Some extra suggestions for the tracer transport assignment:

(this file needs a check-up, I updated the m files after the 2023 version

* There is a dedicated GoTransport for this transport assignment.
* Stuff you need to do can be found as %=> in the code, in this script and in some of the called functions. You might still want to add code at other places too.
* In your\_transport\_geometry .m make a vascular network starting with a single input artery (Source Element 1) and output vein (Source element 2). Your network should eventually not be too small, so you may want to generate the network from some algorithm rather than define it by hand (as was done in the Wheatstone example). However, as a start a simple network would help developing all the code; I made one up for now.
* It is maybe handy to define what are arteries, capillaries and veins: define S.IE.type and label these as ‘A’ for arteries, ‘C’ for capillaries and ‘V’ for veins. See the example in your\_transport\_geometry.
* To derive the advection of contrast into several pieces (rectangles) of tissue, I added:
  + A function defining the brain tissue areas, as a number of rectangles next to each other that cover the brain tissue. I assume your network runs from top to bottom, and you can define the vertical limits S.Ytop at the arterial side and S.Ybottom at the venous side. You can also define the left and right limits of the whole brain, and the number of tissue areas next to each other, S.Xleft and S.Xright and S.N\_Tissue\_Areas.
  + A function that splits up all segments in your network that cross a boundary, such that we get a new node at exactly the boundary. You will need that later. The function is not completely bug-free (it misses some crossings), but is correct for large areas as compared to your element lengths. Bonus points if you solve the bugs!
* Solve the flows in this network: already implemented
* Calculate the velocities in the elements and store these values in the IE.
* Define an arterial input function C(t) for the contrast concentration. It can be as complex and realistic as you want, but also here maybe start simple, e.g. a step 0=>1 at time 0 and 1=>0 at a later time.
* This input function is used to calculate all the contrast advection (in moles/s) into the nodes, see the Jin field in the IN. This is applying Ficks principle (what was that again?). The transport is programmed in Transport, preceded by a function GetTransportOrder that figures out in which order we need to simulate the contrast transport.
* In Transport, a dummy statement is programmed that relates the influx and outflux of an element. You need to implement a function that is physically correct.
* (For now) for this function assume only advection (and not diffusion) and assume that flow velocity is homogeneous over the cross-section of all vessels (the elements).
* While the calculation of advection are already programmed, you should be able to explain how this is done. How is this for a node that only has one upstream node (as in arteries)? How is this for nodes that have two upstream nodes (veins)? How do concentrations and fluxes correlate?
* So we now have all flows and all the transport in all nodes, including those at the boundaries. Use these to calculate the total flow into the tissue areas, and the amount of contrast in these areas as a function of time.
  + S.IN(i).Tissue Areas is a vector of all the TissueAreas of which node i is a boundary node. It is empty for non-boundary nodes and may have 1 or 2 elements, crossing a single or two boundaries.
  + These boundary nodes are so-called 2-nodes: they connect 2 elements, one inside each area. S.IN(i).RunsIn is true if the topological direction is into the area. If flow is positive, this means that flow is also into the area.
  + The total flow into an area should be zero: what goes in goes out. This is a good check, but what is relevant is the total arterial flow, that is perfusing the tissue areas. We labeled the vessels as ‘A’ and so on, this should allow you to figure out total flow.
  + How does the total contrast in the tissue as a function of time depend on inflow and outflow concentration? Think about mass balances…
  + We calculated fluxes in the nodes, but the contrast is in the elements, not the nodes. (How) can you calculate C(t) for the contrast concentration in the elements? Mass balance again…
* I think this should allow you to generate all information that you need for testing if/how well the contrast dynamics in the tissue relate to flow. Up to you to further analyze/plot this.