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### **Shared genetic risk factors in pain conditions**

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Chronic pain conditions show substantial genetic and phenotypic correlations. Our goal for this study is to find and characterize the shared genetic risk components underlying these conditions. Using the UK Biobank dataset, we selected chronic conditions marked by persistent pain across body sites and suspected etiologies. We ran a genome-wide association study (GWAS) on each condition and estimated genetic correlations among them. Next, we used the genomic structural equation modeling (gSEM) framework to perform factor analysis and plotted genetic correlations between all pain traits as a network, extracting graph properties. Our gSEM results show evidence of a bifactor structure, with a prominent general factor explaining most of the shared genetic variance and three specific factors with significant loadings from musculoskeletal, cranio-visceral, and inflammatory disorders. The bifactor model outperforms the model with three specific correlated factors. Network visualization likewise reveals a large cluster of highly inter-connected conditions that share genetic associations. Overall, the results suggest common genetic predispositions for etiologically distinct pain conditions manifesting in different body sites, which may indicate common pathophysiological mechanisms in brain and/or systemic immune processes. These findings contribute evidence for chronic pain as a systemic condition and disease in its own right, whose recognition as such may better inform care for chronic pain patients. Future directions include GWAS on extracted factors to identify single nucleotide polymorphisms (SNPs) associated with genetic predisposition to multiple forms of persistent pain.