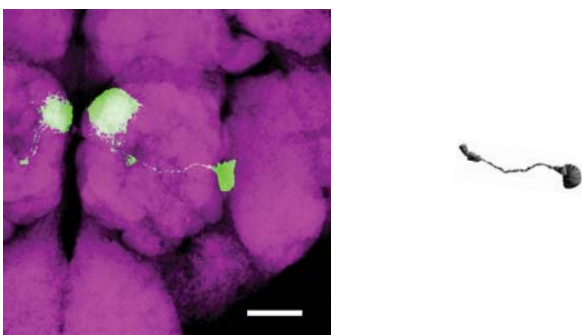
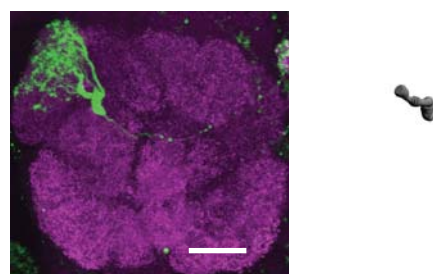


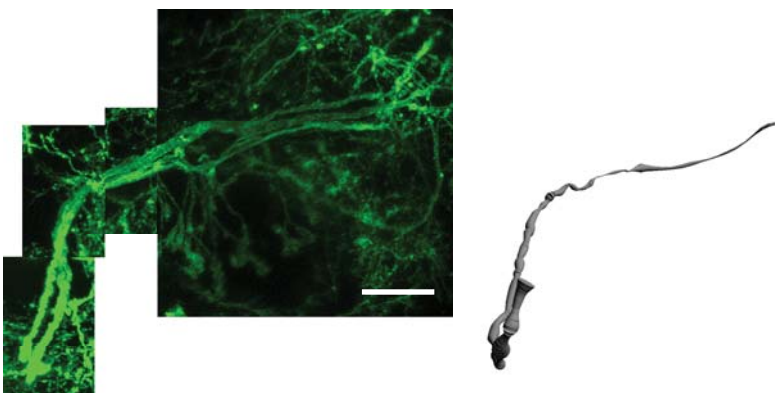
**A** Single cell MARCM clone (soma)



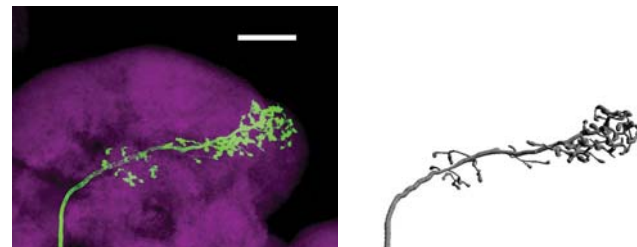
**B** Biocytin fill



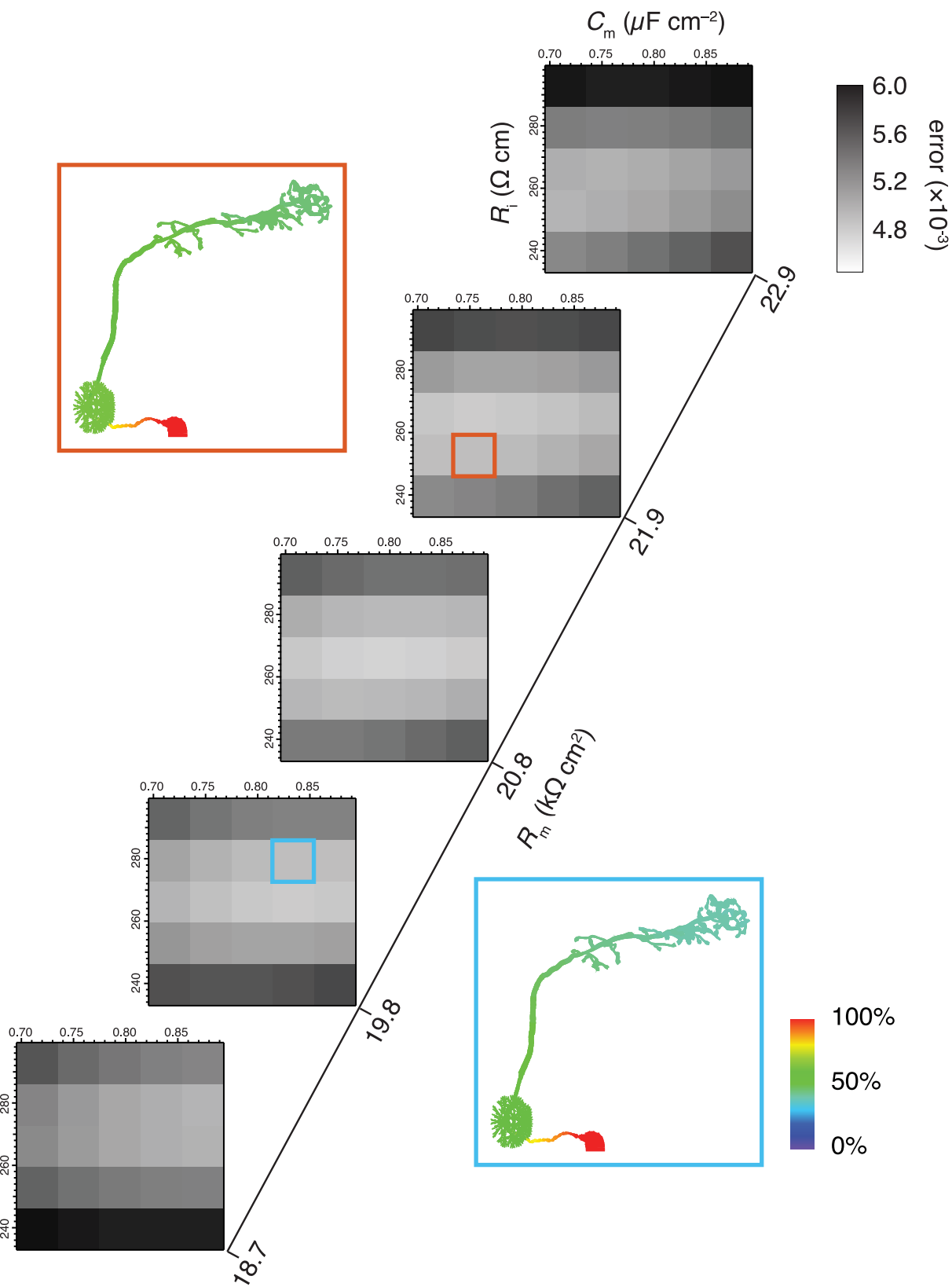
**C** Enhancer trap line



**D** Single cell MARCM clone (axon)



**Supplemental Figure 1.** Reconstruction of subcellular regions of the projection neuron. In all panels, the source confocal image is on the left and the 3D reconstruction is on the right. The biocytin (**B**) or CD8 (others) channel is shown in green, and the nc82 channel is in magenta. All images are maximum projections except the nc82 channels of **A** and **D**, which are mean projections. **A**, Reconstruction of the soma and primary neurite. Scale bar is 30  $\mu\text{m}$ . Image from Jefferis et al. (2007). **B**, Reconstruction of the initial segments of the dendrite and axon. Scale bar is 30  $\mu\text{m}$ . **C**, Reconstruction of the middle segment of the axon. Scale bar is 20  $\mu\text{m}$ . **D**, Reconstruction of the axon terminals. Scale bar is 30  $\mu\text{m}$ . Image from Jefferis et al. (2007).



**Supplemental Figure 2.** The fit error as a function of  $R_m$ ,  $R_i$ , and  $C_m$  displayed as a volume. Lighter shades of gray indicate less error in the fit. Each parameter was varied by up to  $\pm 10\%$  of the values returned by the best-fitting algorithm. The data set to which the model was compared is from Cell 3 (Fig. 4). The morphology used was Dendrite 2 (Fig. 4). Two example plots of steady-state voltage attenuation from the soma are shown. The corresponding location in parameter space is indicated by the similarly-colored square in the plot of the error function.