**TMM LOGISTICS:**

Jonathan rents vehicle (likely Dodge Grand Caravan) from Enterprise on Lomas ~1:30PM on Sunday, May 12th. As an individual, there will be a $150 deposit, and all drivers need to be present to sign paperwork with a $15/driver/day additional fee. It is cheapest to rent the vehicle at the Lomas location on Sunday and then return to the airport immediately upon return on Sunday, May 19th. This will be $506.26 with one driver, plus $105 per additional driver. Nick, Carson, and Jonathan are available that Sunday for signing purposes. It would have been $448 through UNM, including all drivers and returning the car Monday morning rather than Sunday night.

Last trip to TMM, we learned that many of their *Arctodus* specimens were actually casts, with the originals held at Texas Tech in Lubbock. Felisa emailed the collections manager there (and I believe received a positive response?) about us stopping by to collect stable isotopes (and I’m sure Carson would now like to grab microwear) from those bears on a future trip. If it can be arranged, perhaps we could do this on our way back this trip. I think an even better option would be to do another TMM trip in January 2020 coupled with the Society for Integrative and Comparative Biology (SICB) meeting.

Since no Smith grad students are going to SVP 2019 in Brisbane, I propose that we attend both GSA in Phoenix, AZ in September **and** SICB 2020 in Austin, TX from 1/3-1/7, while coupling the conference with another TMM trip.

**PI-LEVEL QUESTIONS THAT INFLUENCE RETURNS AND GOALS:**

1. **Do we care about shrews?** All but *Blarina* (short-tailed shrews)and the very rare *Scalopus aquaticus* (Eastern moles) are too tiny for individual-level SIA. Jonathan is already planning to do SIA on *Blarina* as a contrast to *Onychomys*. Toothless mandibles for all other shrews are 30mg or less. To make matters worse, some previous project identified most *Notiosorex* to the species level, and I assume TMM would want us to match that. While I don’t have the specifics, I know the easiest ID method involves counting individual tooth cusps, and many specimens lack teeth... (yet the previous project apparently ID toothless mandibles using more subtle traits?). There are also several thousand shrews available between already accessioned specimens and unID vials marked shrew jaws or Insectivora/Soricidae.
2. **What methods are we using for Kate’s community abundance project?**  We have now pulled virtually every unID vial containing small mammals from the TMM cabinets. I have identified all possible specimens from 000-100cm and 215-355cm. There is much more material from 100-215cm, which we will be processing in lab for probably the next year. At TMM, there are hundreds of pre-accessioned specimens for common species (e.g. *Chaetodipus* and *Perognathus*) in boxes. I did not take many of these since I got the sample size I needed from unID specimens, and I assumed we could get abundance from Toomey’s dissertation/TMM spreadsheets. If I was wrong, we’d need to pull them on this trip.
3. **Do we care about rare taxa for SIA?** We have a few individual *Dipodomys, Synaptomys, Ochrotomys,* etc… Are they safe to return? *Dipodomys* was originally ID as a focal taxon for the grant, but last semester we decided to shift to superabundant *Chaetodipus* instead.

**HALL’S CAVE MICRO/MESO/MEGAMAMMAL STATUS RECORDS:**

I started the micromammal records as a way to more efficiently accession small mammals to prevent scenarios like accessioning 500 individual *Chaetodipus* from the 145-150cm stratum. I was planning to use these twelve taxa under 1lb as my Hall’s Cave chapters’ focal taxa, with some caveats. *Perognathus* is too small for individual-level SIA from mandibles. Dave Fox has offered to share his individual-level IDs for those specimens and CT data, but his specimens are returned to TMM after use. I propose we combine multiple specimens assigned to the same species for SIA after those analyses, which punts them toward the end of this project, but it would allow us to examine responses of the smallest granivores on the landscape relative to larger ones (i.e. *Chaetodipus*). *Blarina* looks very incomplete right now, but that’s an artifact of me telling the undergrads to set shrews aside rather than accessioning them. *Neotoma* and *Sigmodon* also look very incomplete, and that’s an artifact of me not having access to the previous loaned specimens that have been returned. They were not returned to the shelves following past returned loans, so I assume I’ll need to find where those live in the museum now.

**TMM RETURNS:**

Dante has prepared at least one, small box of *Sylvilagus* and *Lepus* for return. Jonathan has a large box of specimens for remaining unID material from small mammals, surplus bulk accessioned material, and rare or truly tiny taxa. I just need to know whether we’re safe to return non-*Blarina* shrews, boxes of Toomey-accessioned taxa for which we already have good sample sizes (e.g. *Chaetodipus*), and rare taxa.   
  
  
**INDIVIDUAL GOALS/WISH LIST:**

**Jonathan:**

1. Either check out the youngest and oldest raw matrix bins (000-005cm and 350-355cm) OR, ideally, check out bags of sieved material from multiple bins. It would take a minimum of **four** TMM trips to flesh out sample sizes for known missing time bins at just two bins per trip.
2. Go through previous returned *Neotoma, Sigmodon,* and *Onychomys* (?) material to find complete tooth rows (for CT-scanning) or complete sets of dental alveoli (for body size analyses). These are a bargain because we already have isotopes for those specimens. *Neotoma* and *Sigmodon* are undersampled in my records, but obviously not in the Hall’s Cave record. And I know their material was not back in the shelves/cabinets on our last trip, so it must still be in the back or some other location.
3. Make a final pass through the Hall’s Cave drawers checking for missed material. On our last trip, I went through 000-150cm and 355-215cm, but I missed the middle part of the record, for which Amelia did pull specimens on her solo trip. However, I found many specimens she didn’t realize were rodents in the strata that she and I both examined, so it is wort checking through these drawers again.
4. 3D scan/photogrammetize megafauna? If we want to do any sort of megafaunal morphology, we now have the technology… And it would be neat to 3D print a real mammoth skull from the Edwards Plateau…

**Catalina:**

1. Sample modern mammals, especially small mammals, from the Edwards Plateau for SIA (take a rib when possible). **(This would really help Jonathan too.)**
2. Take a trip out to a site near Hall’s Cave to sample vegetation for SIA for mixing models.

**Carson:**

1. Sample fossil bears from the Edwards Plateau for SIA and dental microwear.
2. Sample modern bears in TMM’s collection for isotopes and (especially) dental microwear. (Consulting with Jonathan to avoid bears killed in National Parks before garbage policy reforms).

**Nick:**

1. Nick wants to do some morphology while he’s here, so he proposes to look at changes in body size in mesomammals (especially felids) pre- and post-extinction.

**Photographing at TMM:**

I think we should always have someone manning the camera since modern photos and SIA are constant goals. The camera used for the inter/intra-observer error study is a Canon EOS 70D with 20.4 megapixels. I recently purchased a Canon 5DS R with 50.6 megapixels. I propose to leave the 70D in Smith Lab so undergrads and postbacs can continue to take pre/post-photos in preparation for a major small mammal isotope session when I return from TMM. We can get even better images with new camera, and it will be good for me to get more experience with it anyway.