

CS548

ASSIGNMENT 0 (DUE FEB 6, 2020)

Computer Science Department
Colorado State University

January 30, 2020

1. Summary of cancer bioinformatics papers [50 pts].

Read the following papers and also recursive references therein and summarize the topic covered by these papers. You need to understand and summarize the general problem that these works are trying to solve, the motivation for the problem and various solution approaches.

- Farzad Abdolhosseini, Behrooz Azarkhalili, Abbas Maazallahi, Aryan Kamal, Seyed Abolfazl Motahari, Ali Sharifi-Zarchi, Hamidreza Chitsaz. Cell Identity Codes: Understanding Cell Identity from Gene Expression Profiles using Deep Neural Networks, Scientific Reports 9, Article number: 2342, 2019
- Behrooz Azarkhalili, Ali Saberi, Hamidreza Chitsaz, Ali Sharifi-Zarchi. DeePathology: Deep Multi-Task Learning for Inferring Molecular Pathology from Cancer Transcriptome, Scientific Reports 9, Article number: 16526, 2019
- Runpu Chen, Le Yang, Steve Goodison, Yijun Sun. Deep-learning approach to identifying cancer subtypes using high-dimensional genomic data, Bioinformatics, btz769, 2019
- Bong-Hyun Kim, Kijin Yu, Peter C W Lee. Cancer classification of single-cell gene expression data by neural network, Bioinformatics, btz772, 2019

2. Summary of RNA-RNA interaction bioinformatics papers [50 pts].

Read the following papers and also recursive references therein and summarize the topic covered by these papers. You need to understand and summarize the general problem that these works are trying to solve, the motivation for the problem and various solution approaches.

- Hamidreza Chitsaz, Raheleh Salari, S. Cenk Sahinalp, Rolf Backofen. A Partition Function Algorithm for Interacting Nucleic Acid Strands, Bioinformatics 25(12): i365-i373; (doi:10.1093/bioinformatics/btp212) Also, 17th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB/ECCB) 2009, Stockholm, Sweden
- Ali Ebrahimpour-Boroogeny, Sanjay Rajopadhye, Hamidreza Chitsaz. BPPart and BPMax: RNA-RNA Interaction Partition Function and Structure Prediction for the Base Pair Counting Model, arXiv, arXiv:1904.01235 [q-bio.BM]

- Gong J, Shao D, Xu K, Lu Z, Lu ZJ, Yang YT, Zhang QC. RISE: a database of RNA interactome from sequencing experiments, *Nucleic Acids Res.* 46(D1):D194-D201, 2018
- Jiri Sponer, Giovanni Bussi, Miroslav Krepl, Pavel Banas, Sandro Bottaro, Richard A. Cunha, Alejandro Gil-Ley, Giovanni Pinamonti, Simon Poblete, Petr Jurecka, Nils G. Walter, and Michal Otyepka. RNA Structural Dynamics As Captured by Molecular Simulations: A Comprehensive Overview, *Chem Rev.* 118(8): 4177–4338, 2018

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