

***Histone Modification – Cause or Consequence?***

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**Abstract:**

There exist a variety of transcription factors, regulating gene expression. On the other hand, it has been recently reported that histone modifications have correlations with gene expression patterns, suggesting histone codes as regulators. Which is dominant in the cell?

Benveniste *et al.* [1] investigated databases of histone modification and transcription factor binding patterns [2, 3]. They reported that DNA sequence can fairly well predict how likely the corresponding histone is modified, and transcription factor binding (TF ChIP-Seq) data can even better predict the histone modification. This result suggests that histone modifications are not necessarily direct regulators of gene expression; their association with gene expression can be explained equally well by interactions between transcription factors and histone-modifying complexes.

This work is a purely informatics study on static, ensemble-averaged data. Contrasting with the study, I would like to discuss also the potential of our “physical” studies including dynamics, to elucidate the causality in such processes.

**References:**

1. D. Benveniste, H.-J. Sonntag, G. Sanguinetti, D. Sproul, “Transcription factor binding predicts histone modifications in human cell lines”, *Proc. Natl. Acad. Sci. USA* **111**, 13367 (2014).
2. ENCODE datasets <https://www.encodeproject.org/>
3. ENSEMBL database <http://www.ensembl.org/>