TrackerAutomatedScript (arguments)

* Tracks, linkedTracks, rawTracks

finalTracks = processTracks (folder)

* finalTracks - structure (path, speed, etc)

compareTwoGenotypes\_HMM\_useN2HMM (folder, with 2 subfolders, name of 1st = 1\_n2)

* figure (state durations, turning, speed), saves “TrackInfo” for each genotype

Channelrhodopsin

Make StimFile – seconds w/ lighton, power, etc

showChOPHits\_CopperRing\_comparePoolsToN2\_useN2HMM

takes N2 control data and actual data, along with StimFile