michael Joyce, Jiang Zhu, Gary Nabel, Peter Kwong and Ivelin Georgiev. Bioinformatics Prediction Of N-linked Glycosylation Incorporating Structural Properties and Patterns

Chan-Shuo Wu, Chun-Ying Yu, Ching-Yu Chuang, Hung-Chih Kuo and Trees-Juen Chuang. Identification and analysis of trans-splicing in human embryonic stem cells by transcriptome sequencing

Sayed Mohammad Ebrahim Sahraeian and Byung-Jun Yoon. NAPAbench: a comprehensive network alignment benchmark

Leonid Nazarov, Yan Stirmanov, Sergey Larionov, Sergey Rybalko, Eugene Ryadchenko and Alexander Loskutov. The Nature of Extremophiles Genomes Clusterization by Detrended Fluctuation Analysis

Aida Ouangraoua, Krister Swenson and Anne Bergeron. On the comparison of sets of alternative transcripts

Chih-Hung Chang, Hsiang-Iu Wang, Hsiang-Chia Lu, Hong-Hwa Chen, Chuan Yi Tang and Hsin-Hung Yeh. A hierarchical screening strategy for gene functional analysis using RNA interference

Oscar Flores and Modesto Orozco. Automatic annotation of nucleosome positions: from peaks to reads

Mario Fasold, David Langenberger, Hans Binder, Peter F. Stadler and Steve Hoffmann. DARIO: A ncRNA detection and analysis tool for next-generation sequencing experiments

Mahdi Belcaid, Anne Bergeron, Aida Ouangraoua, Philippe Lavoie-Mongrain, Nicolas Massoulier and Guylaine Poisson. Duplications in tape measure proteins

Shih-Yi Chao and A-Mei Huang. Metastatic Pathway Identification – a case study of prostate cancer

Yan Jing, Ping Han and Xiaofeng Song. Intracellular protein stability correlated with the features of the solvent accessible surface

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Florian Rasche, Kerstin Scheubert, Franziska Hufsky, Marco Kai, Ales Svatos and Sebastian Böcker. Characterisation of unknown metabolites by tandem mass spectrometry

Tobias Rausch, Thomas Zichner, Andreas Schlattl, Adrian Stütz, Vladimir Benes and Jan Korbel. DELLY: Structural variant discovery at single-nucleotide resolution

Rocio Rebollido-Rios, Stanislav Jakuschev and Daniel Hoffmann. HOW DOES THE CALCIUM BINDING COULD AFFECT THE SUSPECTED PROTEASE ACTIVITY OF SONIC HEDGEHOG?

Nadia El-Mabrouk, Yves Gagnon and Mathieu Blanchette. Ancestral Genome Reconstruction based on Gapped Adjacencies

Sangcheol Kim, Seulji Lee, Byungwook Lee, Sanghyuk Lee, Sungwon Kwon and Johan Lim. Stouffer's Test in a Large Scale Simultaneous Hypothesis Testing

Lydia Hopp, Henry Wirth, Mario Fasold, Markus Loeffler and Hans Binder. Portraying the expression landscapes of cancer subtypes

Krister Swenson and Nadia El-Mabrouk. Correcting Errors in Reconciliation

Asif Naqvi, Shaymaa Bahnassy, Kuldeep Uchadia, Rinkesh Goyal, Luccky Sharma and Aruna Devi. Study to test the inhibitory activity of THC- Δ9-tetrahydrocannabinol and its derivatives on Acetylcholinesterase (AChe) enzyme: A Molecular Modeling Study

Philippe Serhal and Sébastien Lemieux. Correction of spatial bias in oligonucleotide array data

Atsushi Niida, Seiya Imoto, Teppei Shimamura and Satoru Miyano. Statistical model-based testing for identification of recurrent genomic aberrations

Byungwook Lee. Quantification of transcriptome from RNA-Seq data by effective length normalization

Matthias Scholz. A missing data approach to validate nonlinear PCA

Çiğdem Sevim Bayrak and Burak Erman. Predicting the Most Probable Conformations of a Given Peptide Sequence in the Random Coil State

Thibaut Hourlier, Daniel Barrell, Susan Fairley, Magali Ruffier, Carlos Garcia Giron, Rishi Nag, Simon White, Andreas Kähäri, Amonida Zadissa, Bronwen Aken, Stephen Searle and Tim Hubbard. Ensembl and RNA-Seq: towards better genome annotation!

Melanie Schirmer, Christopher Quince, William T. Sloan and David Taylor. Benchmarking of Viral Haplotype Reconstruction Programs

H.M.Mahadeva Swamy, Ramasamy Asokan and Riaz Mahmood. Bacillus thuringiensis Cry1I and Cry3A Coleopteran-active insecticidal crystal Proteins: Homology-based 3D Modelling and Implications for Toxin Activity

Rahul Agarwal, Matthew Kent, Eli Grindflek, Maren Van Son and Sigbjørn Lien. Whole-Genome Resequencing Identifies Variants Within QTL Regions for Boar Taint

Kwang Su Jung and Kiejung Park. An aCGH-based Tool for Detecting Genomic Variation

Reshmi G, Sona Charles and Radhakrishna .M Pillai. Systems-Level Dynamical Network Modeling for Identifying Interactomes of Innate Immune Pathways in Dengue Hemorrhagic Fever

Mar Gonzàlez-Porta, Miquel Calvo, Michael Sammeth and Roderic Guigó. Estimation of alternative splicing variability in human populations

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Marie Trussart, Davide Bau, Marc A. Marti-Renom, Eva Yus Najera and Luis Serrano Pubul. The three-dimensional genome conformation of Mycoplasma pneumoniae

Ionas Erb, Juan Ramon González-Vallinas, Giovanni Bussotti, Enrique Blanco, Eduardo Eyras and Notredame Cedric. Use of ChiP-Seq data for the design of a multiple promoter-alignment method

Joao Curado, Hagen Tilgner and Roderic Guigo. Modeling splicing from chromatin

Juliane C. Dohm, Andre E. Minoche, Daniela Holtgraewe, Thomas Rosleff Sörensen, Richard Reinhardt, Hans Lehrach, Bernd Weisshaar and Heinz Himmelbauer. Drafting a large genome at high quality: Multi-platform sequence assembly and integration with genetic and physical maps of sugar beet (Beta vulgaris)

Sumeet Dua and Afolabi Olomola. Functional Model Discovery from Gene Expression Time Series using Markov Models

Fernando Meyer, Stefan Kurtz and Michael Beckstette. Fast and flexible approximate database search for RNA sequence-structure patterns

Md Jamiul Jahid and Jianhua Ruan. A randomized Steiner-tree approach for biomarker discovery and classification for breast cancer metastasis

Ines de Santiago, Tom Carroll and Ana Pombo. SeqGI: Sequence Read Enrichment at Genomic Intervals

Danielle Hyun-Jin Choi and Brett Tyler. Mathematical Modeling of Phytophthora sojae Effector Gene Evolution

Youn-Jae Kim, Jong-Eun Lee, Heon Yoo, Seung-Hoon Lee and Jong Bae Park. Lung cancer brain metastasis-specific mutations identified by exome sequencing

Yuri Pritykin and Mona Singh. Confirmation of Date and Party Hubs across Organisms

Seung Gu Park and Sun Shim Choi. Evolutionary non-random flow of synonymous codon usage in multiple organisms

Jae Yong Nam, Seung Gu Park and Sun Shim Choi. Analysis of evolutionary characteristics of protein secondary structural units

Biter Bilen and Mihaela Zavolan. Probabilistic framework to identify crosslinked positions in RNA-binding protein crosslinking and immune-precipitation data

José Ignacio Lucas Lledó and Mario Cáceres. Detection of chromosomal inversions with paired-end sequencing

Jascha Casadio, Oriol Fornés, Elena Hidalgo, José Ayté, Isabel Calvo Arnedo, Patricia Garcia and Baldo Oliva. A computational analysis of the regulation of oxidative stress genes in S. pombe by Pap1 and Prr1

Nikita Alexeev. Random matrix approach and Combinatorial topology approach to Sorting by transpositions

Fahad Syed, Mikko Arvas, Marja Ilmen and Tiina Nakari-Setala. Comparison of Bacterial Genomes

Thomas Bonfert, Gergely Csaba, Ralf Zimmer and Caroline C. Friedel. A context-based approach to identify the most likely mapping for RNA-seq experiments

Santi González, Bàrbara Montserrat-Sentís, Friman Sánchez, Montserrat Puiggròs, Enrique Blanco, Laura Martinez, Alex Ramirez and David Torrents. Prediction of regulatory regions using ReLA

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Oznur Tastan, Yanjun Qi, Jaime G. Carbonell and Judith Klein-Seetharaman. Refining Literature Curated HIV-1, Human Protein-Protein Interactions Using Expert Opinions

Juan González-Vallinas and Eduardo Eyras. Predicting and characterizing active enhancers in cancer using high-throughput sequencing data

Arnald Alonso, Sara Marsal and Antonio Julià. CNStream2: a fast and highly accurate tool for SNP and CNV genotyping with Illumina microarrays

Jairo Rocha and Ricardo Alberich. The Significance of the ProtDeform Score for Structure Prediction and Alignment

Sonja Althammer, Amadis Pages and Eduardo Eyras. Models of regulatory genomics

Ole Schulz-Trieglaff, Elizabeth Murchison, Zemin Ning and Anthony Cox. The devil is in the detail: mining and annotating genomic variants in the Tasmanian Devil facial tumour genome

Paweł P. Łabaj and David P. Kreil. Improving RNA-Seq precision with MapAl

Tobias Marschall, Ivan Gesteira Costa, Stefan Canzar, Markus Bauer, Gunnar W. Klau, Alexander Schliep and Alexander Schoenhuth. CLEVER: Clique-Enumerating Variant Finder

Sílvia Bonàs, Josep M. Mercader and David Torrents. Empirical evaluation of different modern reference panels for imputation and their implication for Genome Wide Association Studies.

Hayan Lee and Michael Schatz. Genomic Dark Matter: The reliability of short read mapping illustrated by the Genome Mappability Score

Boris Fedorov, Leonid Zaslavsky, Vyacheslav Chetvernin, Stacy Ciufo, Boris Kiryutin, Kathleeen O'Neill, Alexandre Souvorov, Igor Tolstoy and Tatiana Tatusova. Integrated system for bacterial pan-genome analysis

Miler Lee, Ariel Bazzini, Polloneal Ocbina, Carter Takacs and Antonio Giraldez. Computational analysis of ribosome profiling data to characterize translational dynamics in Zebrafish

Itrat Fatima and Shaneen Singh. Computational Analysis of GRAM domains in the model plant Arabidopsis thaliana.

Irina Khrebtukova, Ryan Kelley, Shujun Luo, Tim Hill, Patrick Lau, Jennifer Chiniquy, Kathryn Stephens, Semyon Kruglyak and Gary P Schroth. Automated workflow for RNA-Seq analysis: application and testing with various types of RNA-Seq protocols

Jennifer Fang, Siddarth Selvaraj, Jesse Dixon, Feng Yue, Ming Hu, Ke Deng, Zhaohui Qin, Yixin Zhu, Jun Liu and Bing Ren. 3D Chromosome Structure Visualization from Hi-C Data

Orion Buske, Ashokkumar Manickaraj, Seema Mital and Michael Brudno. Identification of deleterious synonymous variants in human genomes

James Morton, Patricia Abrudan, Chun Liang and John Karro. Tools for Cleaning NGS Transciptome Data

Andreas Untergasser, Ioana Cutcutache, Triinu Koressaar, Jian Ye, Brant C. Faircloth, Maido Remm and Steve Rozen. Primer3 - New Capabilities and Interfaces

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Jeeyoung Shin, Minkyu Shin and Yangseok Kim. Association Investigator: The intelligent for investigating the relationship between genomics data and clinical variables

Ray Marin and Jiri Vanicek. PACCMIT: Prediction of ACcessible and/or Conserved MIcroRNA Targets

Marta Mele, Roderic Guigó and Tomàs Marquès. Studying lncRNAs in great ape evolution

Merja Oja, Paula Jouhten, Eija Rintala, Mervi Toivari, Marilyn Wiebe, Laura Ruohonen and Merja Penttilä. Systems biology for studying the physiology of acid producing yeast

Jeongkyun Kim, Hee-Jin Lee, Jong C. Park and Hyunju Lee. A search engine for recommending cancer-related genes based on literature evidence

Catarina Allegue, Óscar Campuzano, Lucía Quintana, Carles Ferrer, Sergio Castillo, Eduardo Salas, Mónica Bayés, Simon Heath, Anna María Iglesias, Mónica Coll and Ramon Brugada. VALIDATION OF A NGS STRATEGY FOR GENETIC SCREENING OF SUDDEN CARDIAC DEATH

Panagiotis Papasaikas and Juan Valcarcel. Multiple Links between Splicing Regulation and Chromatin Revealed by an Integrated Analysis of High-throughput Chromatin and Splicing Perturbation Data.

Juan Ramon Tejedor, Panagiotis Papasaikas and Juan Valcarcel. Reconstruction of a Splicing Regulatory Circuitry Involved in Cell Proliferation and Apoptosis.

John R. .Mcpherson, Yingting Wu, Patrick Tan and Steve Rozen. Identifying Genomic Copy Number Alteration and Loss of Heterozygosity in Next-Generation Sequence Data

Teppei Shimamura, Seiya Imoto, Atsushi Niida and Satoru Miyano. Identification of key methylated genes from patient-specific gene networks

Agata Wesołowska, Louise Borst, Marlene Dalgaard, Louise Helt, Hans Madsen, Hanne Marquart, Peder Wehner, Morten Rasmussen, Eske Willerslev, Thomas Gilbert, Søren Brunak, Kjeld Schmiegelow and Ramneek Gupta. Relating genomic variation to drug response in childhood acute lymphoblastic leukemia

Baeksoo Kim and Hyunju Lee. A cancer text ranking algorithm based on cancer-related terms

Andreas Leha, Tim Beißbarth and Klaus Jung. Predicting Ordinal Response in High-Dimensional Datasets

Nikolay Chekanov, Egor Prokhortchouk, Artem Artemov, Artem Nedoluzhko, Eugenia Bulygina, Sergey Rastorguev, Svetlana Tsygankova, Natalia Gruzdeva and Konstantin Skryabin. A family study of early-onset Alzheimer's disease

Sònia Casillas, Can Alkan, Evan E Eichler and Mario Cáceres. Calling inversions from Next-Generation Sequencing Paired-End Mapping data with GRIAL

Evrim Besray Unal, Maria Lluch, Eva Yus, Yogi Jaeger and Luis Serrano. Reverse Engineering of Mycoplasma pneumoniae Gene Regulatory Network

Paweł Bednarz, Agnieszka Podsiadło, Joanna Giemza, Norbert Dojer and Bartek Wilczynski. BNFinder2: efficient software for learning Bayesian networks

Cemal Erdem, Alper Demir, Ahmet Gül and Burak Erman. Mathematical Modeling of a Human Immune-Mediated Auto-Inflammatory Disease

Ian Streeter, David Thybert, Klara Stefflova, Laura Clarke, Duncan Odom and Paul Flicek. A comparison of read-mapping and de novo assembly methods for calling inter-species variants between Mus caroli and Mus musculus

Prerna Dua, Chaitanya Pinnamaneni, Pradeep Chowriappa and Walter Lukiw. A Co-expression Network Based Approach for Gene Expression Analysis in Alzheimer's' Disease Progression

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Alexander Martinez Fundichely, Meritxell Oliva Pavia, Juan Ramon Gonzalez Ruiz, Sònia Casillas and Mario Cáceres. Accurate prediction of inversions in the human genome from paired-end mapping data with the GRIAL algorithm.

Layla Oesper, Anna Ritz, Sarah Aerni, Ryan Drebin and Ben Raphael. Reconstructing Cancer Genomes from Paired-end Sequencing Data

Maike Ahrens, Jörg Rahnenführer, Christian Stephan and Martin Eisenacher. Detecting features from OMICS data that contain subgroups of patients with differential values

Sinan Erten, Salim A. Chowdhury, Xiaowei Guan, Rod K. Nibbe, Jill S. Barnholtz-Sloan, Mark R. Chance and Mehmet Koyuturk. Identifying stage-specific protein subnetworks for colorectal cancer

Derya Aydın, Meltem Muftuoglu and Burak Erman. Identifying small molecule inhibitors targeting base excision repair enzymes DNA polymerase γ and β to increase the effects of cancer treatment

Rachita Yadav, Klaus Bønnelykke, Thomas Nordahl Petersen, Anne Mølgaard, Hans Bisgaard and Ramneek Gupta. Machine learning risk prediction of childhood asthma.

David Dufour and Marc A. Marti-Renom. RNA structure prediction by knowledge-based statistical potentials and Selective 2′-Hydroxyl Acylation and Primer Extension (SHAPE)

Susanne Balzer, Ketil Malde, Inge Jonassen and Markus A. Grohme. Filtering duplicate reads from 454 pyrosequencing data

Oliver Drechsel, Rubayte Rahman and Stephan Ossowski. Clinical application and computational analyses of Exome-seq for disease studies

Kalliopi Tsafou, Damian Plichta, Branka Radić, Uwe Rix, Giulio Superti-Furga, Irene Kouskoumvekaki and Ramneek Gupta. Investigating the Genomic Landscape of Ewing Sarcoma

Matthew Ruffalo, Mehmet Koyuturk, Soumya Ray and Thomas Laframboise. Accurate Estimation of Short Read Mapping Quality for Second-Generation Genome Sequencing

Jon Hallander, Petter Lindgren, Pär Larsson and Andreas Sjödin. A microbial forensic approach using Ultra-Deep Sequencing (UDS) for analysis of haplotype spectra in clonal bacterial strains

Yuichi Shiraishi, Yusuke Sato, Aiko Sato-Otsubo, Yusuke Okuno, Shigekatsu Maekawa, Hidewaki Nakagawa, Seishi Ogawa and Satoru Miyano. Fusion gene detection by using soft clipping information

Juris Viksna, Karlis Freivalds and Paulis Kikusts. Application of graph clustering and visualization methods for detection of evolutionary related groups of proteins

Chiara Fornari, Francesca Cordero, Marco Beccuti, Stefania Lanzardo, Laura Conti, Federica Cavallo, Gianfranco Balbo and Raffaele Calogero. Multi-level model for the investigation of oncoantigen-driven vaccination effect

Marc Friedländer, Esther Lizano, Eulàlia Martí and Xavier Estivill. NATA: a combined wetlab and drylab method for naïve transcriptome analysis

Oriol Fornes and Baldo Oliva. Prediction of DNA-binding specificities using statistical potentials

Eva König, Lars Feuerbach, Barbara Hutter, Matthias Schlesner, Qi Wang, Benedikt Brors and Thomas Lengauer. Improving loss of heterozygosity identification by tumor purity estimation

Matthew Edwards and David Gifford. High-resolution genetic mapping with pooled sequencing

Joseph Herman, Ádám Novák, Rune Lyngsø and Jotun Hein. A probabilistic framework for incorporating alignment uncertainty into multiple sequence analysis

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Abhishek Mitra and Maga Rowicka. Instant-Seq:- an integrated tool with web interface for fast analysis of ChIP-Seq data

Dhany Saputra, Thomas Sicheritz Pontén and Ole Lund. Reads2Type: An Online Tool for Rapid Bacterial Typing

Sana Ben Mustapha, Hend Ben Tamarzizst, Ghada Baraket and Amel Salhi Hannachi. SSR markers and sequences of the trnL intron to study polymorphism in Tunisian plum

Ornella Cominetti, David Smith, Nick Jones, Radek Erban, Philip Maini and Climent Casals-Pascual. Identification of new pathobiological clusters in severe malaria using unsupervised methods

Anna Ritz, Suzanne Sindi, Ali Bashir and Benjamin Raphael. A Probabilistic Method for Structural Variant Prediction from Strobe Sequencing Data

Anne Wenzel, Erdinc Akbasli and Jan Gorodkin. RIsearch: fast yet accurate RNA-RNA interaction search

Fabio Vandin, Hsin-Ta Wu, Eli Upfal and Ben Raphael. Algorithms to Find Mutated Pathways in Cancer

Jon Sveinbjornsson and Bjarni Halldorsson. BAM Region Viewer: A Viewer Application For BAM

Sonia Boughattas. SNPs identification, multiple alignment and network construction to analyze the polymorphism of Tunisian strains of the parasite Toxoplasma gondii

Maga Rowicka, Nicola Crosetto, Abhishek Mitra, Maria Joao Silva, Magda Bienko, Philippe Pasero and Ivan Dikic. BLESS: mapping DNA double-strand breaks by next-generation sequencing

Myungguen Chung and Kie-Jung Park. Automated analysis support system for Imputed Genotype based Case-Control Study with a Disease by using next-generation sequencing data

Nathan Boley. Integrative De Novo Transcriptome Assembly in Fruit Fly

Manway Liu, Anupama Reddy, Alan Huang, Giordano Caponigro and Joseph Lehar. Network Analysis of Pharmacologic, Genomic, and Transcriptomic Assays in Cancer Cell Lines

Alejandro Caceres, Suzanne Sindi, Benjamin Raphael, Mario Caceres and Juan Gonzalez. Identification of Polymorphic Inversions from Genotypes

Jin Zhang, Jiayin Wang and Yufeng Wu. Calling Structural Variations with Low-coverage Sequencing Data by Mapping to Focal Region

Jeanre Smit, Misha Le Grange, Phelelani Mpangase, Michal Szolkiewicz and Fourie Joubert. Discovery: a resource for the rational selection of drug target proteins and leads for the malaria parasite, Plasmodium falciparum