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## Neuroinformatics with the Insight ToolKit

Recent interest in the human connectome has led to the application of graph theoretical analysis to human brain structural networks, in particular white matter connectivity inferred from diffusion imaging and fiber tractography. While these methods have been used to study a variety of patient populations, there has been less examination of the reproducibility of these methods. These graph metrics typically derive from fiber tractography, however a number of tractography algorithms exist and many of these are known to be sensitive to user-selected parameters. We examine how these algorithm and parameter choices influence the reproducibility of proposed graph metrics.

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This is a footnote

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- 43 • Concluding Remarks

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85 Authors should provide relevant information relating to how the peptide/protein matches were undertaken,  
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87 and threshold or cut-off rates for peptide and protein matches. Further information could include  
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89 processing methods, mass tolerances used for matching, variable/fixed modifications, allowable missed  
90 cleavages, etc.  
91 Authors should provide as supplementary material information used to identify proteins and/or peptides.  
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93 matched mass, peptide/protein scores, peptide modification, miscleavages, peptide sequence, match rank,  
94 matched species (for cross species matching), number of peptide matches, ambiguous protein/peptide  
95 matches should be indicated, etc. For quantitative proteomics analyses authors should provide information  
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97 uncertainty and the methods used for calculating error.  
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100 annotated spectra or submit data to an online repository (recommended option). Authors are encouraged  
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#### ACKNOWLEDGEMENT

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#### SUPPLEMENTAL DATA

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