Supplementary Figures

Table of contents

1 Supplementary Figures

1.1 Figure S1. Scree plot of eigenvalues

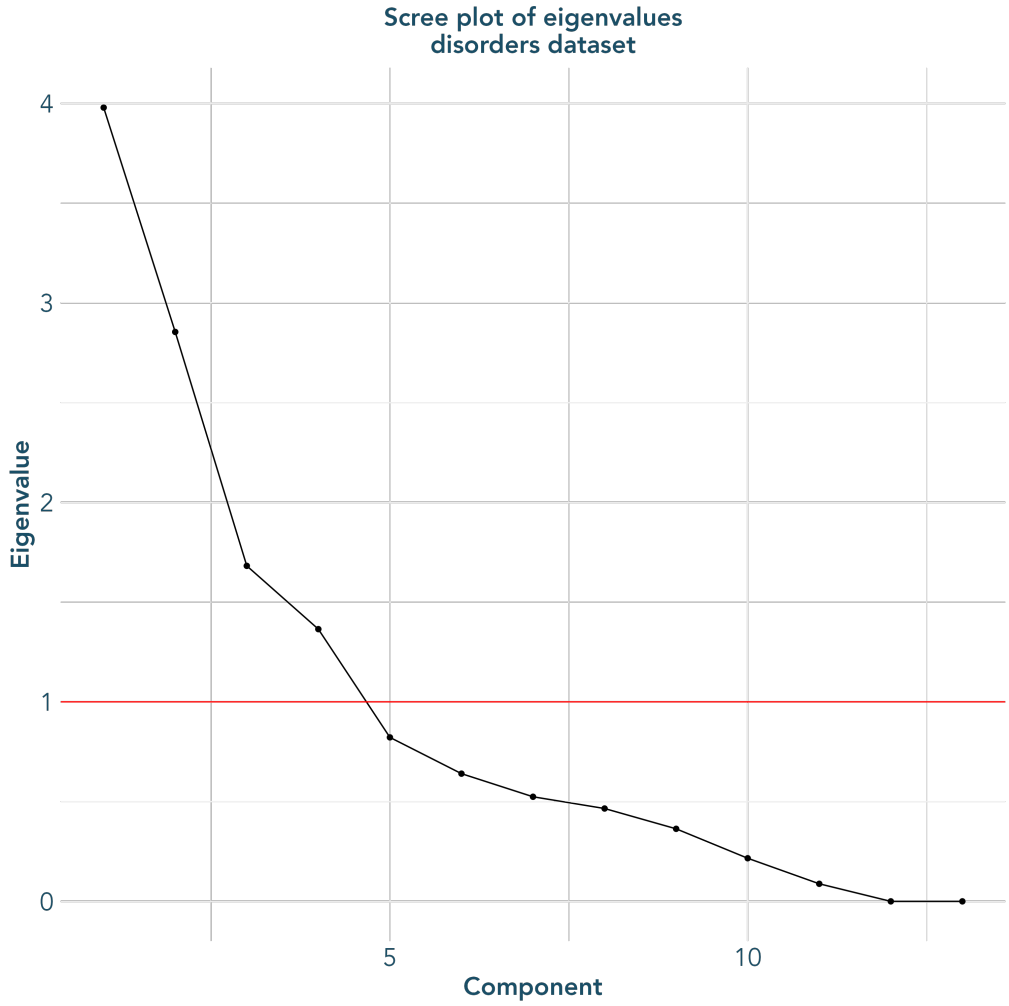

Figure 1: *Scree plot of eigenvalues from the LDSC-derived genetic correlation matrix.* Blue points/lines show observed eigenvalues; the red dashed line marks the Kaiser threshold (= 1). The elbow occurs around the 3rd–4th component, suggesting diminishing returns after 3 factors.

1.2 Figure S2. Parallel analysis

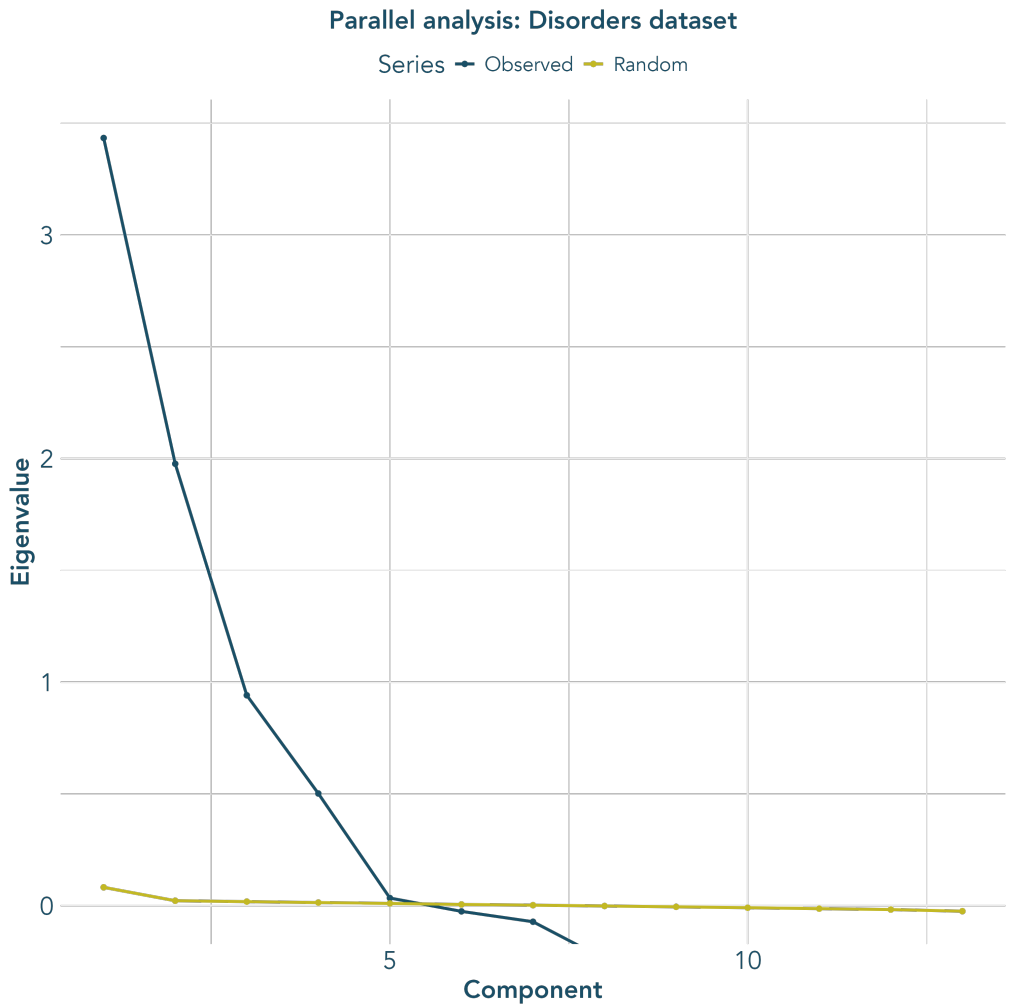

Figure 2: *Parallel analysis results for the LDSC-derived genetic correlation matrix of the disorders dataset.* Observed eigenvalues (blue) exceeded simulated random eigenvalues (yellow) through approximately the fifth component, although the incremental variance explained beyond the third factor was minimal. The curve shows a clear inflection ("elbow") after the third factor and asymptotes near zero thereafter, suggesting that a three-factor solution captures the major common variance structure, with additional factors contributing negligible unique information.

1.3 Figure S3. Scree plot: Symptoms

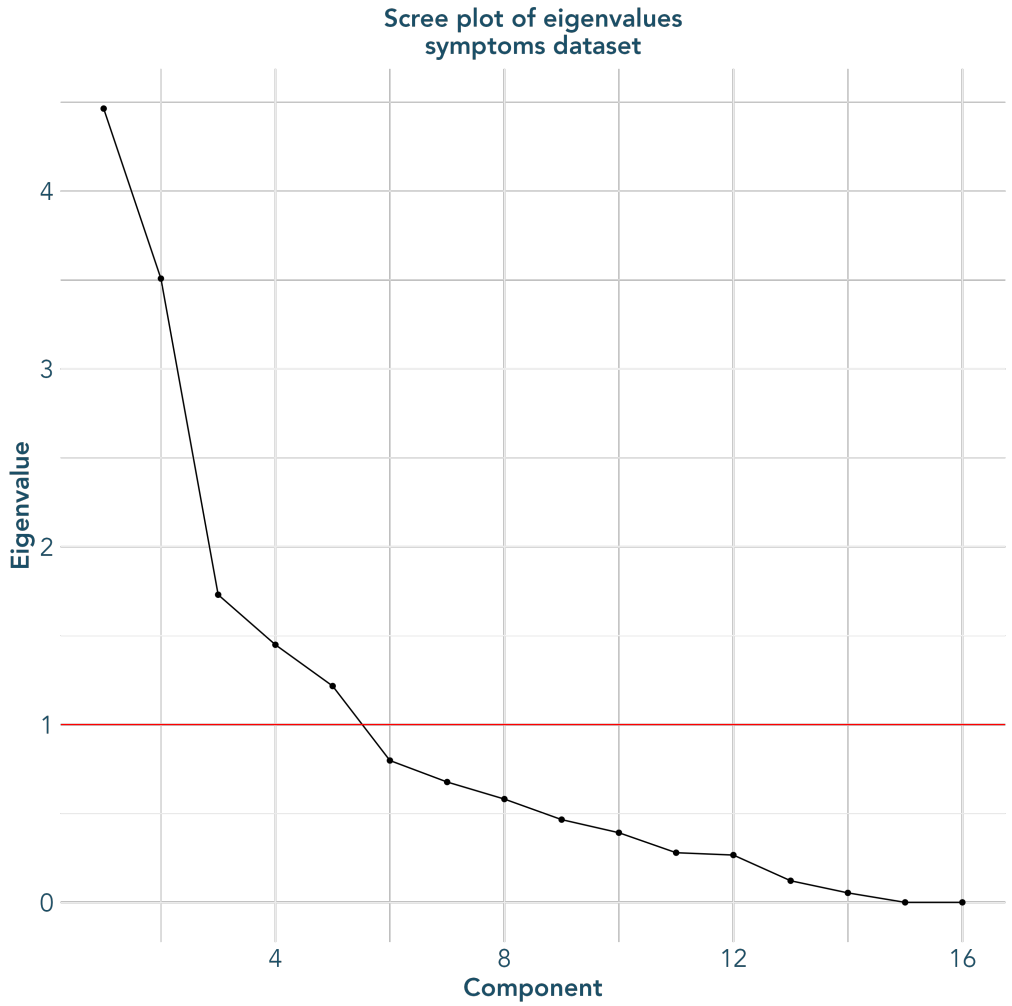

Figure 3: *Scree plot of eigenvalues from the LDSC-derived genetic correlation matrix.* Blue points/lines show observed eigenvalues; the red dashed line marks the Kaiser threshold (= 1).

1.4 Figure S4. Parallel Analysis

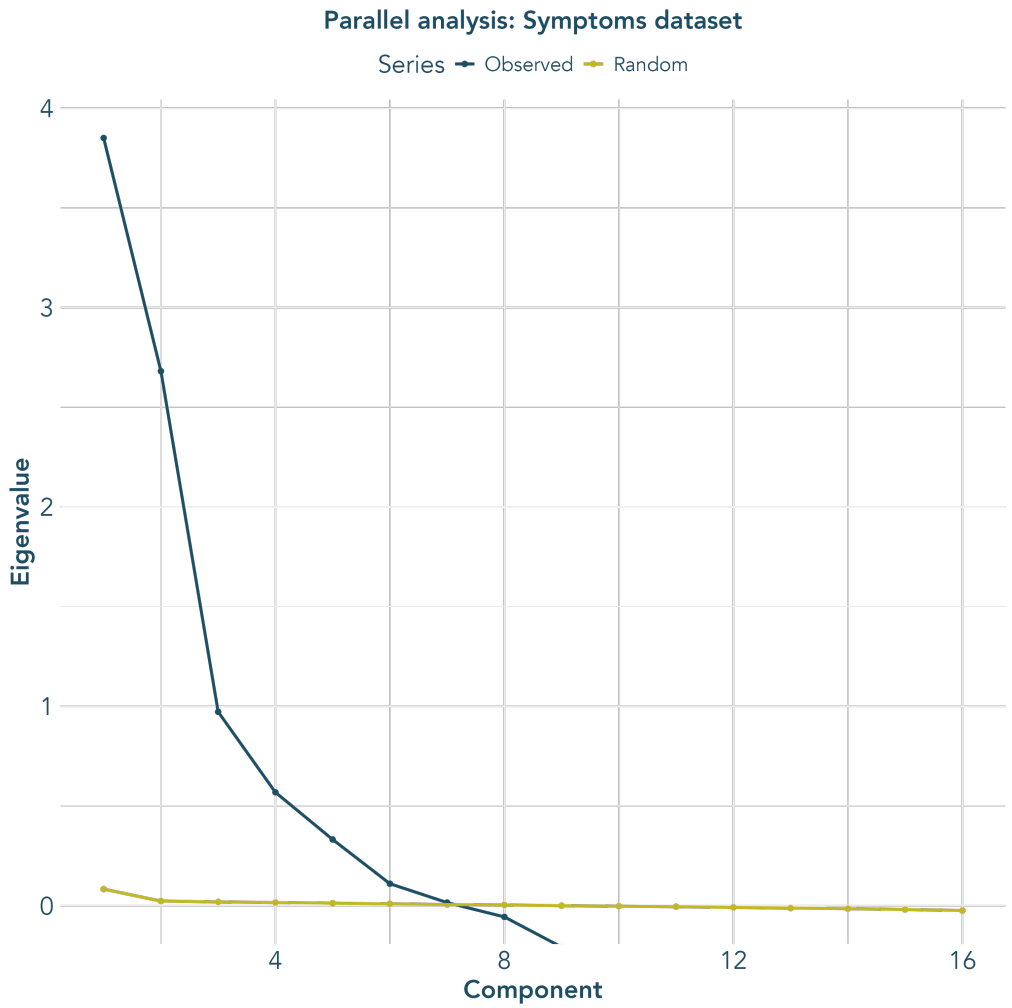

Figure 4: *Parallel analysis results for the LDSC-derived genetic correlation matrix of the disorders dataset.* Observed eigenvalues (blue) exceeded simulated random eigenvalues (yellow) through approximately the fifth component, although the incremental variance explained beyond the third factor was minimal. The curve shows a clear inflection ("elbow") after the third factor and asymptotes near zero thereafter, suggesting that a three-factor solution captures the major common variance structure, with additional factors contributing negligible unique information.