We might be able to take advantage of other cytoskeleton segmentation tools, or to at least know how well these do to compare against. Most seem to be Image-J plugins so we may not be able to take advantage of transfer learning.

Examples (from a brief search):

CytoSeg2.0  
<https://academic.oup.com/bioinformatics/article/36/9/2950/5714735?login=false>

JFilament  
<https://onlinelibrary.wiley.com/doi/10.1002/cm.20481>