

Figure 1. Schematic and Simulations

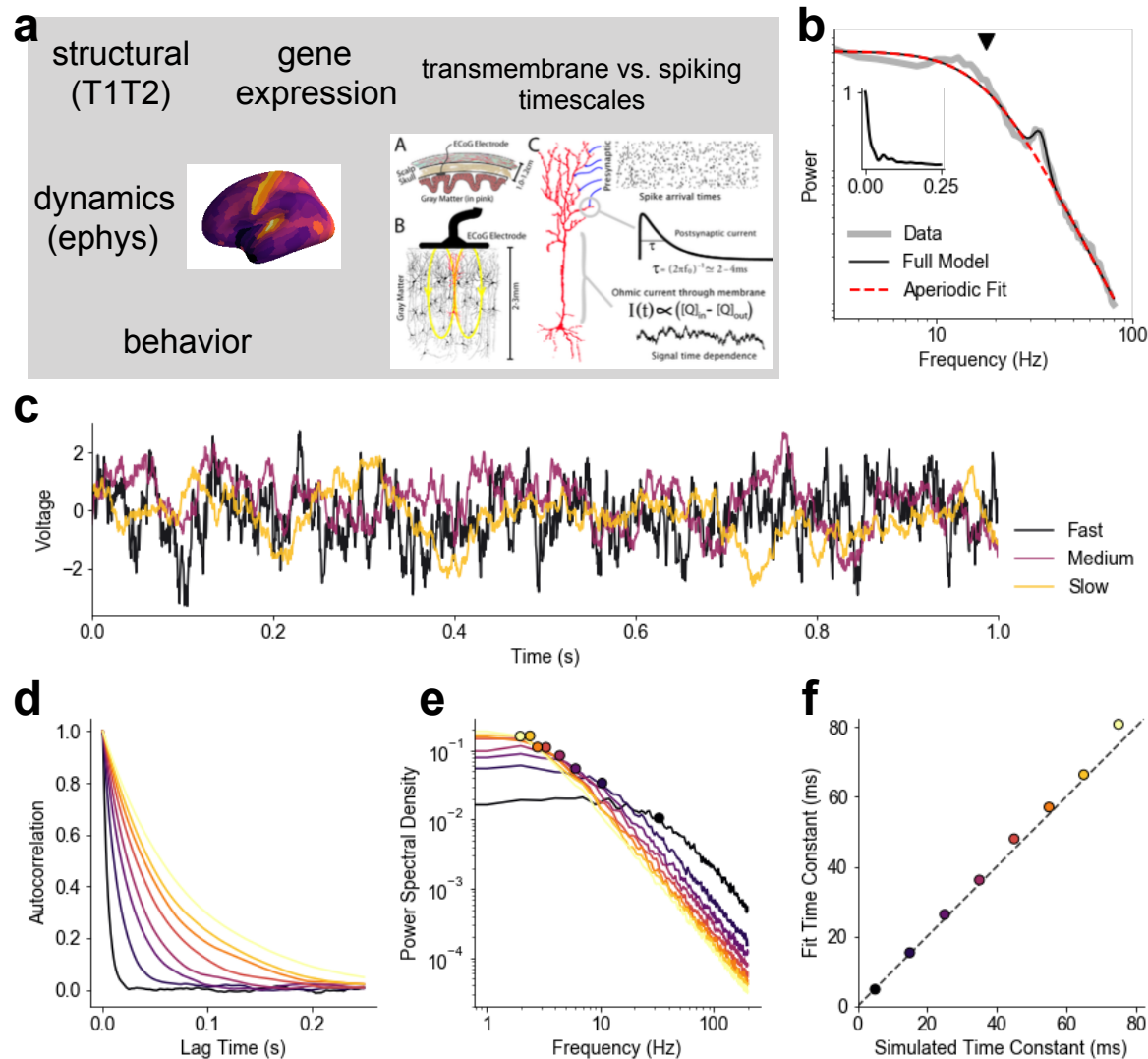


Figure 1| Schematic of study, method, & simulation. a, we estimate cortical synaptic and transmembrane timescales from surface ECoG recordings, and compare with spiking population timescales, anatomical hierarchy, and gene expression gradients, as well as investigate their dynamic modulation during behavior. b, characteristic timescale (decay time constant) of a system can be estimated from its power spectral density as the frequency of power drop-off (black triangle) via eq. 2. An example ECoG PSD is shown, with the corresponding model fit; inset: autocorrelation function. c-f, simulated time series (c) with increasing (longer) autocorrelation decay time constants (d), which can be accurately estimated from the PSD (e), retrieving the ground truth parameter values (f).

Figure 2. Monkey ECoG vs. SU

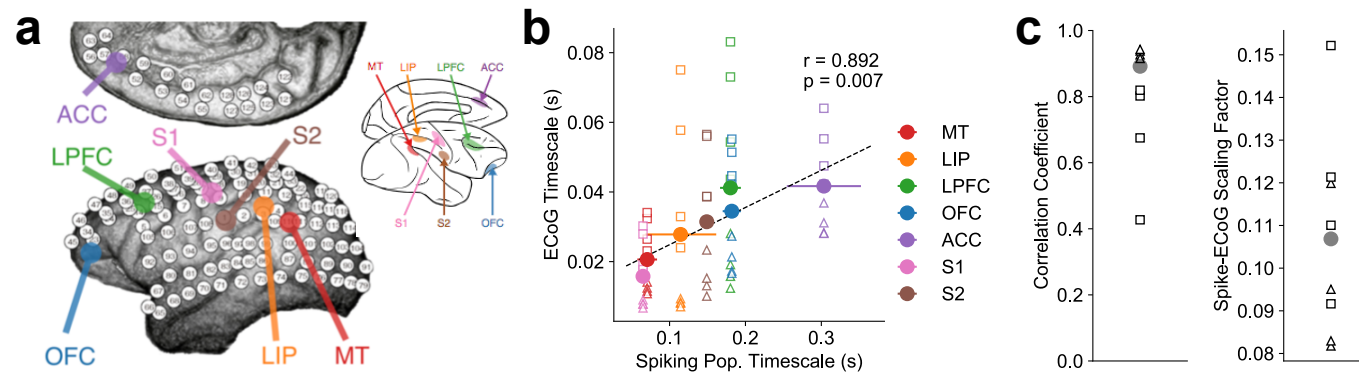


Figure 2| Local transmembrane timescale scales with population spiking timescale across macaque cortex, following functional hierarchy. a, whole-cortex ECoG grid is shown, highlighting corresponding regions with published single-unit data taken from [ref] (inset). b, Transmembrane (ECoG) timescale increases along cortical hierarchy, and is tightly correlated with spiking timescale estimated from multiple single-unit population spiking autocorrelation in [ref]. Hollow markers denote individual session estimates, shapes denote different animals. Solid circles denote grand average over all sessions and animals. c, linear regression fit to individual sessions show robust correlation between timescale estimates, while transmembrane timescales are consistently an order of magnitude faster than spiking population timescales.

Figure 3. Human ECoG & Gene Expression

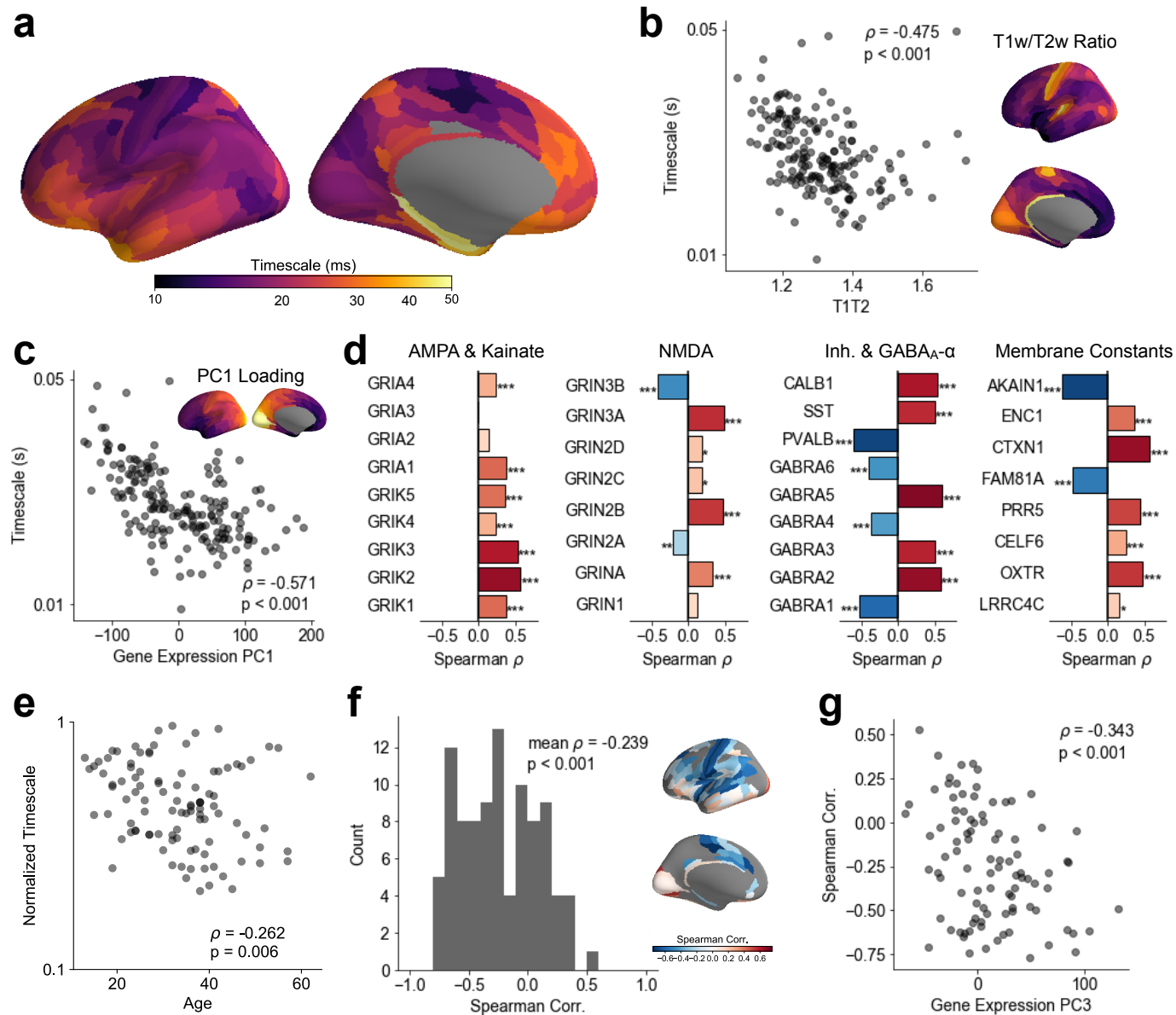
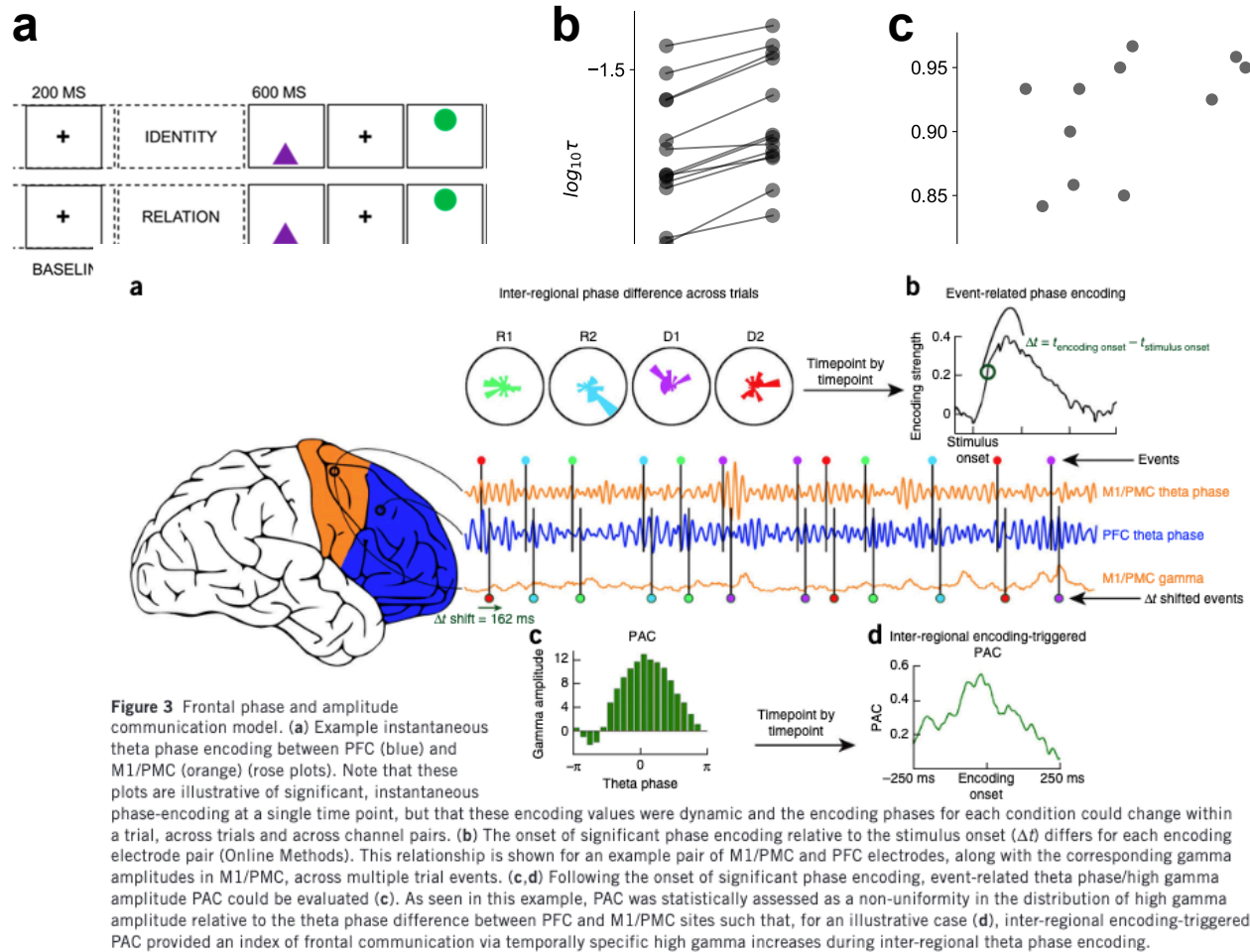


Figure 3|

Figure 4. Human ECoG & Working Memory



task schematic