Filtering datasets

Renata Diaz

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We filter datasets in two stages. First, we filter **prior to trying to sample from the feasible set**, in order to remove communities that have a combined S and N too high for us to sample the feasible set and the reduce the FIA dataset to a manageable size. Second, we filter **after sampling the feasible set but before we aggregate results across communities**, where mathematical constraints result in uninformative results. Below we elaborate on the logic and methods for these filtering processes, including code to allow others to see precisely what we implemented.

## Pre-feasible set sampling

While our algorithm for sampling the feasible set improved our ability to assess the shape of the feasible set for larger communities, there were still computational limits on what we could do. We filtered out all communities with more than 40720 individuals, because this is the largest community we were able to sample given the available resources. This upper limit results in the removal of a total of 4 communities, all of them from the Miscellaneous Abundance Database

For computational reasons, we also created a sub-sample of the FIA dataset, because sampling the feasible set for all 103,343 FIA communities overwhelms our computational pipeline. Because the FIA has so many extremely small communities (92,988 with fewer than 10 species), we decided to randomly select a sample of the small communities for analysis. Thus our FIA dataset consisted of ~20,000 communities comprising all communities with more than 10 species (10,355) plus 10,000 randomly selected communities with 3-10 species.

Code for downloading the data used for this project can be found [INSERT REPO HERE]. The download\_data function downloads raw data files from <https://github.com/weecology/sad-comparison/> (for BBS, Gentry, Mammal Community Database, and FIA) and figshare <http://figshare.com/files/3097079> (for the Miscellaneous Abundance Database). These raw files are stored in working-data\abund\_data and are not edited.

Below code forloading the raw data files and going through the filtering process step by step are provided for each dataset In the analysis this is accomplished by running dataset-specific filtering scripts and saving new .csvs, which are then loaded using load\_dataset. We can manually load the datasets and then compare them to what is returned from load\_dataset.

### Miscellaneous Abundance Database

Misc. Abund includes datasets reported as relative abundance in addition to count data. We don’t want any communities without counts, so we filter out records where abund = 0.

misc\_abund\_raw <- read.csv(here::here("working-data", "abund\_data", "misc\_abund\_spab.csv"))  
  
misc\_abund\_raw <- misc\_abund\_raw %>%  
 dplyr::rename(site = Site\_ID,  
 abund = Abundance)  
  
misc\_abund\_raw <- misc\_abund\_raw %>%  
 mutate(site = as.character(site),  
 dat = "misc\_abund",  
 singletons = F,  
 sim = -99,  
 source = "observed") %>%  
 filter(abund > 0) %>%  
 group\_by(site) %>%  
 arrange(abund) %>%  
 mutate(rank = row\_number()) %>%  
 ungroup()  
  
misc\_abund\_loaded <- load\_dataset("misc\_abund")

any(!(misc\_abund\_loaded$abund == misc\_abund\_raw$abund))

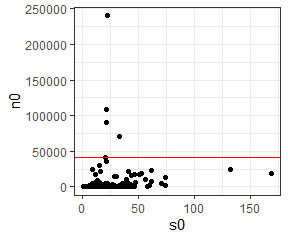
## [1] FALSE

any(!(misc\_abund\_loaded$site == misc\_abund\_raw$site))

## [1] FALSE

Check community sizes to determine whether any exceed the community size limits:

misc\_abund\_statevars <- get\_statevars(misc\_abund\_raw)  
  
ggplot(misc\_abund\_statevars, aes(s0, n0)) +  
 geom\_point() +  
 theme\_bw() +  
 geom\_hline(yintercept = 40720, color = "red")



Misc abund has 4 communities that get removed because they have high numbers of individuals.

The filtered database is saved as a .csv and can be loaded with load\_dataset. We can check that it matches the filtering we have done here:

misc\_abund\_sv\_filtered <- misc\_abund\_statevars %>%  
 filter(n0 <= 40720)  
  
misc\_abund\_filtered <- filter(misc\_abund\_raw, site %in% misc\_abund\_sv\_filtered$site)  
  
misc\_abund\_short\_loaded <- load\_dataset("misc\_abund\_short")  
  
any(!(misc\_abund\_short\_loaded$abund == misc\_abund\_filtered$abund))

## [1] FALSE

any(!(misc\_abund\_short\_loaded$site == misc\_abund\_filtered$site))

## [1] FALSE

#### FIA

* Load raw FIA data
* Add columns to match what we will get from load\_dataset
* Load from load\_dataset

fia\_raw <- read.csv(here::here("working-data", "abund\_data", "fia\_spab.csv"), stringsAsFactors = F, header = F, skip = 2)  
  
colnames(fia\_raw) <- c("site", "year", "species", "abund")  
  
fia\_raw <- fia\_raw %>%  
 mutate(site = as.character(site),  
 dat = "fia",  
 singletons = F,  
 sim = -99,  
 source = "observed") %>%  
 filter(abund > 0) %>%  
 group\_by(site) %>%  
 arrange(abund) %>%  
 mutate(rank = row\_number()) %>%  
 ungroup()  
  
fia\_loaded <- load\_dataset("fia")

any(!(fia\_loaded$abund == fia\_raw$abund))

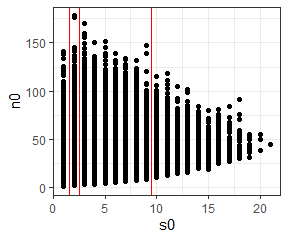
## [1] FALSE

any(!(fia\_loaded$site == fia\_raw$site))

## [1] FALSE

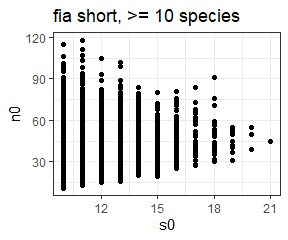
Check community sizes to determine whether any exceed the community size limits:

fia\_statevars <- get\_statevars(fia\_raw)  
  
ggplot(fia\_statevars, aes(s0, n0)) +  
 geom\_point() +  
 theme\_bw() +  
 geom\_vline(xintercept = c(1.5, 2.5, 9.5), color = "red")

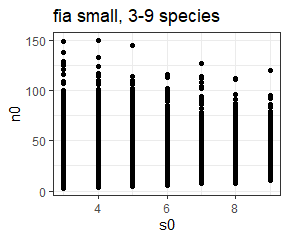


FIA has no extremely large datasets; the largest number of individuals is 178. However, it has 103343 communities, of which 92988 have fewer than 10 species. This many communities overwhelms our computational pipeline. We therefore sample all 10355 communities with 10 or more species, and a random subsample of 10,000 communities with 3-9 species. We then run these through the pipeline as two separate databases. fia\_short is the communities with 10 or more species, and fia\_small is the 10,000 communities with 3-9 species. We re-combine them as “FIA” for aggregate analyses.

fia\_sv\_short <- fia\_statevars %>%  
 dplyr::filter(s0 >= 10)  
  
fia\_short <- fia\_raw %>%  
 dplyr::filter(site %in% fia\_sv\_short$site) %>%  
 dplyr::mutate(dat = "fia\_short")  
  
fia\_short\_statevars <- get\_statevars(fia\_short)  
  
ggplot(fia\_short\_statevars, aes(s0, n0)) +  
 geom\_point() +  
 ggtitle("fia short, >= 10 species") +  
 theme\_bw()



fia\_sv\_small <- fia\_statevars %>%  
 dplyr::filter(s0 >= 3) %>%  
 dplyr::filter(s0 <= 9)  
  
 set.seed(1977)  
 fia\_sv\_small <- fia\_sv\_small[ sample.int(nrow(fia\_sv\_small), size = 10000, replace = F), ]  
  
  
  
fia\_small <- fia\_raw %>%  
 dplyr::filter(site %in% fia\_sv\_small$site) %>%  
 dplyr::mutate(dat = "fia\_small")  
  
fia\_small\_statevars <- get\_statevars(fia\_small)  
  
ggplot(fia\_small\_statevars, aes(s0, n0)) +  
 geom\_point() +  
 ggtitle("fia small, 3-9 species")



The “short” and “small” datasets are saved as .csvs and can be loaded using load\_dataset:

fia\_small\_loaded <- load\_dataset("fia\_small")  
  
any(!(fia\_small\_loaded$abund == fia\_small$abund))

## [1] FALSE

any(!(fia\_small\_loaded$site == fia\_small$site))

## [1] FALSE

fia\_short\_loaded <- load\_dataset("fia\_short")  
  
any(!(fia\_short\_loaded$abund == fia\_short$abund))

## [1] FALSE

any(!(fia\_short\_loaded$site == fia\_short$site))

## [1] FALSE

### BBS

* Load raw BBS data
* Add columns to match what we will get from load\_dataset
* Load from load\_dataset

bbs\_raw <- read.csv(here::here("working-data", "abund\_data", "bbs\_spab.csv"), stringsAsFactors = F, header = F, skip = 2)  
  
colnames(bbs\_raw) <- c("site", "year", "species", "abund")  
  
bbs\_raw <- bbs\_raw %>%  
 mutate(site = as.character(site),  
 dat = "bbs",  
 singletons = F,  
 sim = -99,  
 source = "observed") %>%  
 group\_by(site) %>%  
 arrange(abund) %>%  
 mutate(rank = row\_number()) %>%  
 ungroup()  
  
bbs\_loaded <- load\_dataset("bbs")

Compare loaded to raw:

any(!(bbs\_loaded$abund == bbs\_raw$abund))

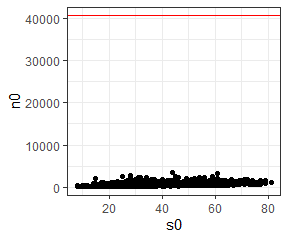
## [1] FALSE

any(!(bbs\_loaded$site == bbs\_raw$site))

## [1] FALSE

Check community sizes:

bbs\_statevars <- get\_statevars(bbs\_raw)  
  
ggplot(bbs\_statevars, aes(s0, n0)) +  
 geom\_point() +  
 theme\_bw() +  
 geom\_hline(yintercept = 40720, color = "red")



No communities in BBS have more than 40720 individuals, so all are initially included in the analysis.

### Gentry

* Load raw Gentry data
* Add columns to match what we will get from load\_dataset
* Load from load\_dataset

gentry\_raw <- read.csv(here::here("working-data", "abund\_data", "gentry\_spab.csv"), stringsAsFactors = F, header = F, skip = 2)  
  
colnames(gentry\_raw) <- c("site", "year", "species", "abund")  
  
gentry\_raw <- gentry\_raw %>%  
 mutate(site = as.character(site),  
 dat = "gentry",  
 singletons = F,  
 sim = -99,  
 source = "observed") %>%  
 group\_by(site) %>%  
 arrange(abund) %>%  
 mutate(rank = row\_number()) %>%  
 ungroup()  
  
gentry\_loaded <- load\_dataset("gentry")

Compare loaded to raw:

any(!(gentry\_loaded$abund == gentry\_raw$abund))

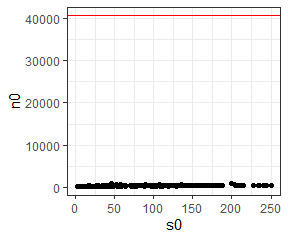
## [1] FALSE

any(!(gentry\_loaded$site == gentry\_raw$site))

## [1] FALSE

Check community sizes:

gentry\_statevars <- get\_statevars(gentry\_raw)  
  
ggplot(gentry\_statevars, aes(s0, n0)) +  
 geom\_point() +  
 theme\_bw() +  
 geom\_hline(yintercept = 40720, color = "red")



No communities in Gentry have more than 40720 individuals, so all are used at this stage.

### Mammal Community Database

* Load raw MCDB data
* Add columns to match what we will get from load\_dataset
* Load from load\_dataset

mcdb\_raw <- read.csv(here::here("working-data", "abund\_data", "mcdb\_spab.csv"), stringsAsFactors = F, header = F, skip = 2)  
  
colnames(mcdb\_raw) <- c("site", "year", "species", "abund")  
  
mcdb\_raw <- mcdb\_raw %>%  
 mutate(site = as.character(site),  
 dat = "mcdb",  
 singletons = F,  
 sim = -99,  
 source = "observed") %>%  
 group\_by(site) %>%  
 arrange(abund) %>%  
 mutate(rank = row\_number()) %>%  
 ungroup()  
  
mcdb\_loaded <- load\_dataset("mcdb")

Compare loaded to raw:

any(!(mcdb\_loaded$abund == mcdb\_raw$abund))

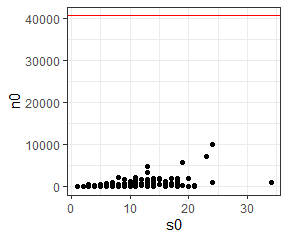
## [1] FALSE

any(!(mcdb\_loaded$site == mcdb\_raw$site))

## [1] FALSE

Check community sizes:

mcdb\_statevars <- get\_statevars(mcdb\_raw)  
  
ggplot(mcdb\_statevars, aes(s0, n0)) +  
 geom\_point() +  
 theme\_bw() +  
 geom\_hline(yintercept = 40720, color = "red")



No high N communities; so all are included at this stage.

## Post-sampling

Some communities fall into mathematically odd spaces where basic constraints prevent informative results. We removed all communities that fell into any of the below scenarios: 1) When communities have only 1 mathematically possible SAD (S = 1, N = S, or N = S + 1), 2) When the sampled feasible sets yield more than 20 unique values for skewness/evenness. If there are fewer than 20 unique values in the comparison vector, it’s impossible to be in the 5th or 95th percentile, 3) When a community consists of only 2 species we did not analyze their skewness because e1071::skewness() always = 0 if S = 2.

Below is the code use used to implement the dataset filtering that occurred post-sampling of the feasible set. First we can load all\_di (“all diversity indices”), which is the combined results across all the communities in all the datasets. Every community that was included for sampling is included in all\_di. (Additionally, every community has a “singletons” counterpart, which is the same analysis run adjusted for rarefaction. That analysis is discussed elsewhere, and we ignore the rarefaction-adjusted versions here).

all\_statevars <- bind\_rows(bbs\_statevars, fia\_short\_statevars, fia\_small\_statevars, gentry\_statevars, mcdb\_statevars, misc\_abund\_sv\_filtered)  
  
  
all\_di <- read.csv(here::here("analysis", "reports", "all\_di.csv"), stringsAsFactors = F)  
  
all\_di <- all\_di %>%  
 filter(!singletons) %>%  
 mutate(dat = ifelse(grepl(dat, pattern = "fia"), "fia", dat),  
 dat = ifelse(dat == "misc\_abund\_short", "misc\_abund", dat)) %>%  
 mutate(Dataset = dat,  
 Dataset = ifelse(Dataset == "fia", "Forest Inventory and Analysis", Dataset),  
 Dataset = ifelse(Dataset == "bbs", "Breeding Bird Survey", Dataset),  
 Dataset = ifelse(Dataset == "mcdb", "Mammal Community DB", Dataset),  
 Dataset = ifelse(Dataset == "gentry", "Gentry", Dataset),  
 Dataset = ifelse(Dataset == "misc\_abund", "Miscellaneous Abundance DB", Dataset))  
  
head(all\_di)

## sim source dat site singletons s0 n0 nparts skew shannon  
## 1 -99 observed bbs 4002 FALSE 35 816 4.070604e+24 1.973575 2.655380  
## 2 -99 observed bbs 4003 FALSE 26 439 1.765612e+17 1.502247 2.609893  
## 3 -99 observed bbs 4004 FALSE 27 445 3.100591e+17 1.802663 2.748364  
## 4 -99 observed bbs 4006 FALSE 29 471 1.689307e+18 2.728160 2.432257  
## 5 -99 observed bbs 4007 FALSE 24 575 1.424232e+19 1.216833 2.491605  
## 6 -99 observed bbs 4009 FALSE 21 534 6.506488e+17 1.848653 2.420594  
## simpson skew\_percentile shannon\_percentile simpson\_percentile  
## 1 0.9016995 69.60 0.050 1.375  
## 2 0.9009605 50.75 8.800 15.225  
## 3 0.9138139 64.45 23.775 28.450  
## 4 0.8597058 92.65 0.425 0.800  
## 5 0.8915962 36.80 4.550 11.475  
## 6 0.8785787 79.55 8.050 11.325  
## skew\_percentile\_excl simpson\_percentile\_excl skew\_range simpson\_range  
## 1 69.60 1.375 5.013388 0.1071673  
## 2 50.75 15.225 4.406489 0.1807068  
## 3 64.45 28.450 4.384616 0.3824770  
## 4 92.65 0.800 4.369746 0.1462940  
## 5 36.80 11.450 4.293175 0.1741853  
## 6 79.55 11.300 3.932031 0.1747465  
## nsamples skew\_unique simpson\_unique skew\_2p5 skew\_97p5 skew\_95 skew\_min  
## 1 4000 4000 3445 0.7046398 3.358540 2.998938 0.05485603  
## 2 4000 4000 2860 0.5050514 3.157090 2.846737 -0.19707578  
## 3 4000 4000 2883 0.5441635 3.182604 2.879527 0.02681027  
## 4 4000 4000 2948 0.5689934 3.270669 2.928296 -0.16145549  
## 5 4000 4000 3283 0.4274895 2.971295 2.710518 -0.21809489  
## 6 4000 4000 3267 0.3496395 2.780707 2.531622 -0.38791363  
## simpson\_max simpson\_2p5 simpson\_5 simpson\_97p5 skew\_95\_ratio\_2t  
## 1 0.9631061 0.9064803 0.9144545 0.9551500 0.5293626  
## 2 0.9517697 0.8671956 0.8799140 0.9437090 0.6018485  
## 3 0.9522030 0.8740614 0.8860598 0.9451334 0.6017496  
## 4 0.9562164 0.8815458 0.8929864 0.9484996 0.6182684  
## 5 0.9501822 0.8638114 0.8769887 0.9396030 0.5925231  
## 6 0.9418353 0.8506425 0.8631493 0.9325567 0.6182726  
## simpson\_95\_ratio\_2t skew\_95\_ratio\_1t simpson\_95\_ratio\_1t Dataset  
## 1 0.4541467 0.5872441 0.4539785 Breeding Bird Survey  
## 2 0.4234121 0.6907570 0.3976368 Breeding Bird Survey  
## 3 0.1858206 0.6506195 0.1729337 Breeding Bird Survey  
## 4 0.4576662 0.7070780 0.4322117 Breeding Bird Survey  
## 5 0.4351207 0.6821556 0.4202049 Breeding Bird Survey  
## 6 0.4687608 0.7425008 0.4502870 Breeding Bird Survey

nrow(all\_di) == nrow(all\_statevars)

## [1] TRUE

We remove communities with only one possible SAD (N = S, N = S + 1, or S = 1).

all\_di %>%  
 group\_by\_all() %>%  
 mutate(only\_one\_sad = sum(s0 == n0, s0 == 1, n0 == (s0 + 1)) > 0) %>%  
 ungroup() %>%  
 group\_by(dat) %>%  
 summarize(total\_only\_one\_sad = sum(only\_one\_sad),  
 total\_sites = dplyr::n()) %>%  
 ungroup() %>%  
 mutate(all\_sites\_one\_sad = sum(total\_only\_one\_sad),  
 all\_sites = sum(total\_sites))

## # A tibble: 5 x 5  
## dat total\_only\_one\_sad total\_sites all\_sites\_one\_sad all\_sites  
## <chr> <int> <int> <int> <int>  
## 1 bbs 0 2773 258 24647  
## 2 fia 176 20355 258 24647  
## 3 gentry 0 224 258 24647  
## 4 mcdb 56 730 258 24647  
## 5 misc\_abund 26 565 258 24647

all\_di\_filtered <- all\_di %>%  
 filter(s0 != n0,  
 s0 != 1,  
 n0 != (s0 + 1))  
  
nrow(all\_di\_filtered)

## [1] 24389

Removing those with only one SAD results in the removal of 258 sites total. 176 from FIA, 56 from MCDB, and 26 from Misc. Abund.

Finally, we will restrict aggregate analyses to sites whose feasible sets have more than 20 unique values for whichever shape metric we’re interested in, **and** we will restrict analyses with skewness to sites with >2 species. This results in these final totals:

all\_di\_filtered %>%  
 filter(simpson\_unique > 20) %>%  
 group\_by(dat) %>%  
 summarize(sites\_for\_evenness = dplyr::n()) %>%  
 ungroup() %>%  
 mutate(total\_sites\_for\_evenness = sum(sites\_for\_evenness))

## # A tibble: 5 x 3  
## dat sites\_for\_evenness total\_sites\_for\_evenness  
## <chr> <int> <int>  
## 1 bbs 2773 22142  
## 2 fia 18113 22142  
## 3 gentry 224 22142  
## 4 mcdb 542 22142  
## 5 misc\_abund 490 22142

all\_di\_filtered %>%  
 filter(skew\_unique > 20, s0 > 2) %>%  
 group\_by(dat) %>%  
 summarize(sites\_for\_skewness = dplyr::n()) %>%  
 mutate(total\_sites\_for\_skewness = sum(sites\_for\_skewness))

## # A tibble: 5 x 3  
## dat sites\_for\_skewness total\_sites\_for\_skewness  
## <chr> <int> <int>  
## 1 bbs 2773 22325  
## 2 fia 18300 22325  
## 3 gentry 223 22325  
## 4 mcdb 537 22325  
## 5 misc\_abund 492 22325