RE: [External] RE: topography

From: **Patrick Lyden** | plyden@usc.edu Tuesday, Jun 8, 3:19 PM

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

Cc: **Diniz, Marcio A** | Marcio.Diniz@cshs.org, **'Andre Rogatko (Andre.Rogatko@cshs.org)'** | Andre.Rogatko@cshs.org, **Jessica Lamb** | lambj@usc.edu, **Karisma A Nagarkatti** | nagarkat@usc.edu

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What do you think?

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From: **Ryan Cabeen** | Ryan.Cabeen@loni.usc.edu Tuesday, Jun 8, 3:26 PM

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Great to hear, and exciting! I appreciate the opportunity to work on sharing these results,

For #1, I'll start making overlays of the anatomical regions like you describe. We can also make 3D surface renderings in case they are able to show more too. For #2, I think Marcio only shared the cases with 0 & 1, but not the intermediate cases. So if the full table can be shared, then I can also look at those cases with intermediate values and do those additional tests. Maybe after that we could go over to discuss and plan any remaining pieces before writing?

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Email: rcabeen@loni.usc.edu
Web: cabeen.io
www.ini.usc.edu

From: **Marcio A** | Marcio.Diniz@cshs.org Tuesday, Jun 8, 3:49 PM

Hi Ryan,

To match with your data, please use enro_animal_id. The variable corner_index_d28 indicates whether it is 0 or 1.

Let me know if you need anything else,

Marcio

From: **Ryan Cabeen** | Ryan.Cabeen@loni.usc.edu To: **Patrick Lyden** | plyden@usc.edu Tuesday, Jun 8, 3:42 PM

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From: **Patrick Lyden** | plyden@usc.edu Thursday, Jun 10, 1:30 PM

To: **Diniz, Marcio A** | Marcio.Diniz@cshs.org, **'Andre Rogatko (Andre.Rogatko@cshs.org)'** | Andre.Rogatko@cshs.org

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

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Ryan's fabulous results (see attached) confirm our theory: the "0" animals (all right turns) have striatal lesions and the "1" animals (all left turns) have mainly cortical and thalamic lesions. There is very little overlap in the frequency distributions. Ryan and I are going to start working on a paper, and I would like you involved too. I think it would be very interesting to next map the intermediate scores. Marcio, can you send Ryan a list of IDs for the animals who scored within a range of 0.5, say 0.4 to 0.6?

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From: **Ryan Cabeen** | ryan.cabeen@loni.usc.edu Friday, Jun 11, 2:02 PM

To: **Patrick Lyden** | plyden@usc.edu

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From: **Patrick Lyden** | plyden@usc.edu Friday, Jun 11, 3:01 PM

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

Yes, I would like to see the plots that show each group separately as well.

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From: **Diniz, Marcio A** | Marcio.Diniz@cshs.org Friday, Jun 11, 4:06 PM

To: **Patrick Lyden** | plyden@usc.edu, **Rogatko, Andre** | Andre.Rogatko@cshs.org
Cc: **Ryan Cabeen** | Ryan.Cabeen@loni.usc.edu

Hi Patrick and Ryan,

That's look exciting! Apologies for my delay, I was taking care of randomization for stage 2 with Jessica.

I created a variable corner_index_cat that includes the following categories 0, 0.01 – 0.2, 0.21 – 0.4, 0.41 – 0.6, 0.61 – 0.8, 0.81 – 0.99 and 1. Please see corner_test_categorized.csv.

I also filtered only mice with corner test between 0.4 and 0.6 as requested. Please see corner_test_only_4_6.csv.

Let me know if you need the data in different format, Ryan.

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> MC2821
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plyden@usc.edu

From: **Patrick Lyden** | plyden@usc.edu Friday, Jun 11, 5:11 PM

To: **Diniz, Marcio A** | Marcio.Diniz@cshs.org
Cc: **Rogatko, Andre** | Andre.Rogatko@cshs.org, **Ryan Cabeen** | Ryan.Cabeen@loni.usc.edu

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From: **Ryan Cabeen** | ryan.cabeen@loni.usc.edu Monday, Jun 14, 9:43 PM

To: **Diniz, Marcio A** | Marcio.Diniz@cshs.org

Hi Marcio,

One more thing, I just wanted to loop you in on a few tests I did for validating the MRI pipeline. Dr Ayata suggested comparing early timepoint lesion volume and late timepoint tissue volume (atrophy). Our idea was that this would be some indication of the quality of the imaging pipeline, since they should have a strong association (seems to be the case empirically). The results are attached — thought I'd share with you in case they are useful, or if you might have some additional insights.

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plyden@usc.edu

From: **Diniz, Marcio A** | Marcio.Diniz@cshs.org Thursday, Jun 17, 11:03 AM

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

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To: **Ryan Cabeen** | Ryan.Cabeen@loni.usc.edu
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Thank you for the explanation! Now, I completely understand the colormaps in the videos. It was really helpful. Is your plan to produce multiple pairwise comparisons to incorporate intermediate corner test scores?

I totally agree that a voxel-based analysis would be more appropriate. Patrick and I discussed one additional analysis using the data of lesion fractions by region, but I have not been able to obtain clear results as you did. Given your much large experience with statistical analysis for imaging than mine, please feel free to take the lead on addressing this question and let me know whatever I can help you from the statistical side.

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From: **Marcio A** | Marcio.Diniz@cshs.org Tuesday, Jun 8, 3:49 PM

Hi Ryan,

To match with your data, please use enro_animal_id. The variable corner_index_d28 indicates whether it is 0 or 1.

Let me know if you need anything else,

Marcio

From: **Ryan Cabeen** | Ryan.Cabeen@loni.usc.edu To: **Patrick Lyden** | plyden@usc.edu Tuesday, Jun 8, 3:42 PM

I think just two lists of the cases that make up the groups, corner test = 0 and corner test = 1. I don't think I have the behavior outcome measures on my end.

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From: **Patrick Lyden** | plyden@usc.edu Tuesday, Jun 8, 3:38 PM

Thanks. What do you need to pull it off?

From: **Ryan Cabeen** | Ryan.Cabeen@loni.usc.edu To: **Patrick Lyden** | plyden@usc.edu Tuesday, Jun 8, 3:26 PM

Sounds like a great idea to me -- I'd be glad to implement it and make visualizations that we can review.

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From: **Patrick Lyden** | plyden@usc.edu Tuesday, Jun 8, 3:19 PM

Ryan,

We are still struggling to understand our corner test data, using your analysis of cortical vs striatal vs thalamic lesion volumes. I would like to try to simplify the problem, and I recalled your most excellent frequency map in which you plotted in 3-d the lesions and showed a beautiful lesion frequency map. I would like to try the same thing but first, split the data into two populations: corner test = 0 and corner test = 1. These are the extreme values, and if lesion location plays a role in turning direction, this two groups should differ in their lesion locations. Then you make the frequency map again, but show the two populations in different colors. The two distributions should center in different locations.

What do you think?

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