# Sept. 11 meeting with Betsy

Overall question: Do similar forest communities converge in EM communities after fire??

Three questions:

1. Do we see changes in diversity or community composition as a function of fire in the Santa Catalina Mts. and Pinaleno Mts.?
   * Yes, we do.
   * ~~Fig. 2 and 3 combine into panels~~
   * ~~Check NMDS analysis of SCM and PM. Are the numbers right?~~
     + Checked analyses numbers came out the same
     + Similar results seen when root tip abundance data was used instead of sequence abundance data
   * Diversity tells us that the communities have recovered (no sig. difference between burned and unburned), but the below tells us that they do not converge
2. Do communities converge after fire?
   * No
   * Fig. 4B 🡪 4A
   * Fig. 4A 🡪 4B
   * Insert fig. 5 as an inset to figures 4A and 4B
3. Are the same taxonomic lineages present in both ranges?
   * No, there is a lack of convergence at both the species level and at higher taxonomic levels.

*Frame work for intro:*

* Fires are important for forest health and function
* Trees and soils are affected
* Can affect symbiotic EM communities directly and indirectly.
* Often studies of fire occur at relatively small special scales making it difficult to generalize across forest 🡪 show scholarship here, what do we know
* Sky islands of AZ and Mexico offer opportunity to look at fire in similar forests with different precipitation regimes
* Goal of study is to evaluate whether such forests converge on similar communities after fire.

*Methods:*

Study range focusing on the similarity of sites

* Incorporate plot data
* ~~Temperature did not differ (add stats to Table 1 description)~~
* ~~Precipitation did (add stats to table 1 description)~~
  + ~~Range comparison, do not include fire; t-test~~
  + Address this difference in the discussion
* Soil
  + All soil characteristics or just those important to EM…DECIDE
  + Redo analyses PCA of characteristics, FU sites only scm vs pm
* All of this will account for background noise

\*Check fire unaffected NMDS, is this significantly different??? Same stats as FA

**Fix supplementary figures**

*Table 1*

* Show mean ± sd for prec and temp; add stats for t-tests
* Check that have same number of digits for all.
* ~~No decimal for elevation~~
* ~~Remove forest type~~
* Remove tree and site names (think about this, can they be simplified, are they necessary for other tables/figures?)

|  |  |
| --- | --- |
| sc1 | 1 |
| sc2 | 2 |
| p1 | 3 |
| p2 | 4 |
| sc3 | 5 |
| sc4 | 6 |
| p3 | 7 |
| p4 | 8 |

* ~~Group by unburned (SCM, PM), burned (SCM, PM)~~

*Table 2*

* Means ± SD, group by fire history, range, and site
* ~~Group by unburned (SCM, PM), burned (SCM, PM)~~

*Table S1*

* ~~Remove outliers from table~~
* Why don’t Shannon samples for outliers also look weird
  + LB021
  + NF19
  + F4
  + F11
  + F12
  + F14
* ~~Group by unburned (SCM, PM), burned (SCM, PM)~~

*Table S2*

* Make main result table

*Discussion*

We sample longer than the regular fire interval

# To keep consistent

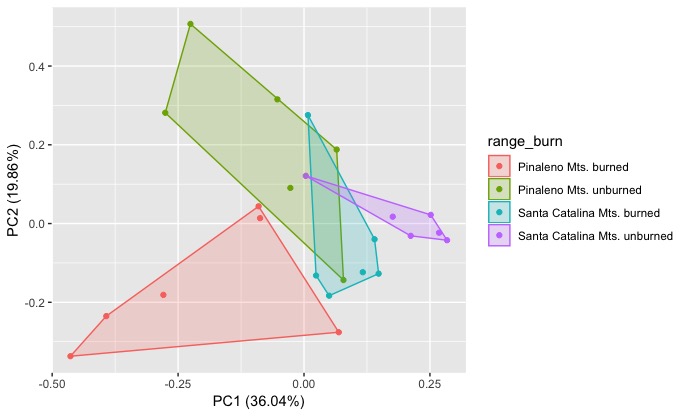
* Use a space on either side of =, <, or >.
* Two decimal points
* Unburned (SCM, PM) then burned (SCM, PM)
* Keep axes the same so graphs across are easier to compare
* Reduce usage of acronyms (SCM, PM, FU, FA)
* Severity and intensity differences

# Environment

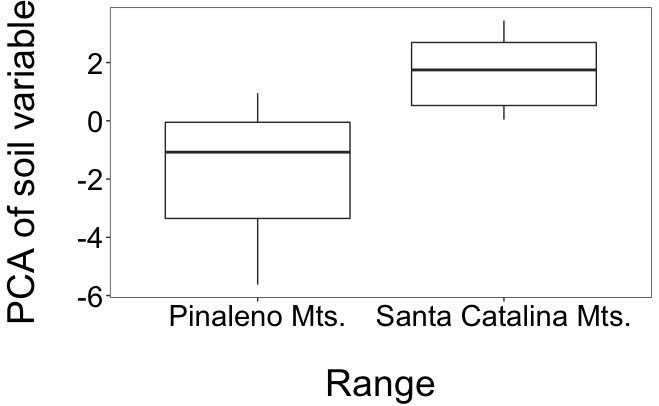
* Are there significant differences between climate and soil between ranges?
* Between burned and unburned sites?

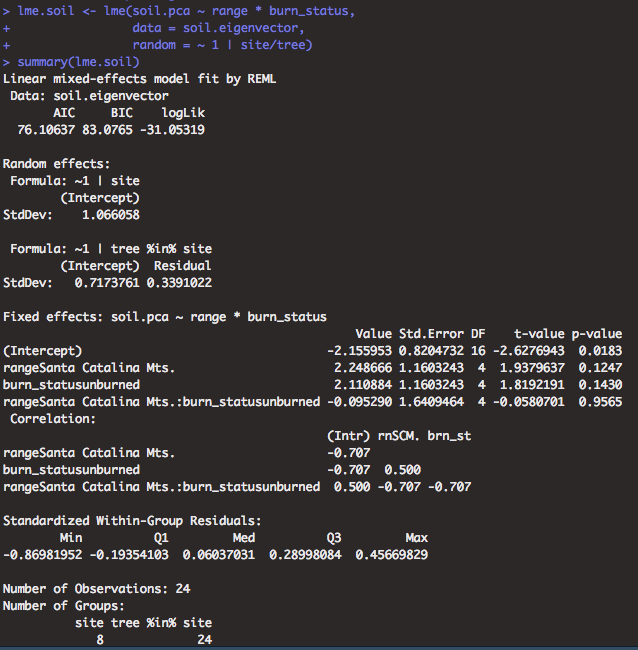
Soil: Seems to differ by both range and burn status, but range has a stronger difference (based on cluster dendrogram and multiple linear regression.

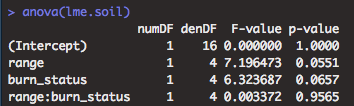
* Based on model fitting (see output below) a model including range only with site as a random factor is the best model.





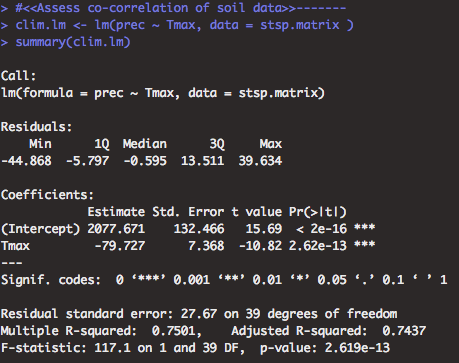


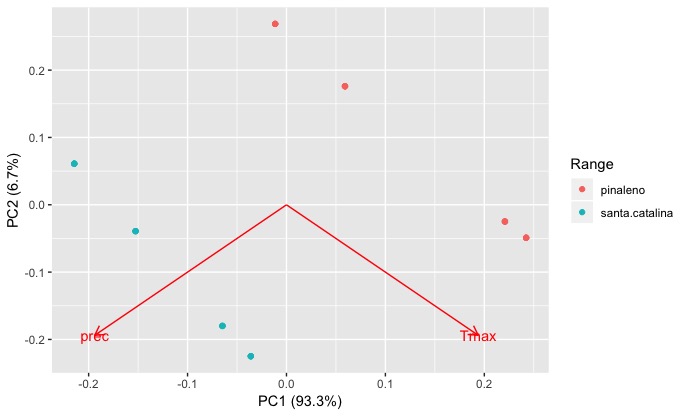


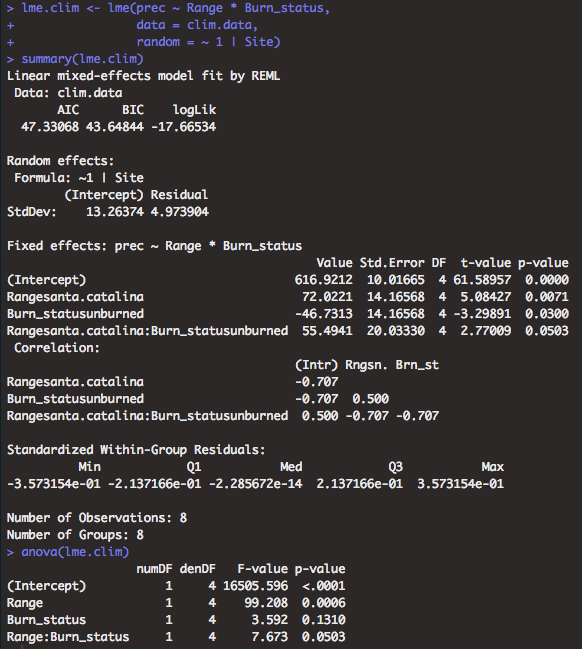


Climate: mainly precipitation is driving differences between ranges in climate.

* Precipitation and temperature are co-correlated



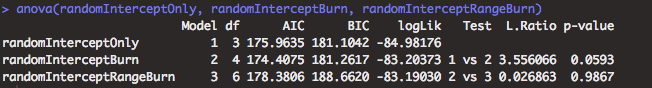
* 

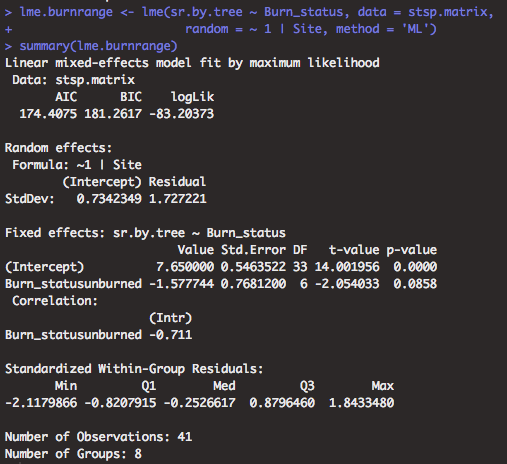


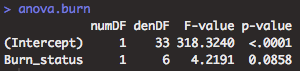
* Do soil differences correspond to differences in forest type?
  + Unable to assess as the there are some plant communities with only 1 site (i.e. no repetition).
  + Assess using PCA instead

# Diversity

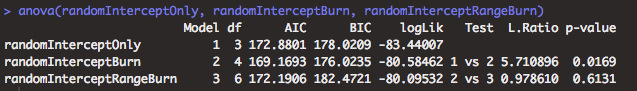
* Species richness with singletons
  + Ran model to assess whether random effects should be included in model
    - Yes, included site as a random factor
    - Including tree as a random variable did not improve the model
  + Model showed that neither range nor burn status improved the model, neither was significant
  + On that note just burn status was marginally significant, so I included it in the model only.

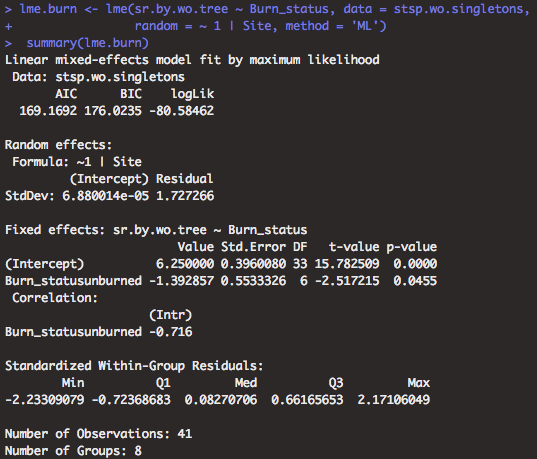


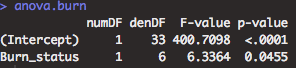




* Species richness without singletons
  + Ran model to assess whether random effects should be included in model
    - Yes, included site as a random factor
  + Model showed that burn status only improved model

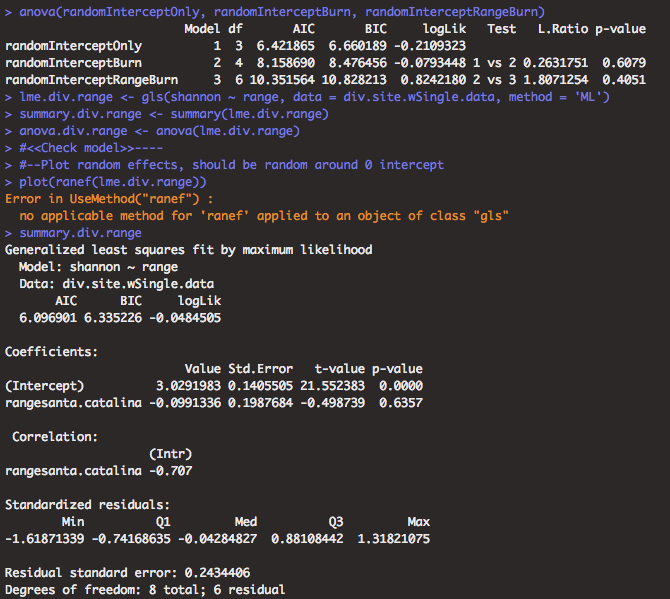


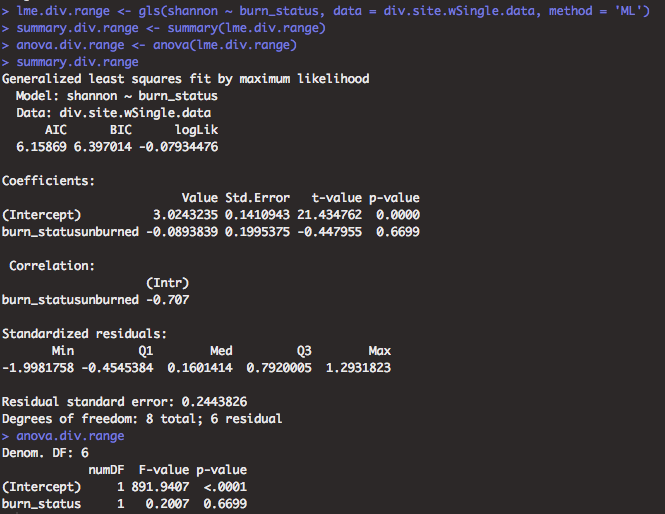




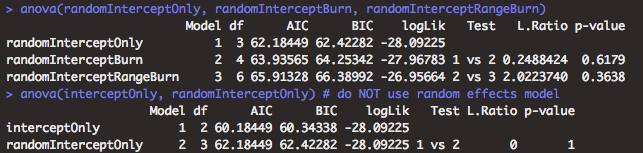
* Diversity with singletons and without singletons
  + Ran model to assess whether random effects should be included in model
    - No, Use a generalized least squares model instead as a linear mixed effects model does not improve the model at all.
  + Not significant for both FA and Shannon’s.

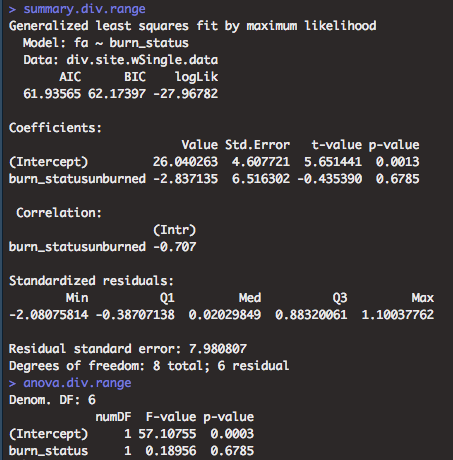
Shannon’s diversity





Fisher’s alpha

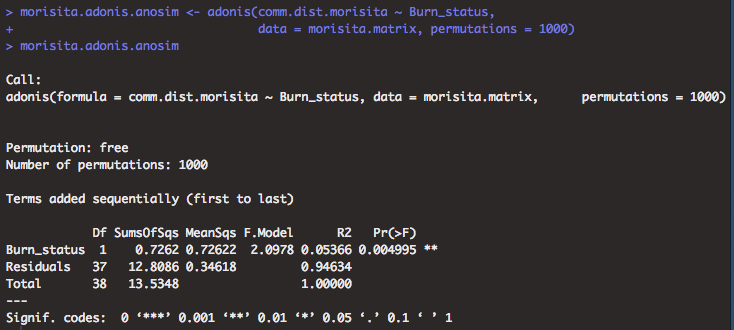




# Community

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| anosim.res | stress.nmds | F.betadisper | df.betadisper.1 | df.betadisper.2 | p.betadisper | r | p |
| jaccard.all | 0.2148 | 0.1281 | 1 | 36 | 0.7225 | 0.0766 | 0.036 |
| morisita.all | 0.205 | 4.2081 | 1 | 37 | 0.0474 | NA | NA |
| jaccard.p | 0.149 | 1.2687 | 1 | 16 | 0.2766 | 0.5291 | 0.001 |
| morisita.p | 0.1632 | 0.0014 | 1 | 16 | 0.971 | 0.5372 | 0.001 |
| jaccard.scm | 0.2253 | 1.5477 | 1 | 18 | 0.2294 | 0.1233 | 0.059 |
| morisita.scm | 0.2285 | 2.7737 | 1 | 18 | 0.1131 | 0.1252 | 0.03 |
| morisita.fa | 0.1915 | 2.6116 | 1 | 18 | 0.1235 | 0.3368 | 0.001 |
| morisita.fu | 0.1523 | 2.7737 | 1 | 18 | 0.1131 | 0.1252 | 0.03 |

* Morisita horn all, NMDS stress = 0.205348; PERMANOVA



PERMANOVA analyses assessing fire history and range

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| test | F.model.burn | r2.burn | p.burn | F.model.range | r2.range | p.range | F.model.burn/range | r2.burn/range | p.burn/range |
| jaccard | 1.5993 | 0.0391 | 0.015 | 2.5042 | 0.0613 | 0.001 | 2.7582 | 0.0675 | 0.001 |
| morisita | 2.3509 | 0.0537 | 0.003 | 3.2541 | 0.0743 | 0.001 | 3.20982 | 0.0733 | 0.001 |

# Taxonomy

* Made file of representative OTU sequences at 97% sequence similarity for UNITE taxonomic analysis
  + dereplicated\_otu97.csv in ‘data\_output/’
  + made a fasta file with the otu name and sequence called dereplicated\_otu97.fasta
* Downloaded the UNITE USEARCH database version 8
  + <https://plutof.ut.ee/#/doi/10.15156/BIO/786345>
  + **When using this resource, please cite it as follows:**  
    UNITE Community (2019): UNITE USEARCH/UTAX release for Fungi. Version 18.11.2018. UNITE Community. [**https://doi.org/10.15156/BIO/786345**](https://doi.org/10.15156/BIO/786345)
* usearch -sintax data\_output/dereplicated\_otu97.fasta -db ~/../../Volumes/Cenococcum/UNITE/utax\_reference\_dataset\_02.02.2019.fasta -tabbedout unite/reads.sintax -strand both -sintax\_cutoff 0.8

00:00 1.5Mb 0.1% Reading /Users/eabowman/../../Volumes/Cenococcum/UNITE/utax\_reference\_dataset\_0200:01 52Mb 19.5% Reading /Users/eabowman/../../Volumes/Cenococcum/UNITE/utax\_reference\_dataset\_0200:01 119Mb 100.0% Reading /Users/eabowman/../../Volumes/Cenococcum/UNITE/utax\_reference\_dataset\_02.02.2019.fasta

00:01 86Mb 0.1% Masking (fastnucleo)

00:03 86Mb 100.0% Masking (fastnucleo)

00:05 87Mb 100.0% Word stats

00:05 87Mb 100.0% Alloc rows

00:08 264Mb 100.0% Build index

00:10 275Mb 100.0% Initialize taxonomy data

00:10 277Mb 100.0% Building name table

00:10 277Mb 39004 names, tax levels min 1, avg 5.8, max 7

WARNING: 3 taxonomy nodes have >1 parent

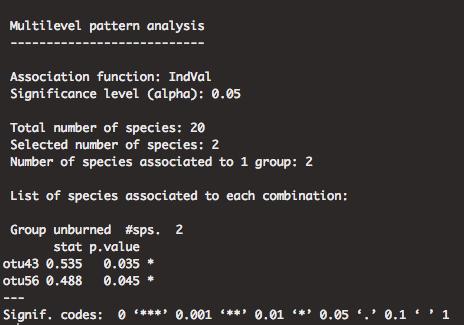
00:13 279Mb 100.0% Processing

* Created Funguild.R script to add taxonomic data to site by species matrix
  + Saved as OTU97\_withTax.csv
* Ran above file on Funguild online site
  + Output file FUNguild/OTU97\_withTax.guilds.txt

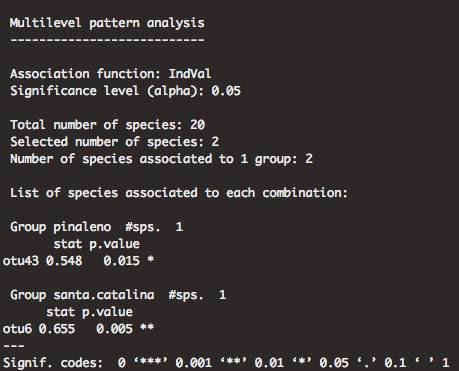
|  |  |  |  |
| --- | --- | --- | --- |
| tests | chi.stat | df | p.value |
| burn.range.class | 44.4790943 | 12 | 0.00001 |
| burn.class | 3.59195026 | 4 | 0.46403551 |
| range.class | 5.66975832 | 4 | 0.22520566 |
| burn.range.genus | 34.9397397 | 17 | 0.00633553 |
| burn.genus | 30.0031003 | 17 | 0.02632273 |
| range.genus | 34.9397397 | 17 | 0.00633553 |

# Indicator species

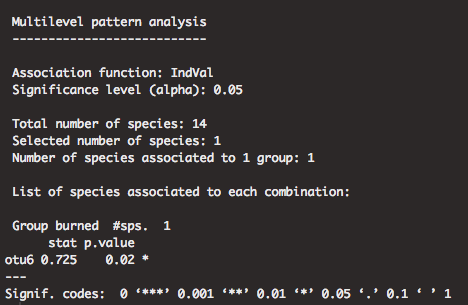
* OTU based
  + Fire history



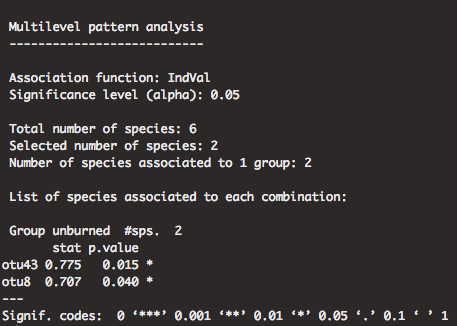
* + Range



* + Santa Catalina Mts.



* + Pinaleno Mts.



# Figures

## Tables

* Table 1: site data
  + Need to add information on weather and plant community
* Table 2: Soil data
* Table 3: diversity

## Figures

* Fig. 1: map of range and sites
* Fig. 2: Species richness and diversity
* Fig. 3: community composition: by range
* Fig. 4: community composition overall
* Fig. 5: Taxonomy???? How to best show this?

Supplementary figures

* Fig. S1: climate data
* Fig. S2: soil data
* Fig. S3: Shannon diversity