

# Connectome-based classification of *BDNF* Met allele carriers



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## Background

### BRAIN-DERIVED NEUROTROPHIC FACTOR

- Protein essential for brain development and long-term potentiation
- Associated gene (*BDNF*) regulates activity-dependent release of BDNF protein [1]
- Alleles: G encodes Valine, A encodes Methionine
- Common single-nucleotide polymorphism known as Val66Met. Prevalence varies: 0.55% in Sub-Saharan Africa, 19.9% in Europe, and 43.6% in Asia [2]
- Carrying the Met allele **reduces** activity-dependent secretion of BDNF [1]
- BDNF facilitates **pruning** of silent axonal branches during development [3,4]
- Two large (n > 400) studies have found **increases** in fractional anisotropy (FA) in Met carriers, relative to Val homozygotes [5,6]

### EXPERIMENTAL DESIGN

- Population (n = 36, 15 Met carriers, 21 Val homozygotes)
- Highly regulated young healthy subjects (18-25y)
- High-resolution T1 MPAGE (1 x 1 x 1 mm<sup>3</sup> voxels)
- Diffusion-weighted MRI (61 directions, b=1000, 2.3 x 2.3 x 2.3 mm<sup>3</sup> voxels)

## Connectome Mapping & Classification

### CONNECTOME MAPPING

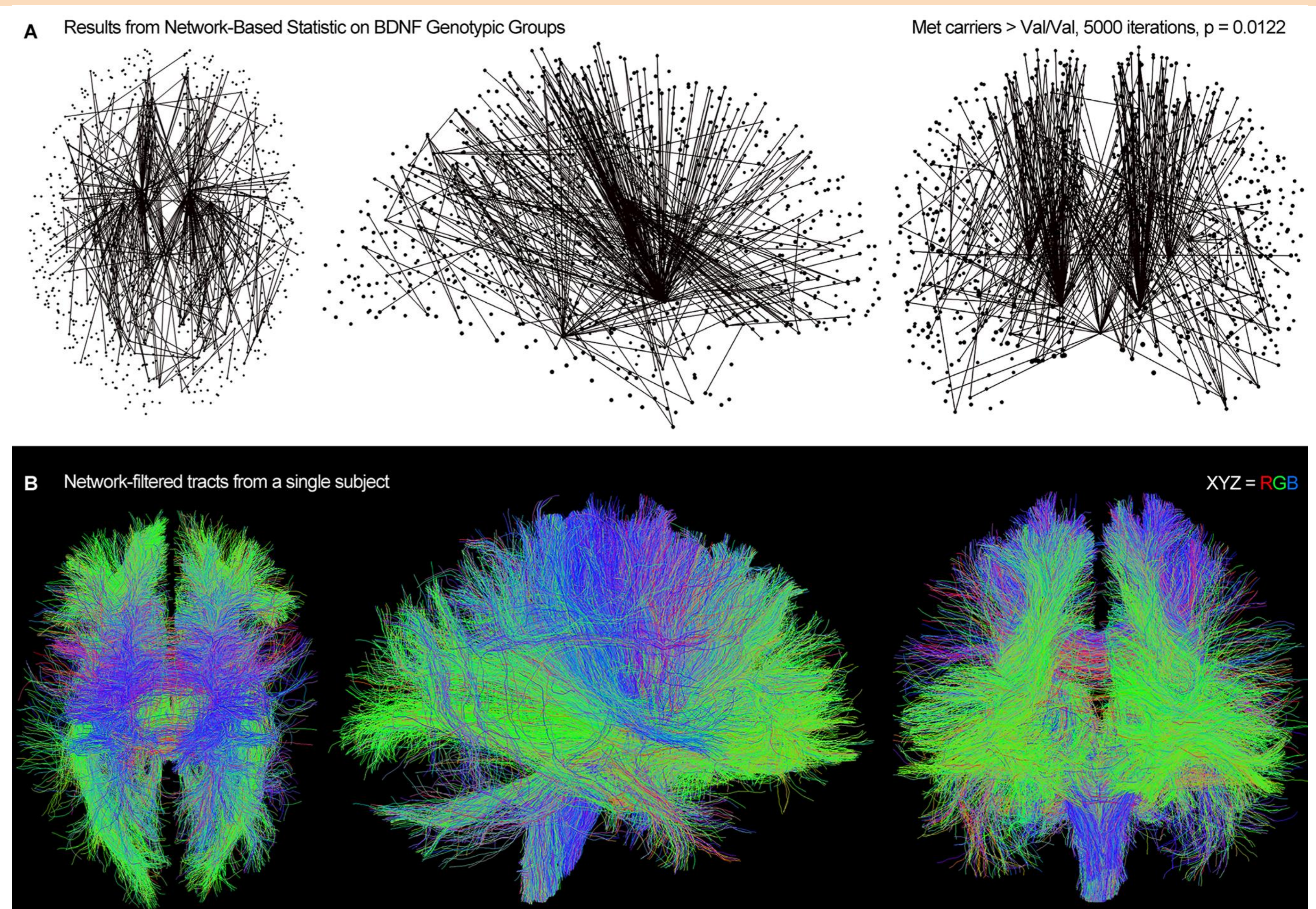
- Whole-brain Probabilistic Tractography
  - Non-negativity constrained spherical deconvolution to obtain orientation distribution functions [7,8]
  - 300,000 fibers, seeded from randomly placed points in the white matter
- Anatomical Parcellation of T1-weighted image
  - Segmentation to Desikan-Killiany atlas (83 regions) [9]
  - Parcellation to Lausanne 1015-region atlas [10,11]
- Connection matrix incremented any time a fiber crossed two regions
- Freely available online as [Nipype Advanced Connectivity Tutorial \(MRtrix\)](#) [12]

### STATISTICS & CLASSIFICATION

- Non-parametric test via “Network-Based Statistic” (5000 permutations, t thresh. = 3) [13]
- Machine learning classification with [Gaussian Processes](#) using the Pattern Recognition Toolbox for Neuroimaging [14]
  - Classifier uses connectivity matrices (edge weights only, no spatial or network topological information)
  - Leave-one-out cross-validation procedure
  - Statistical significance assessed by permutation (n=1000)

## Results (significant at FDR p<.05)

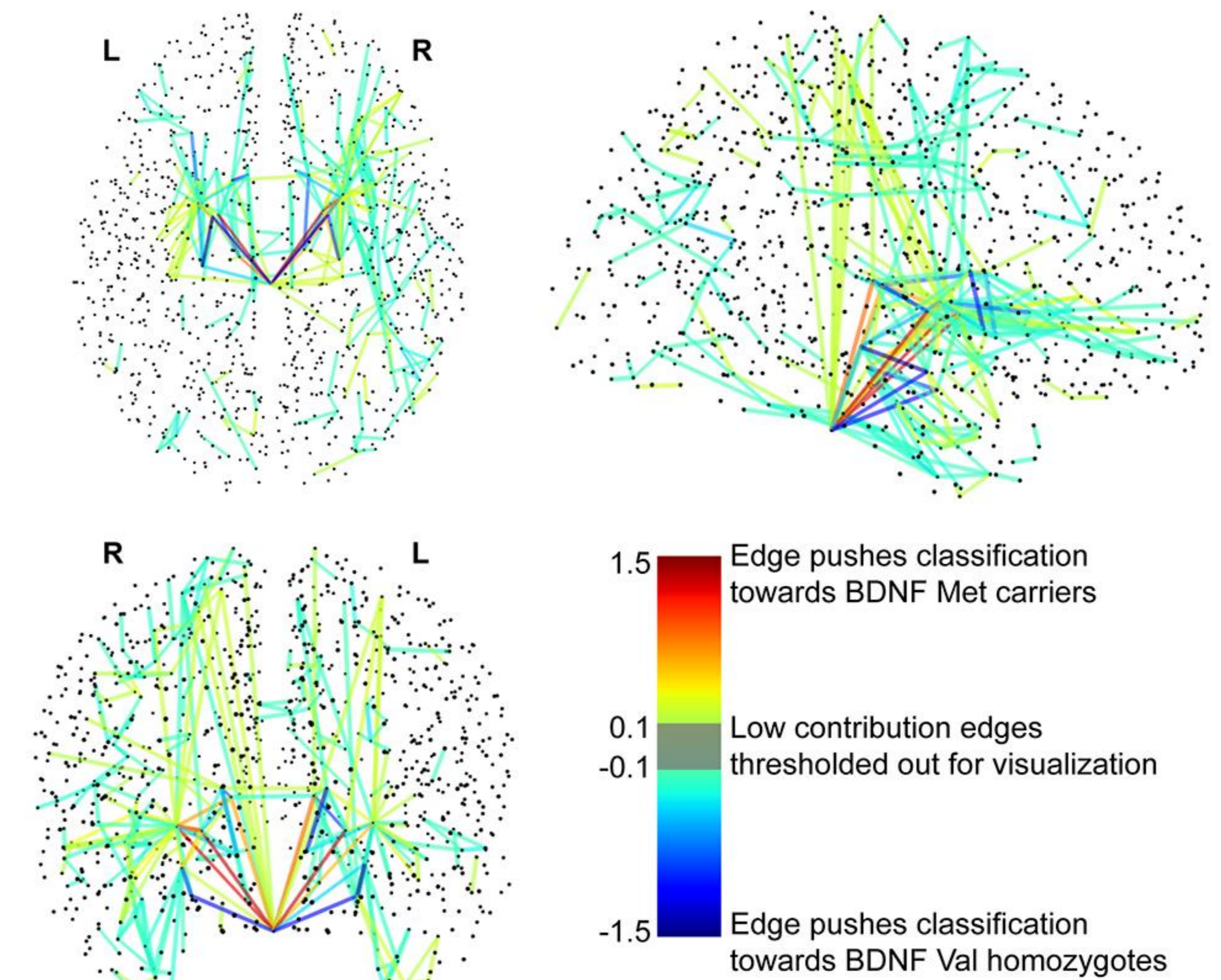
### 1. Apparent increases in connectivity for Met carriers



### 2. Genotype accurately classifiable from brain connectivity

- **Balanced accuracy: 87.14%** (p<.001)
- **Predictive Value (for Val/Val & Met carriers): 94.4% & 77.8%**

Spatial representation of classifier weights (thresholded for display purpose only!)



### 3. No significant difference or classification for either gender or adenosine deaminase (ADA) genotype

## Conclusions

- *BDNF* Met carriers prune less axonal arbors during brain development
- Resulting tracts stay in the brain
  - Seem to provide little or no benefit
  - May protect against age-related deficits
- Extraneous tracts are found as increases in fractional anisotropy
- Various connections have increased fiber count in Met carriers:
  - Connections between bilateral thalami and brainstem
  - Sensorimotor areas of parietal and frontal cortex
  - Ventromedial prefrontal cortex (anterior forceps)
- Occipital, posterior parietal, and temporal areas also differ to a lesser extent.

### REFERENCES

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