Re: picking a lesion threshold

From: **Ryan Cabeen** | ryan.cabeen@loni.usc.edu Wednesday, Jun 30, 2:22 PM

To: **Ayata, Cenk, M.D.** | cayata@mgh.harvard.edu

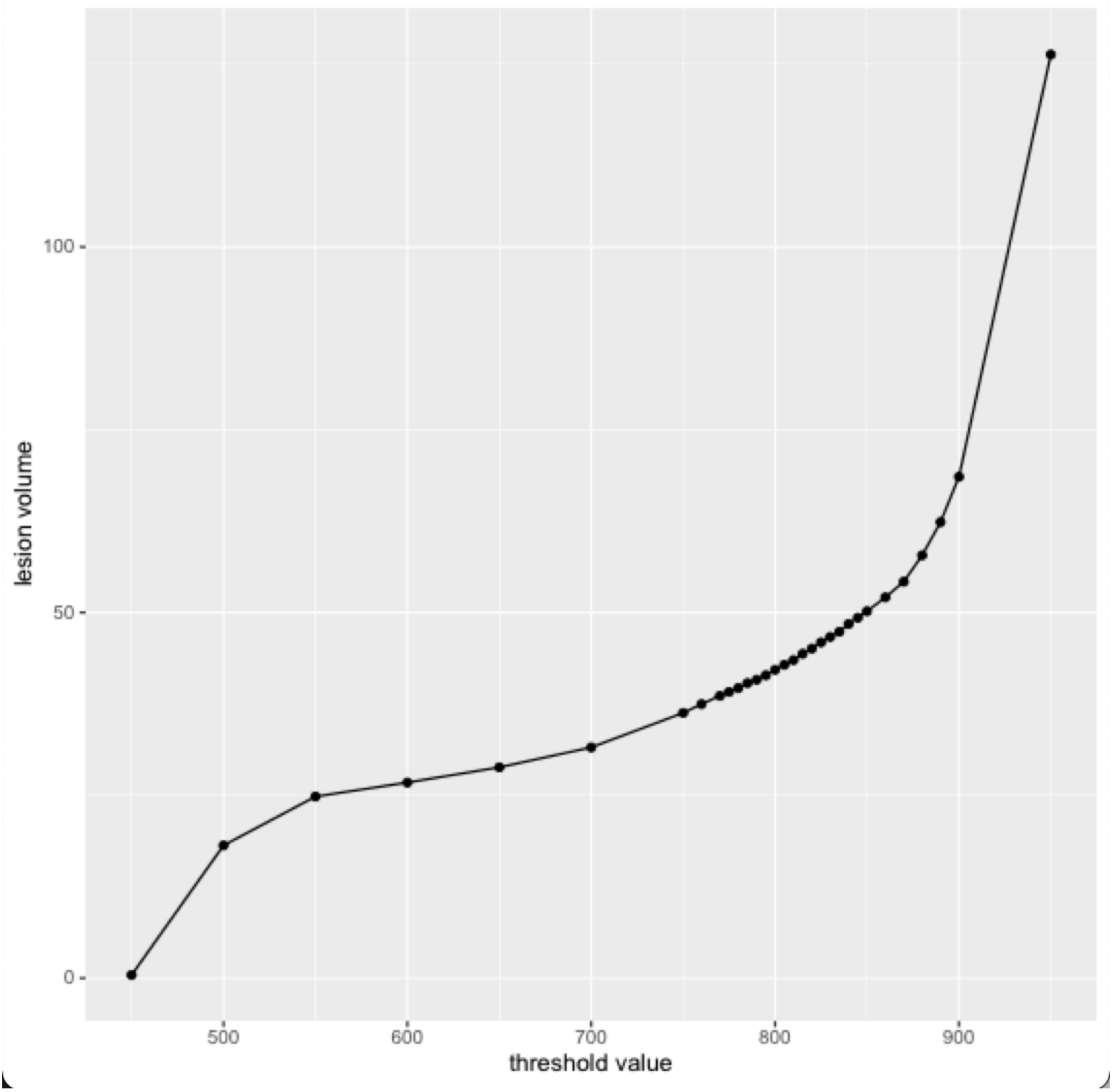
Hi Cenk,

Just wanted to share some food for thought — a first pass at making the threshold vs lesion volume plot for a randomly selected case from stage one. Seems like it has a sigmoidal shape we discussed, although not terribly flat. However, it seems like the derivative is flat in that region, so maybe we can use something like an “elbow criteria” or “knee of the curve” to pick the threshold:

en.wikipedia.org/wiki/Knee_of_a_curve

Anyway, I’ll repeat this for the whole cohort, and we can see how this plays out across individuals and sites, and we can review in detail next week.

Cheers,
Ryan



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From: **Ayata, Cenk, M.D.** | CAYATA@mgh.harvard.edu Wednesday, Jun 30, 3:13 PM

To: **Ryan Cabeen** | Ryan.Cabeen@loni.usc.edu

Awesome, just as we predicted! The flat portion will likely be in similar region horizontally even if the magnitude (vertical axis) is different because of different lesion volumes. We can then look at the slope of the curve and get rid of the vertical axis differences. We could then justify the selection. It will be great to see how this fits at different sites.
C

> From: **Ryan Cabeen** | Ryan.Cabeen@loni.usc.edu Wednesday, Jun 30, 5:22 PM
>
> **External Email - Use Caution**
>
> Hi Cenk,
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> Ryan
>
> <Screen Shot 2021-06-30 at 2.15.19 PM.png>
>
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