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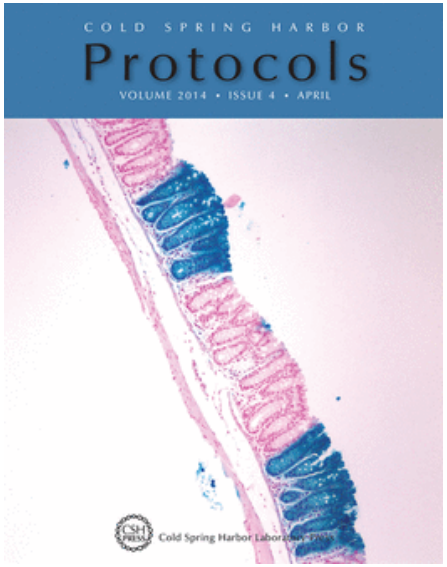

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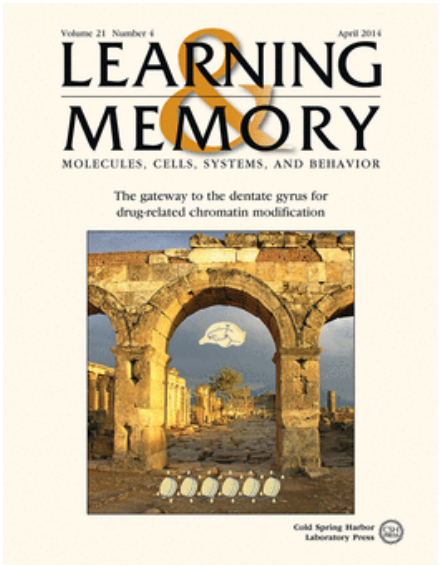

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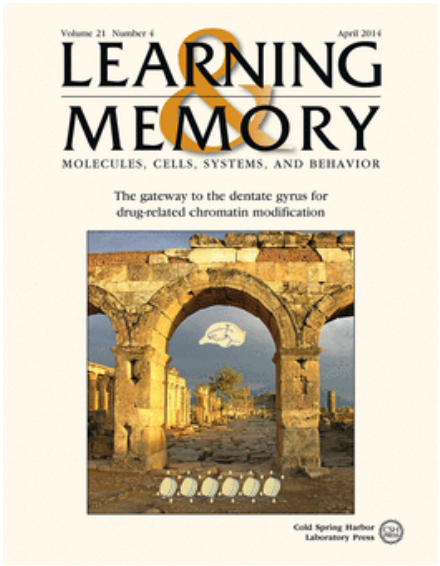

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Breakpoint profiling of 64 cancer genomes reveals numerous complex rearrangements spawned by homology-independent mechanisms

Ankit Malhotra[1], Michael Lindberg[1], Gregory G. Faust[1,2], Mitchell L. Leibowitz[1], Royden A. Clark[1], Ryan M. Layer[1,2], Aaron R. Quinlan[1,3,4,5] and Ira M. Hall[1,3,5]

+ Author Affiliations

Abstract

Tumor genomes are generally thought to evolve through a gradual accumulation of mutations, but the observation that extraordinarily complex rearrangements can arise through single mutational events suggests that evolution may be accelerated by punctuated changes in genome architecture. To assess the prevalence and origins of complex genomic rearrangements (CGRs), we mapped 6179 somatic structural variation breakpoints in 64 cancer genomes from seven tumor types and screened for clusters of three or more interconnected breakpoints. We find that complex breakpoint clusters are extremely common: 154 clusters comprise 25% of all somatic breakpoints, and 75% of tumors exhibit at least one complex cluster. Based on copy number state profiling, 63% of breakpoint clusters are consistent with being CGRs that arose through a single

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doi: 10.1101/gr.143677.112

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Abstract

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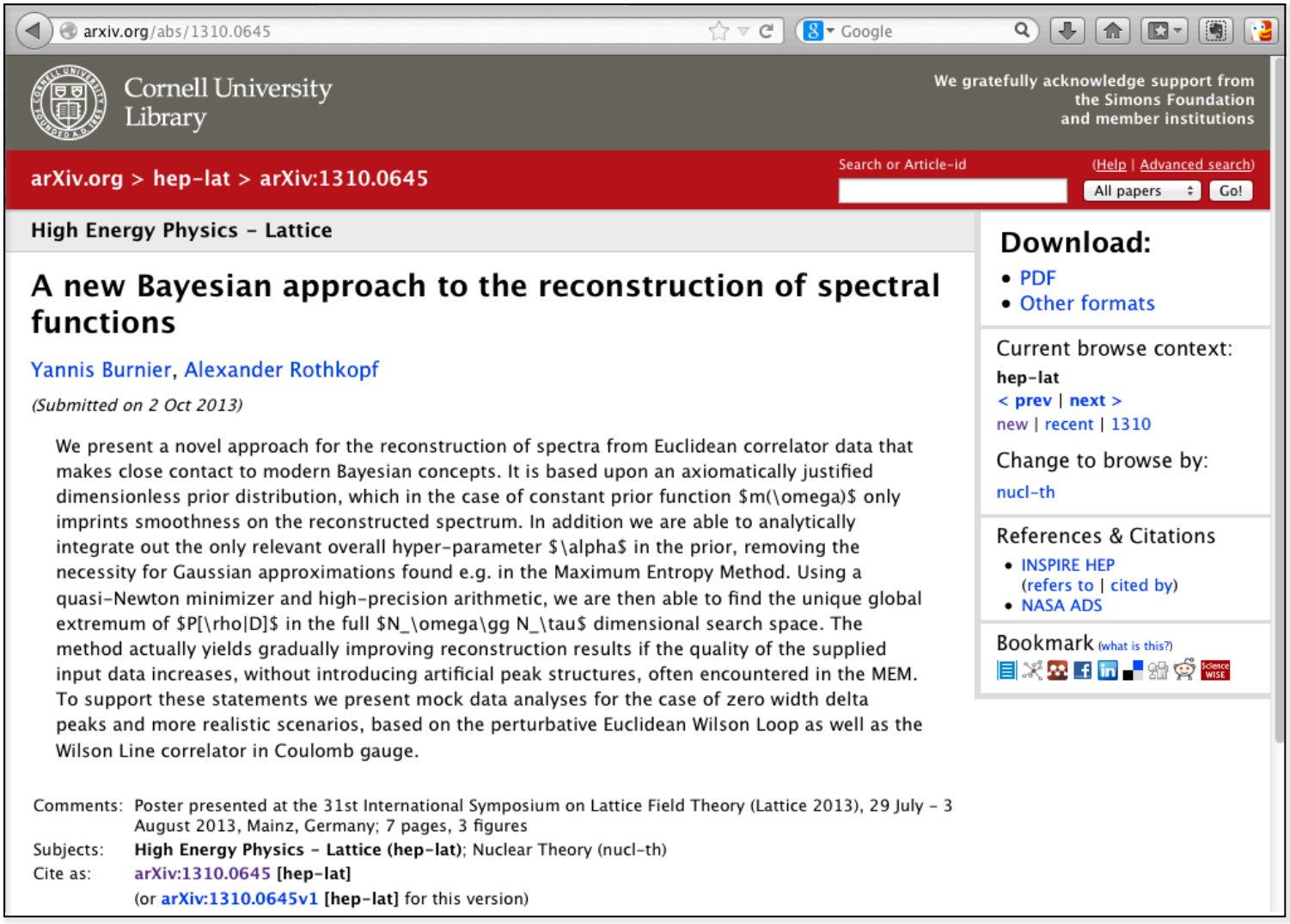

arxiv.org/abs/1310.0645

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We gratefully acknowledge support from the Simons Foundation and member institutions

High Energy Physics - Lattice

A new Bayesian approach to the reconstruction of spectral functions

Yannis Burnier, Alexander Rothkopf

(Submitted on 2 Oct 2013)

We present a novel approach for the reconstruction of spectra from Euclidean correlator data that makes close contact to modern Bayesian concepts. It is based upon an axiomatically justified dimensionless prior distribution, which in the case of constant prior function $m(\omega)$ only imprints smoothness on the reconstructed spectrum. In addition we are able to analytically integrate out the only relevant overall hyper-parameter α in the prior, removing the necessity for Gaussian approximations found e.g. in the Maximum Entropy Method. Using a quasi-Newton minimizer and high-precision arithmetic, we are then able to find the unique global extremum of $P[\rho|D]$ in the full $N_\omega\gg N_\tau$ dimensional search space. The method actually yields gradually improving reconstruction results if the quality of the supplied input data increases, without introducing artificial peak structures, often encountered in the MEM. To support these statements we present mock data analyses for the case of zero width delta peaks and more realistic scenarios, based on the perturbative Euclidean Wilson Loop as well as the Wilson Line correlator in Coulomb gauge.

Comments: Poster presented at the 31st International Symposium on Lattice Field Theory (Lattice 2013), 29 July - 3 August 2013, Mainz, Germany; 7 pages, 3 figures

Subjects: **High Energy Physics - Lattice (hep-lat)**; Nuclear Theory (nucl-th)

Cite as: arXiv:1310.0645 **[hep-lat]**

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Taylor Jensen, Sung K Kim, Zhanyang Zhu, Christine Chin, Claudia Gebhard, Tim Lu, Cosmin Deciu, Dirk van den Boom, Mathias Ehrich

bioRxiv doi: 10.1101/004101 New Results

Filament formation by metabolic enzymes is a specific adaptation to an advanced state of cellular starvation

Ivana Petrovska, Elisabeth Nüske, Matthias C Munder, Gayathrie Kulasegaran, Liliana Malinovska, Sonja Kroschwald, Doris Richter, Karim Fahmy, Kimberley Gibson, Jean-Marc Verbavatz, Simon Alberti

bioRxiv doi: 10.1101/003277 Revised version New Results

Selection signatures in worldwide Sheep populations

Maria-Ines Fariello, Bertrand Servin, Gwenola Tosser-Klopp, Rachelle Rupp, Carole Moreno, International Sheep Genomics Consortium n.a., Magali San Cristobal, simon boitard

bioRxiv doi: 10.1101/001453 Revised version New Results

APRIL 10, 2014

Natural CMT2 variation is associated with genome-wide methylation changes and temperature adaptation

Xia Shen, Jennifer De Jonge, Simon Forsberg, Mats Pettersson, Zheya Sheng, Lars Hennig, Örjan Carlborg

bioRxiv doi: 10.1101/004119 New Results

MixMir: microRNA motif discovery from gene expression data using mixed linear models

LIYANG Diao, Antoine Marcais, Scott Norton, Kevin C. Chen

bioRxiv doi: 10.1101/004010 Revised version New Results

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Joseph Pickrell, David Reich
doi: 10.1101/003517

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Leonid Kruglyak, UCLA and HHMI, in *Nature*