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| A. |
| B. |
| C. |
| Figure 1: Results of fitting models of different number of archetypes, using the first 20 PC’s (covering 17% of the variance in original data). A. Proportion of variance explained. B. Proportion added to explained variance by adding another archetype. C. Variance around archetype position based on bootstrapping of original space. |

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| Figure 2. Archetype position in the original 2-dimensional PC space based on the best fit polygon, a triangle. Green dots indicate archetype position in 200 bootstrapped spaces. Previously published classification of AD patients into subtypes A and B, based on k-means clustering, is represented by blue and red dots, respectively. |

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| A. |
| B. |
| Figure 3. Association of cognitive score (A) and Braak score (B) with sex across the archetypes. Bar height is proportional to deviation from expectation under the null hypothesis of equal representation (i.e, no enrichment), tested using the chi2 statistic. Disease progression proceeds from left to right for both scores. |

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| Figure 4. Association between pseudotime estimates and archetype classification. |

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| Figure 5. GO term enrichment for the top genes associated with each archetype. |

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| Figure 6. Association of archetypes’ top gene sets with previously-published cell-specific marker of brain tissues (REF###). Bar height is proportional to deviation from expectation under the null hypothesis of equal representation (i.e, no enrichment), tested using the chi2 statistic. |

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| Figure 7. Association of archetypes’ top gene sets with previously-published gene expression submodules from the same cohort (REF###). Bar height is proportional to deviation from expectation under the null hypothesis of equal representation (i.e, no enrichment), tested using the chi2 statistic. |

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| Figure 8. Network representation of GWAS results for different phenotypes illustrating overlap among phenotypes in their genetic architecture. Phenotypes include distance from each archetype, archetype assignment, previously-published cluster-based subtypes, CERAD and Braak scores, and cognitive diagnosis. Loci are represented as circles. Edges connect genetic loci to phenotypes. |