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Genome SCORE

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Jonathan B Weitzman

Email: jonathanweitzman@hotmail.com

Deciphering the *cis*-regulatory code hidden within genome sequences is a formidable challenge for the post-genomic era. In the Early Edition of the [Proceedings of the National Academy of Sciences](#), Rebeiz *et al.* report the creation of a [computational method](#) for identifying potential *cis*-regulatory modules and target genes. Their algorithm, called SCORE (Site Clustering Over Random Expectation), evaluates statistically significant enrichment for clusters of binding sites of a particular transcription factor within genome sequence. Rebeiz *et al.* validated this approach by looking for enhancers regulated by [Suppressor of Hairless](#) [Su(H)], a component of the Notch signalling pathway in *Drosophila*. They found over 15,000 potential Su(H)-binding sites in the *Drosophila* genome and used the well-known observation that *bona fide* binding sites are often clustered to identify potentially significant binding sites, within clusters. Many of these clusters fall near genes that are regulated by Notch signalling. Rebeiz *et al.* provide experimental support for their results by showing that one of the clusters regulates Su(H)-dependent expression.

References

1. *Proceedings of the National Academy of Sciences*, [<http://www.pnas.org>]
2. SCORE: A computational approach to the identification of *cis*-regulatory modules and target genes in whole-genome sequence data , [<http://www.pnas.org/cgi/doi/10.1073/pnas.152320899>]
3. Suppressor of hairless directly activates transcription of enhancer of split complex genes in response to Notch receptor activity.