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| **Notation** | **Name** | **Epxression or value** | **Explanation** |
|  | time step |  | time increment in the simulations |
|  | region label |  | indexing regions |
|  | edge label |  | indexing edges |
|  | normal populationin region  | N/A | total number of normal agents in region  |
|  | misfolded populationin region  | N/A | total number of misfolded agents in region  |
|  | normal populationin edge  | N/A | total number of normal agents in edge  |
|  | misfolded populationin edge  | N/A | total number of misfolded agents in edge  |
|  | synthesis rate in region  |  where is the SNCA expression (z-score) in region  | the probability that a new normal agent gets synthesized in each voxel of region per unit time |
|  | clearance rate in region  |  where is the GBA expression (z-score) in region  | the probability that an existing agent (either normal or misfolded) in region gets cleared per unit time |
|  | region size | N/A | voxel counts of region  |
|  | baseline transmission rate |  | the probability for a single misfolded agent to transmit the disease to other agents per unit time |
|  | transmission probability |  | the probability that normal agents get infected (by at least one of the misfolded agents) per unit time |
|  | connection strength of edge  | normalized fiber tracts density between region and  | determining the probability of entering edge when exiting region per unit time |
|  | edge length of edge  | mean length of fiber tracts between region and  | determining the probability of exiting edge per unit time |
|  | the probability of remaining in region  |  for all  | agents in region have equal probability of remaining in region or exiting region per unit time |
|  | functional connectivity of edge  | N/A | biasing agents toward regions showing greater co-activation pattern |
|  | weight of functional connectivity | N/A | controlling the influence of functional connectivity in driving disease spread |
|  | weight of atrophy accrual due to accumulation of misfolded agents |  | controlling the contribution of native misfolded agents to total atrophy growth |
|  | weight of atrophy accrual due to deafferentation |  | controlling the contribution of deafferentation to total atrophy growth |
|  | the ratio of misfolded agents in region  |  | measuring the burden of misfolded agents in region at time  |