

GENETICS

# SPARSE CODING OF SNP/DISEASE ASSOCIATION

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A new feature article in [Nature about sparse coding](#) let me wonder if we could construct also some Waddington-like picture of the SNPxSNP landscape as well as a disease traits and apply such an algorithm to that picture. I did some research but didn't find any example exploiting that idea; maybe it's even more useful with the current shift to full genomes?

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