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Haematopoietic stem cells in perisinusoidal niches are protected from ageing

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Medhanie A. Mulaw⁹, Hartmut Geiger^{1,10} and Maria Carolina Florian^{1,11*}

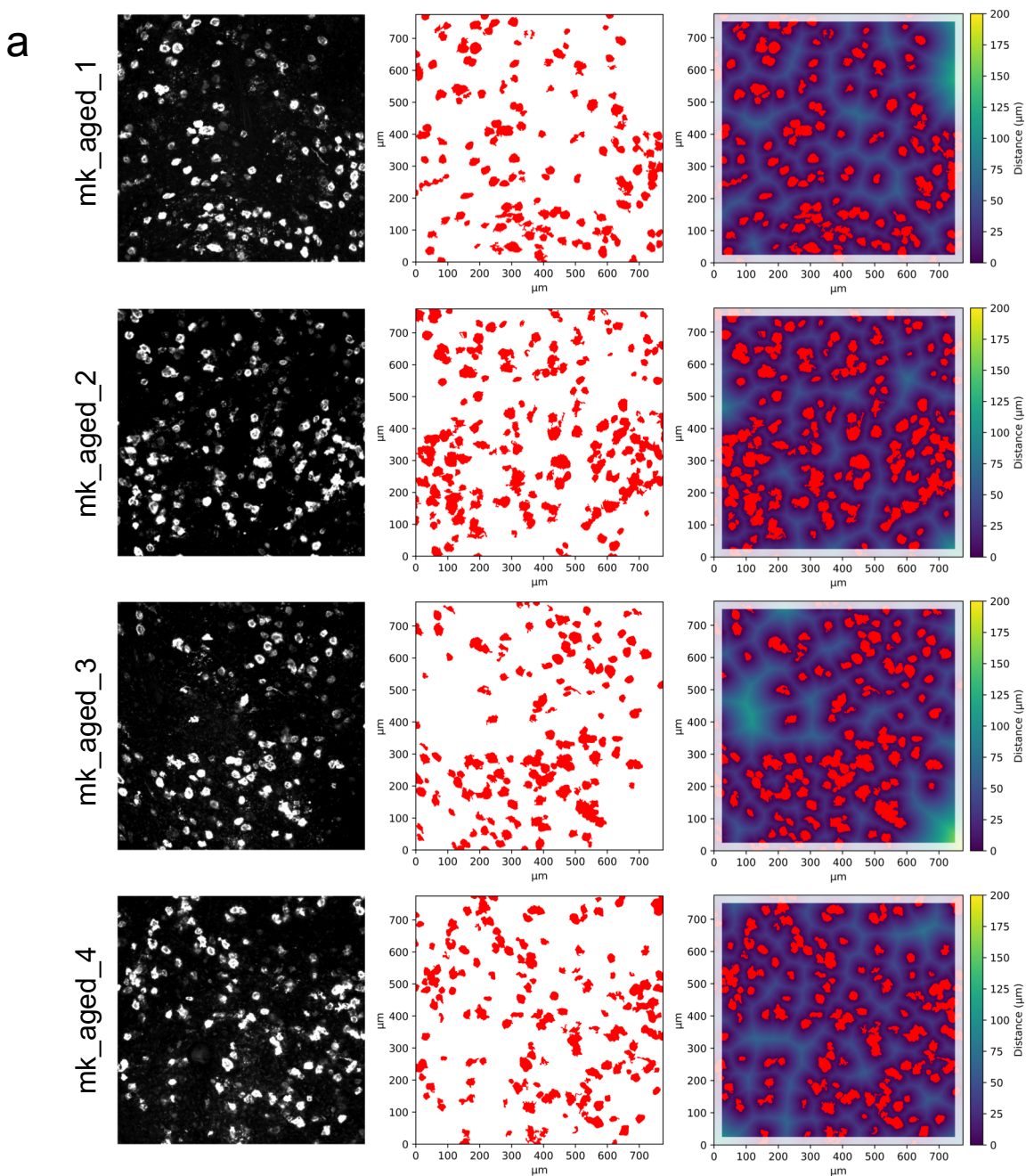
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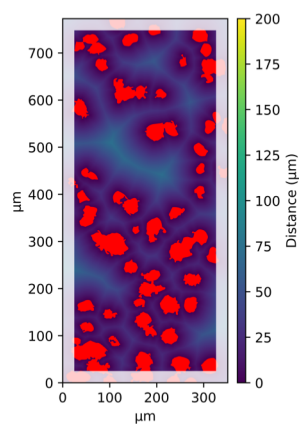
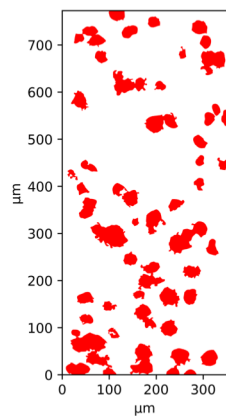
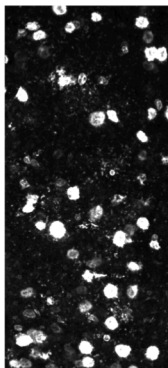
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Supplementary Figure 1: Overview of binary structure maps for the simulation process. Overview of all confocal images (left), corresponding binary maps (middle), and distance transformation (right) used for the in-silico simulation. White areas depict the “empty” domain that was used for distance sampling (in binary maps only), red areas indicate the niche structure from which the distance was measured, and black areas indicate blocked domains (usually bone areas) that were excluded from sampling (both in binary maps and distance transformations). The distance transformations (on the right side) show sampled distances depicted in colormap. Greyed out areas around the images of distance transformations show the cropping that was applied to eliminate boundary artifacts. We simulated the distribution of 10,000 HSCs randomly placed within the BM cavity and calculated the distance between these randomly placed cells and the different niche structures (indicated as “expected” or “in silico” samples). The position of the HSCs was randomly simulated on the bases of each specific niche structure (see Methods for further details). **a-b)** megakaryocytes; **c-d)** endosteum, **e-f)** Nes-GFP^{high} cells, **g-h)** Nes-GFP^{low} cells.

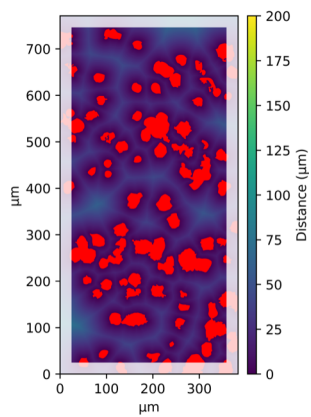
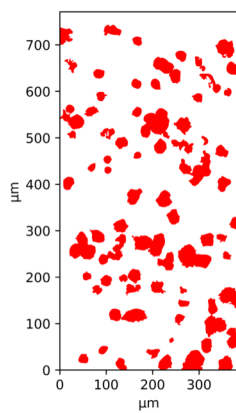
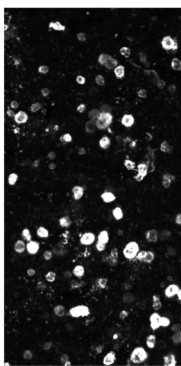


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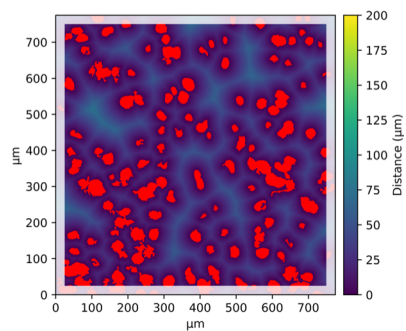
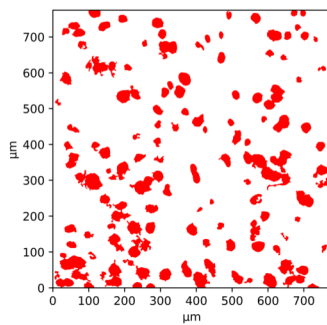
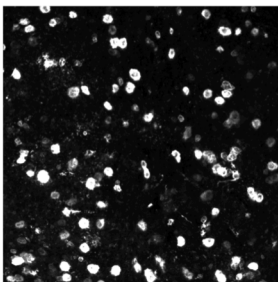
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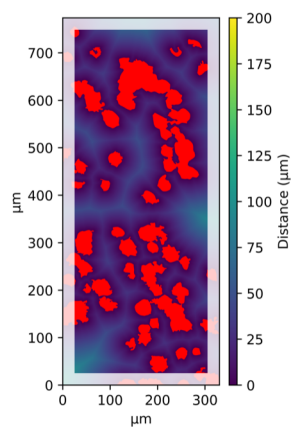
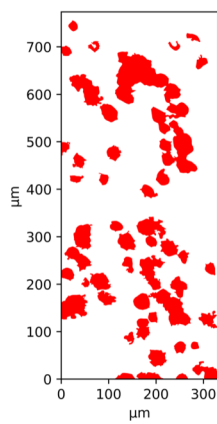
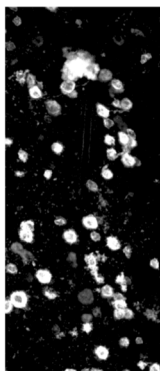
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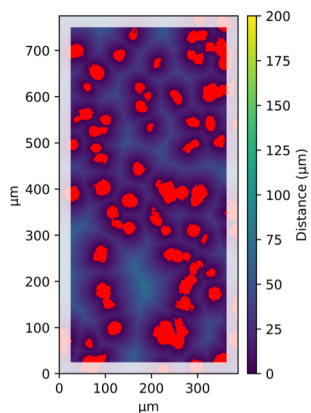
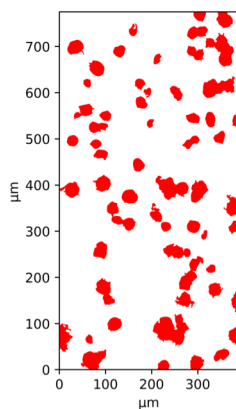
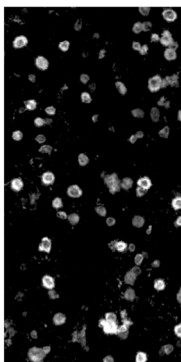
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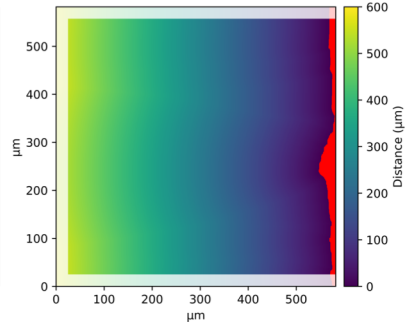
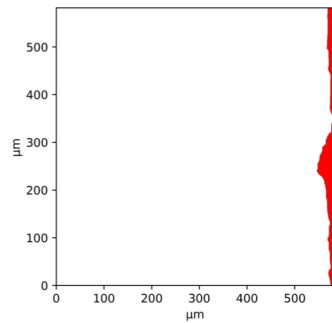
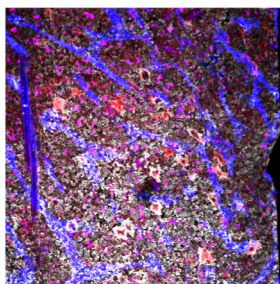


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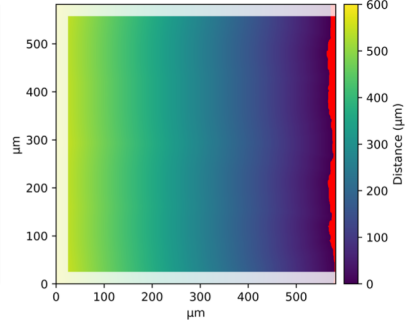
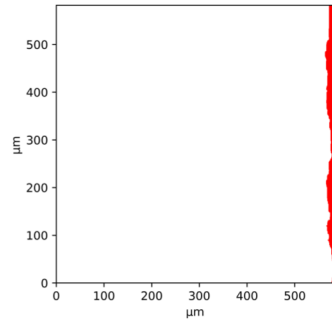
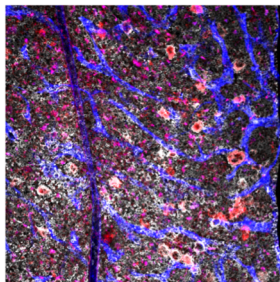


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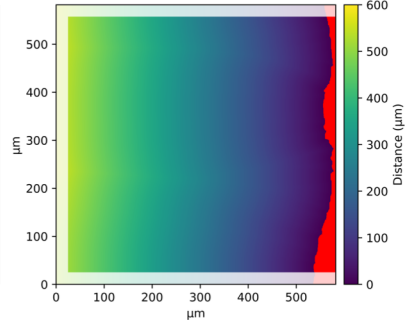
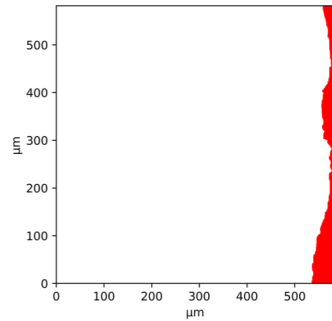
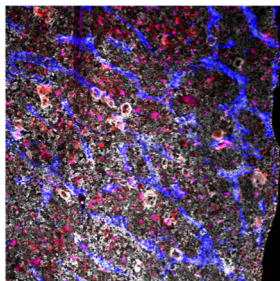
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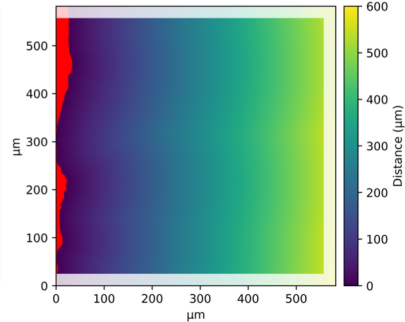
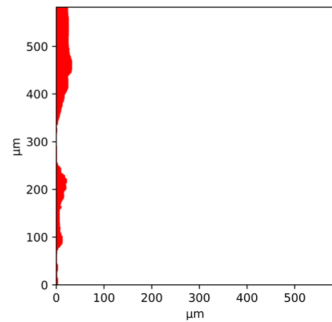
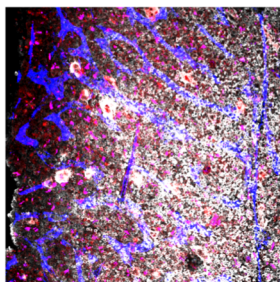
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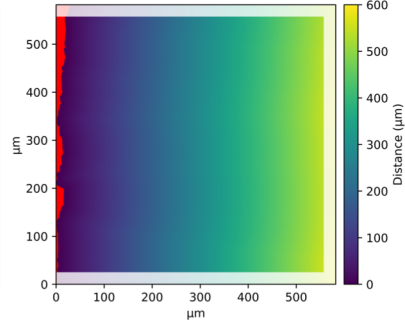
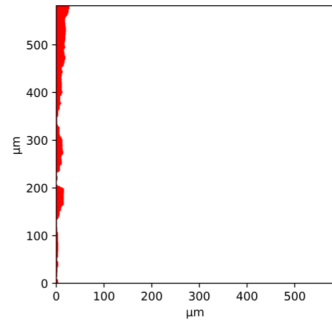
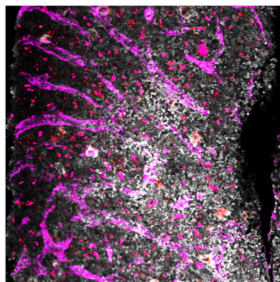
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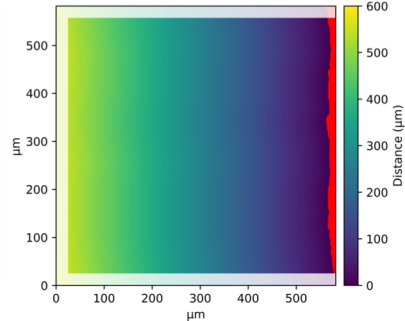
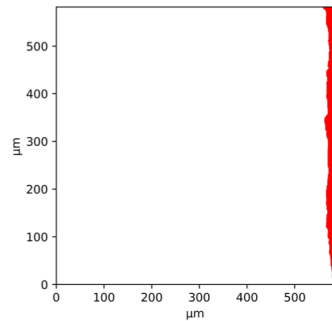
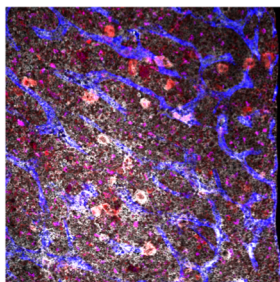
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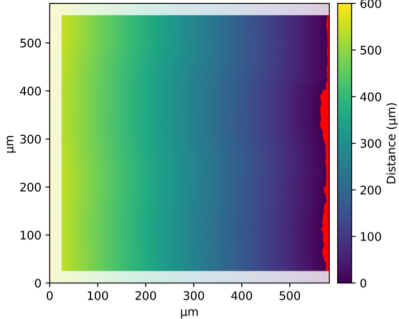
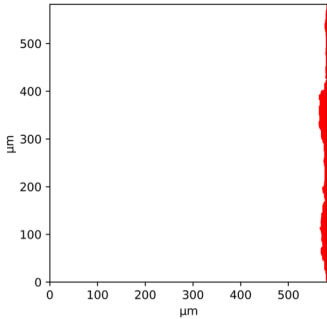
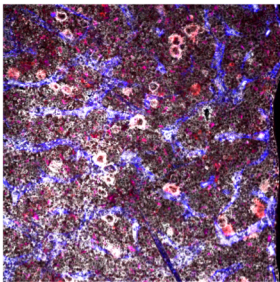


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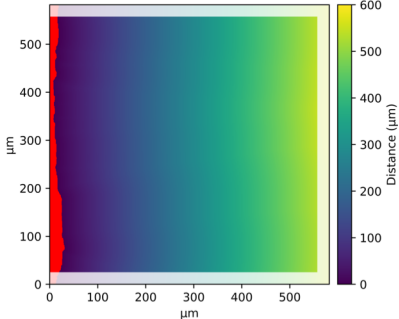
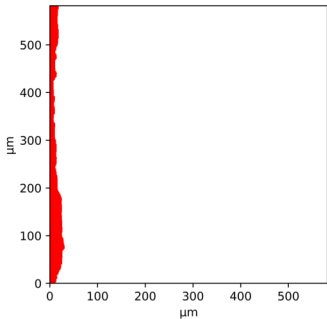
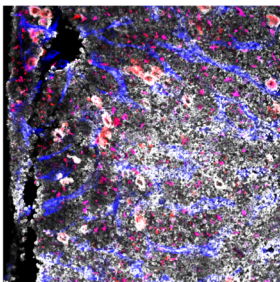


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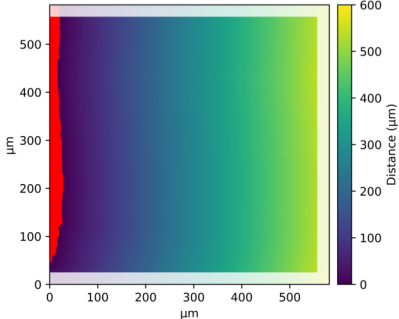
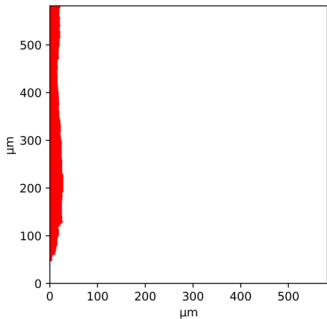
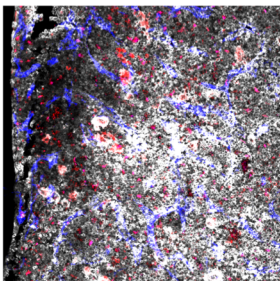
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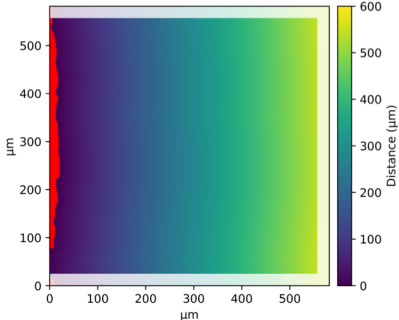
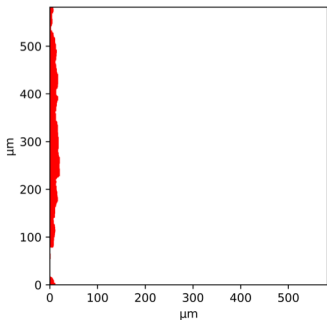
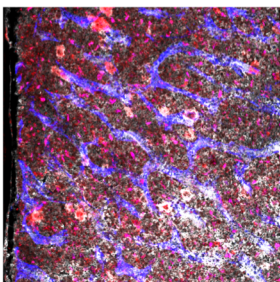
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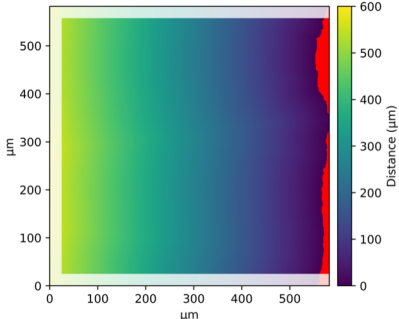
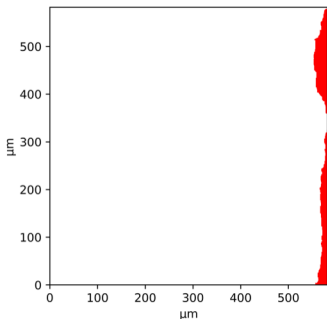
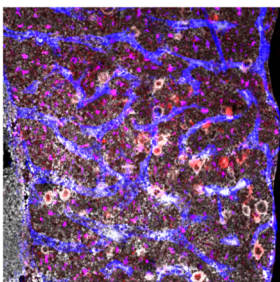
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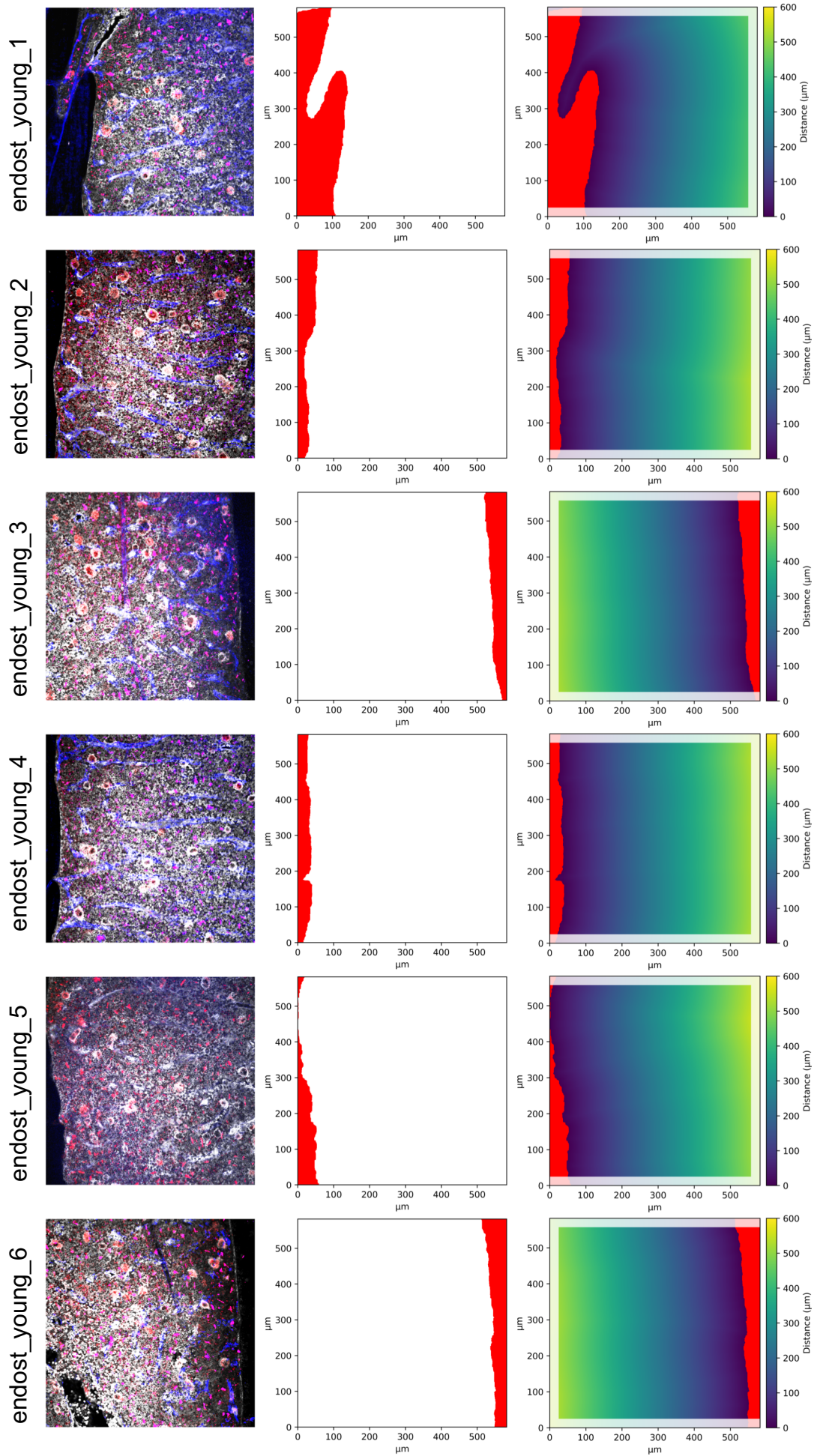
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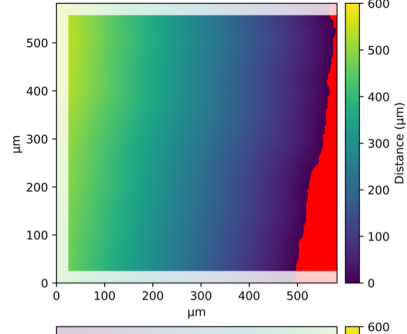
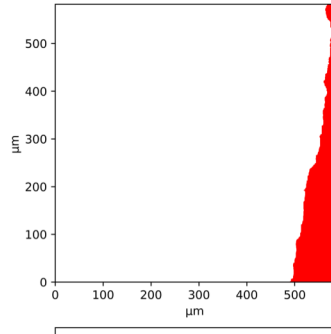
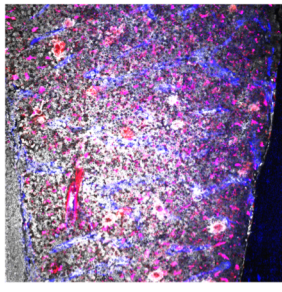


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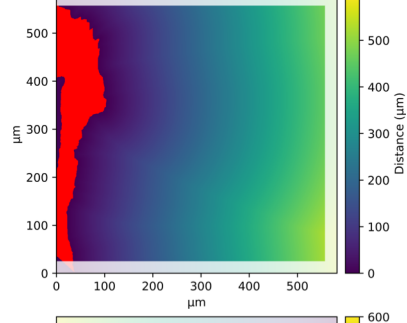
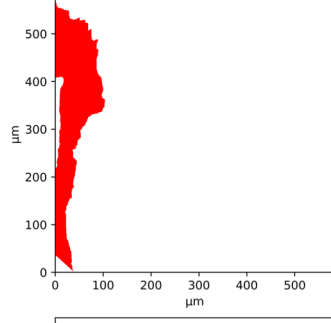
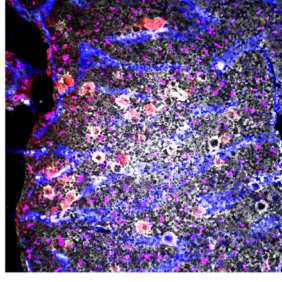


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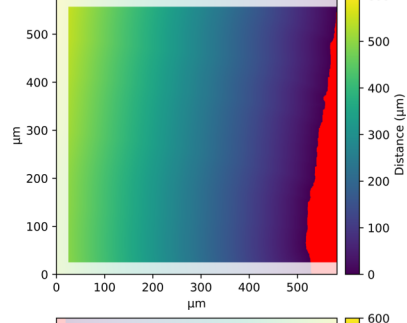
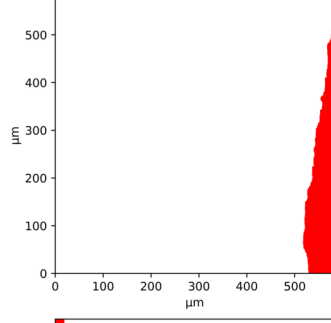
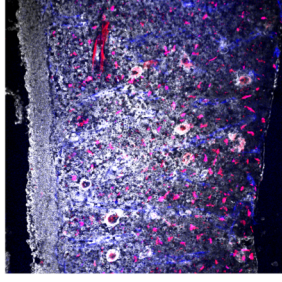
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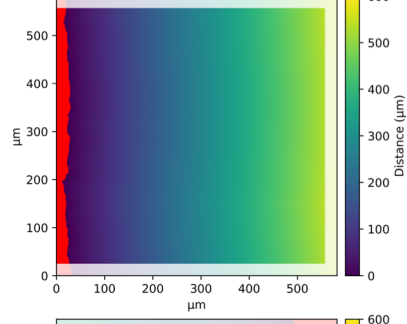
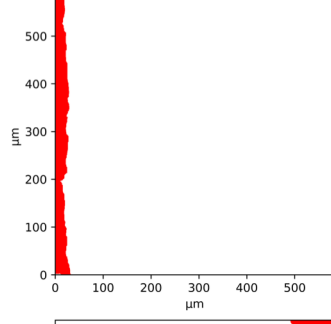
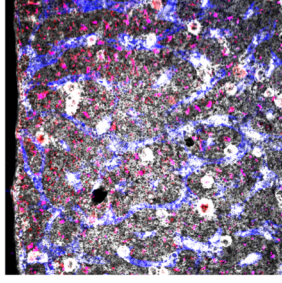
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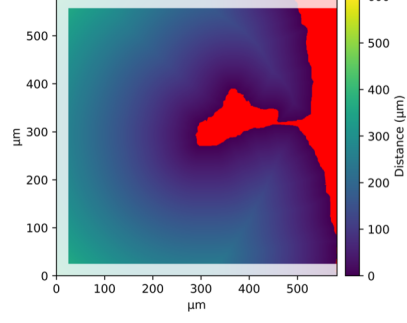
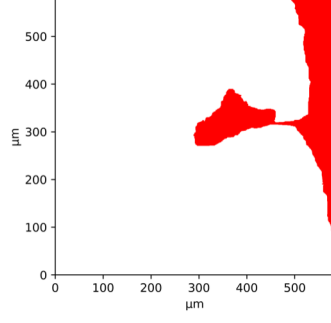
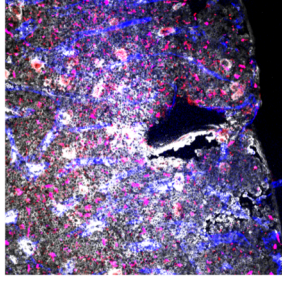
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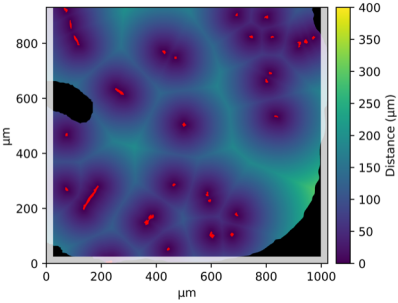
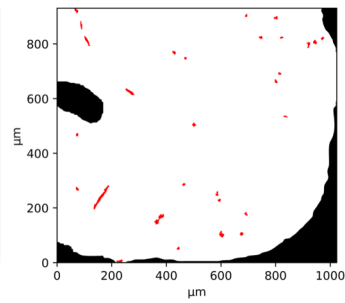
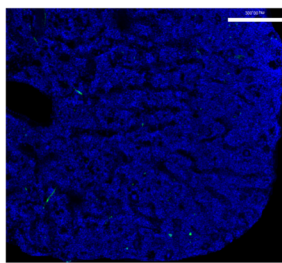


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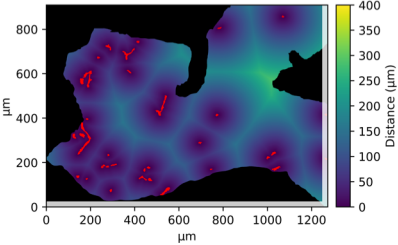
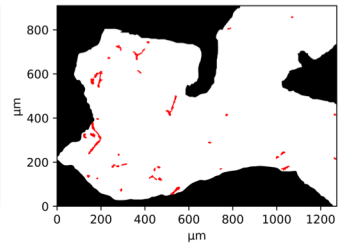
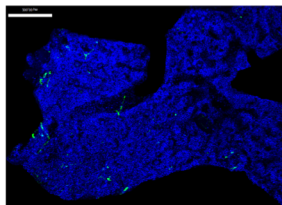


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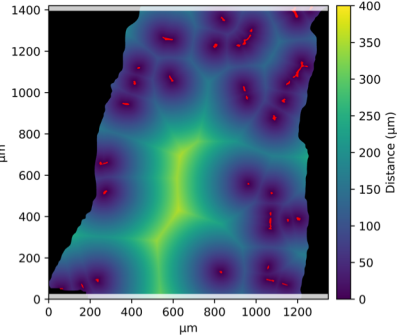
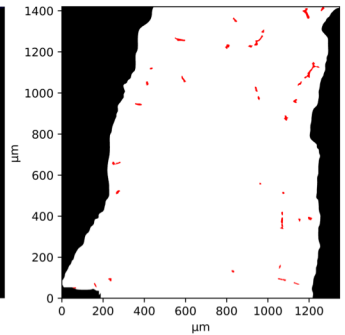
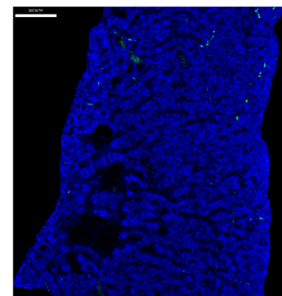
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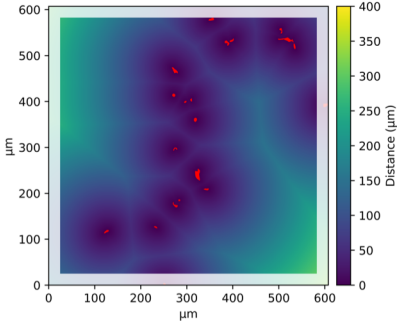
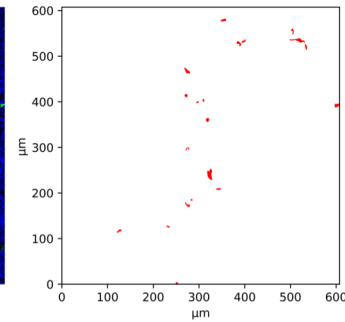
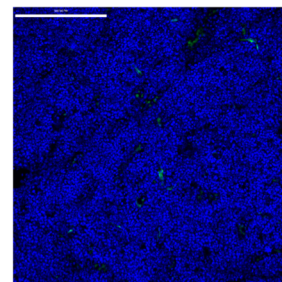
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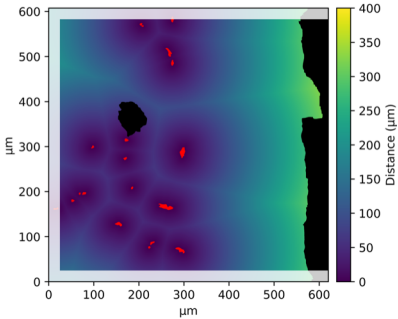
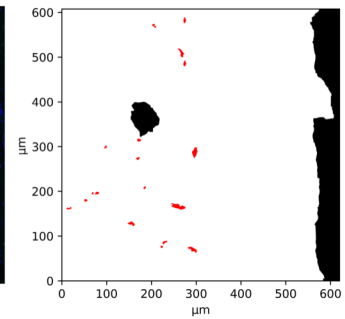
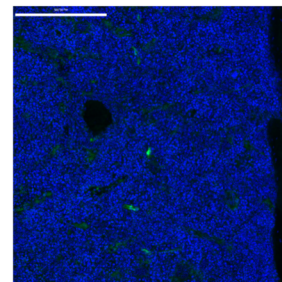
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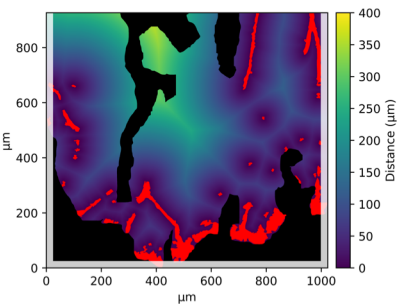
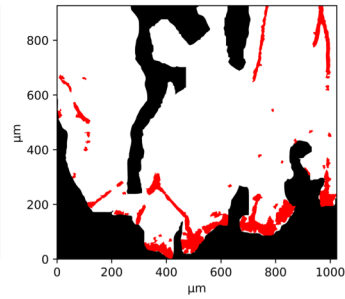
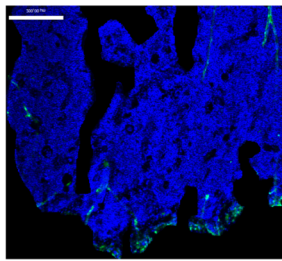


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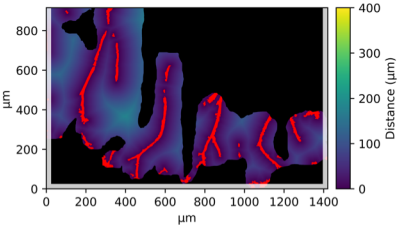
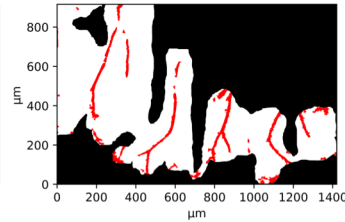
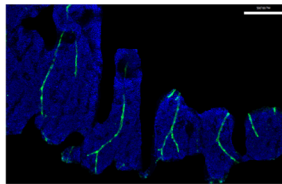


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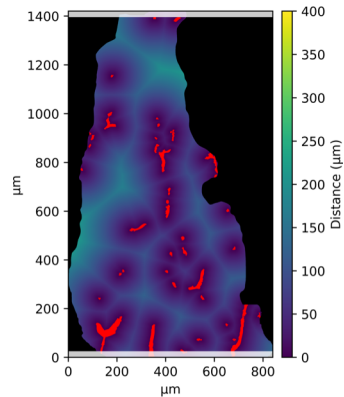
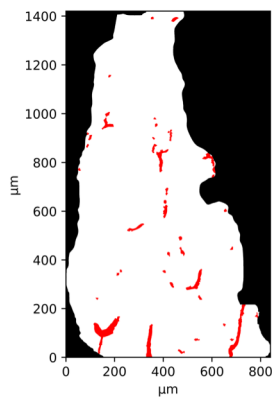
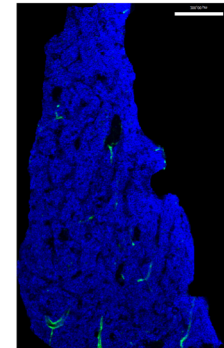
neshigh_young_1



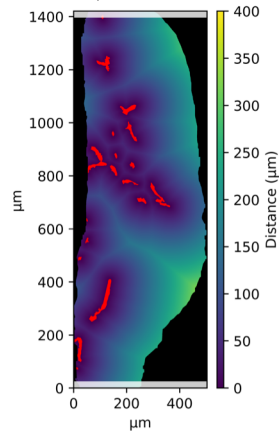
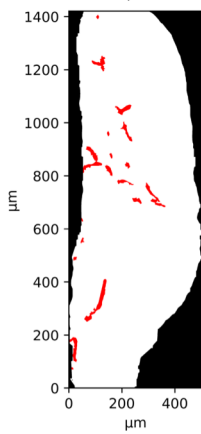
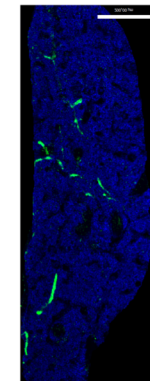
neshigh_young_2



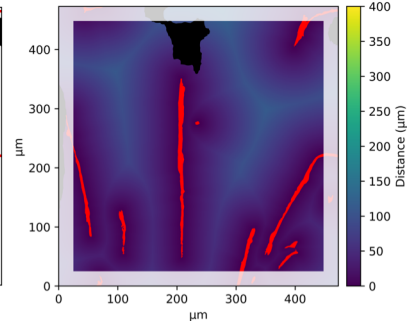
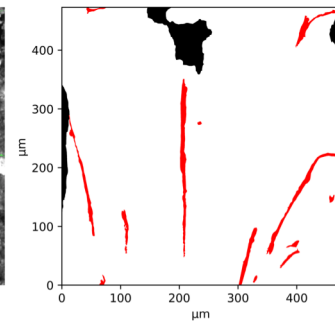
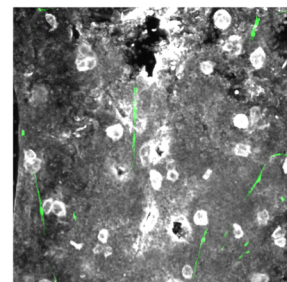
neshigh_young_3



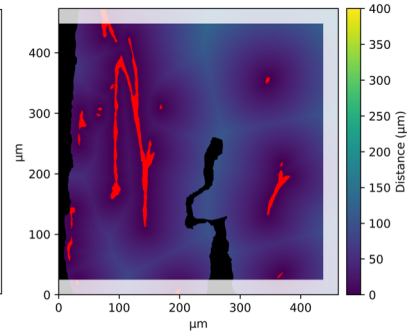
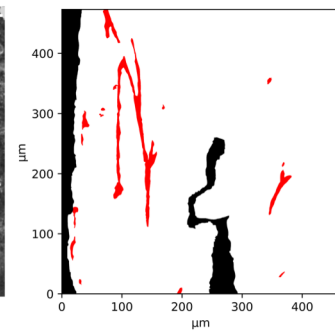
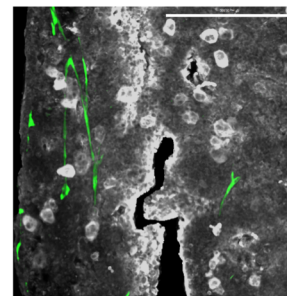
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neshigh_young_5

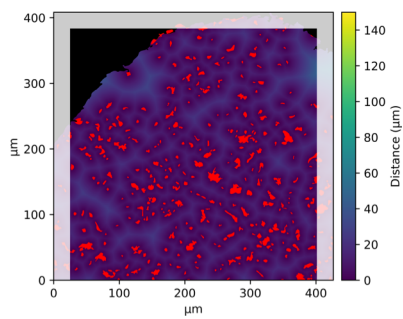
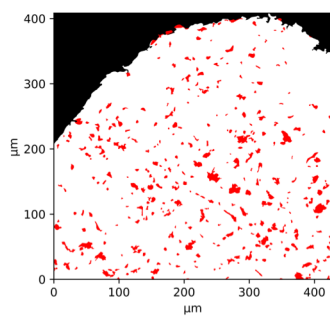
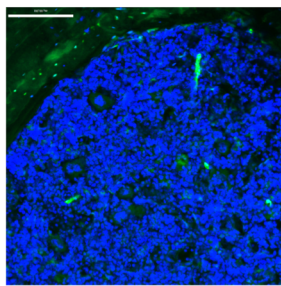


neshigh_young_6

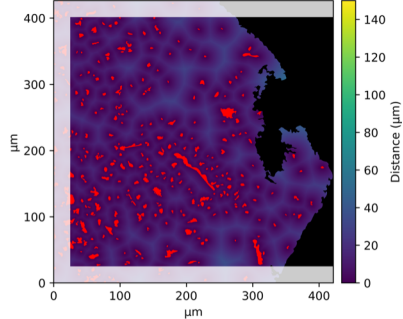
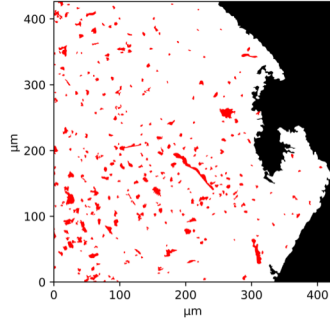
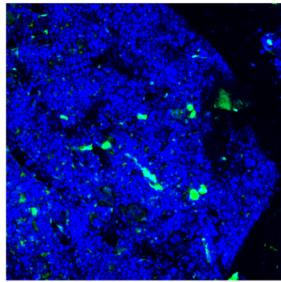


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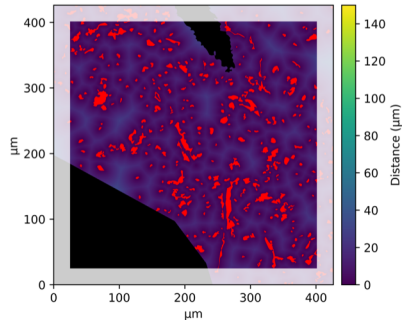
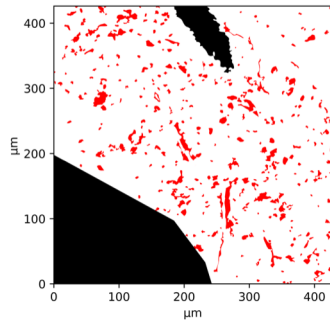
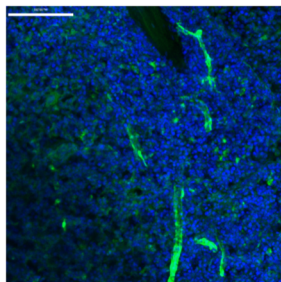
neslow_aged_1



neslow_aged_2

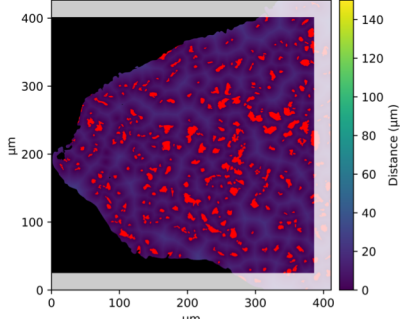
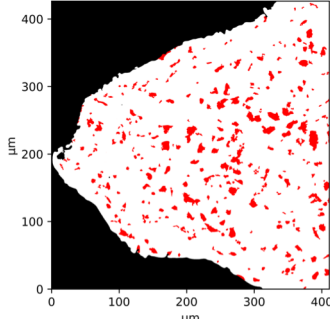
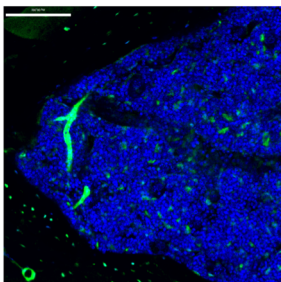


neslow_aged_3

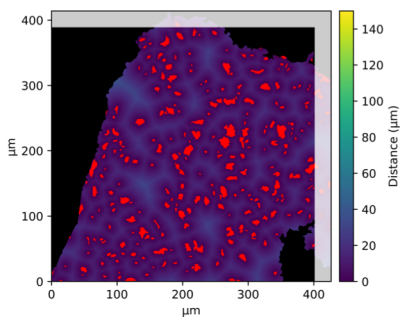
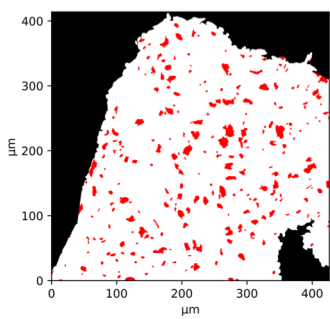
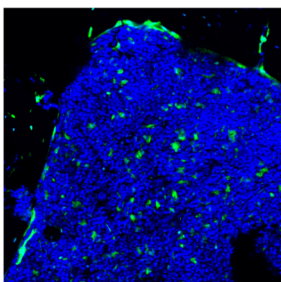


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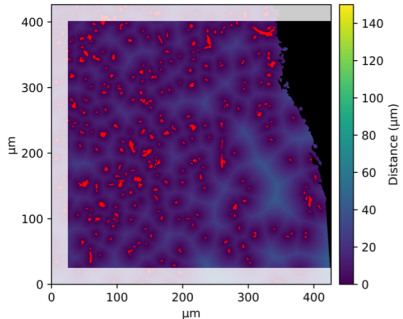
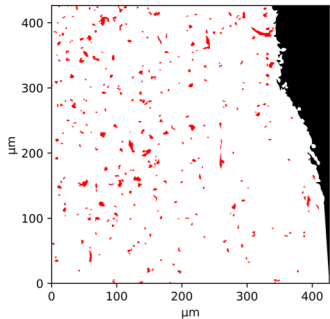
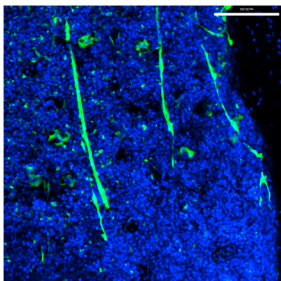
neslow_young_1



neslow_young_2



neslow_young_3



Supplementary Figure 2: LIME Feature Importance Visualization. Hold Out (Test) Set. A representative plot showing a case wise analysis of parameters, either supporting (green) or contradicting (red) that a given sample is aged or young HSC (n = 80 validation cases). Case numbers are indicated, along with label (Yes=Aged; No=Young). Model Probability and level of explanation of the fit are also given for each case.

