Meeting May 19, 2020

From Lyden:

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This is an awesome start. A lot of the data, e.g. site, animal ID, will already be in the
 REDCap database. Machine and image acquisition parameters ‘should’ all be in the file hea
der of the dicom files, assuming all sites comply with the upload instructions.

I want to argue against any manual readouts, such as ‘hemorrhage’ or ‘midline shift’ becau
se we are valiantly tyringto automate all of the image analysis. The less human interventi
on the better, I think. Having said that, hemorrhage is important, and we have not previou
sly discussed it. For the RHAPSODY study, we used a novel protocol from Mark Haacke called
SPIN that automatically quantitated blood. It’s a little late in the game now, but maybe y
ou all can discuss and see if there is an automated process you could implement, if not in
time for STAGE I perhaps by Stage 2.

Variable name:
Data type (numeric vs text vs date, etc):
Variable Length (number of digits or characters):
Allowable range:
Any notes:

For example, lets take volume of stroke as an example.

Variable name: Lesion_Volume
Type: numberic
Length: 7 digits – nnnn.nnn
Range: 0ml to 40ml
Notes: volume is calculated as the measurable void on T2
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From Karen:

For the scan acquisition info we do extract metadata from the image headers (see attached
 from example scans uploaded to SPAN) and store in the database.  For analysis results, if
they are in CSV format they could potentially be pushed into the repository and linked ass
uming that the results dataset contains the image ID.
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https://s3-us-west-2.amazonaws.com/secure.notion-static.com/3ac252fb-8003-40bc-b9aa-e7b4069b3ee9/span.csv

From Joe:

Thanks Ryan. Everything looks pretty good.

A few questions and possible additions to consider now for acquisition and analysis;

1) In our last zoom, you mentioned the potential problem of ADC normalization within a les
ion in at least one of the mice. My assumption from the beginning of this has been that A
DC
will not be reliable at 48 hours, and so I was thinking of this simply as a method to elim
inate CSF, but not as something to be used for lesion segmentation. This is partly/mostly
 a biology question, I think:
what do we do when we see clearly elevated T2 in the core of the lesion but ADC does discr
iminate that area? I was thinking we would ignore ADC in that instance. What do others th
ink?

2) I have some concern about too-small surface coils potentially not covering the space ad
equately (see the last example in your zip). If we get to the spatial normalization soon
 enough,
we may want to add a metric of minimum SNR without the brain mask as a way of seeing drop-
off problems.

3) If we are going to use spatial normalization, which makes sense to me (and which I firs
t suggested but then we dropped because it seemed potentially difficult),
we probably want to specify a stroke side and that animals must be registered in the scann
ers correctly (e.g,, don’t accidentally swap “feet first” vs “head first”).
It would simplify spatial normalization and segmentation to always have the lesion on the
 same side in images. I principle, one could swap coordinate parities, but this is an addi
tional step.

4) Do you have spatial normalization methods that you think will work well in rodents give
n large strokes and the signal roll-off from surface coils?
I have some experience with this, so I’d be happy to chat about it. There probably are a
 variety of methods that would work but the typical strategy of brain extraction usually i
sn’t very good in rodents.

From Ryan:

Thanks Joe — all seem like good considerations! Here are a few thoughts that come to min
d:

1) I noticed this issue in the data too, where T2 and ADC disagree in some cases. I’d hav
e to do some reading to weigh in myself, and happy to update things as folks see fit. I t
hink we can also adjust the ADC threshold to do what you describe.

2) Yes, it does seem like there is inhomogeneity that affects the lesion, and I bet this w
ould be problematic for brain extraction and atlas registration. I’m using N4 bias field
 correction, but it can only do so much for the farthest signal drop.

3) I did some tests with ANTs, and the results seemed encouraging, but it did fail in abou

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t a quarter of the cases. I used a standard T2 template, but I'd guess the differences in
 field of view and contrast may be an issue.  We could possibly make a study-specific (or
 perhaps site-specific) template once the protocol is nailed down and there is more data

4) Would be happy to brainstorm!  I've used ANTs in other rodent datasets, but they don't
 seem to work as well here.  Seems like we can segment the stroke without template registr
ation, but I think we would need it to measure brain/csf volume and to subdivide by hemisp
here.

From Joe:

I typically have not relied upon brain extraction for spatial normalization in rodent spec
ies, mostly due to non-standard image contrasts and unpredictable RF bias.
Instead I simply register into a template-based brain mask to eliminate extra-cerebral sig
nal. The upside is that it eliminates the brain extraction step, and the downside is that
 the "capture range"
on automated alignment is reduced (it typically needs to get "close", like 1/4 FOV, for au
tomated alignment to capture it).  For RF bias, I divide each image (template/source)
by a low-passed version of self, so one can enforce an arbitrary degree of flattening.

One possible strategy would be to segment the lesion in native space and then initialize n
ormalization using the lesion centroid. Then we could align using a series of progressivel
y
increasing flattening to solve the bias and lesion issues. I think in the end the template
should be the normalized average of lesioned mice, so there will be some iteration.
Then final processing occurs in normalized space.

I haven't experimented with ANTs.  It may well be the case that ANTs just works when you u
se a template based upon lesioned mice.
I feel like we shouldn't have to use site-specific templates, but I guess that would be ok
if it enables using some existing method.
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Meeting Notes:

- Add bias field quality control metric

https://s3-us-west-2.amazonaws.com/secure.notion-static.com/4bda01cc-e95c-4440-8b08-0b650b3c035f/MRI_database_entries.xlsx