Explanation of Data Files

Resource availability and heterogeneity shape the self-organization of regular spatial patterning

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| --- | --- |
| File Name | File Description |
| batch\_1.genepop | unfiltered genepop file from STACKS |
| batch\_1.sumstats.tsv | sumstats file from STACKS |
| individual\_genotypes.genepop | filtered genepop file |
| Individual\_metadata.csv | individual termite metadata |
| mean\_mound\_Fij.csv | mean Mound Fij |
| mound\_metadata.csv | mound metadata |
| Fig2A\_data.csv | data for figure 2A |
| Fig2BCD\_data.csv | data for figures 2B, C, and D |
| glade\_NDVI\_data.csv | data for figure 1D |
| FigS2.Rdata | data for figure S2 and null model tests |
| dung\_summary.csv | data for figure S3 |
| CastilloVardaro\_Rcode.R | R code for running analyses |

**batch\_1.genepop**

Unfiltered genotype calls from STACKS.

|  |  |
| --- | --- |
| Row | Description |
| 1 | STACKS header with version info and data |
| 2 | Locus names reported as stack\_basepair |
| 3 | “pop” header |
| 4-696 | individual genotypes with columns for sample name and allele calls |

**batch\_1.sumstats.tsv**

This file contains summary statistics describing every SNP, including the frequecy of alleles, expected/observed heterozygosity, π, FIS, and so on.

**individual\_genotypes.genepop**

Filtered genotype calls.

|  |  |
| --- | --- |
| Row | Description |
| 1 | Locus names reported as stack\_basepair |
| 2-636 | individual genotypes with columns for sample name and allele calls |

**Individual\_metadata.csv**

Metadata for genotyped individuals.

|  |  |  |
| --- | --- | --- |
| Column | Heading | Description |
| 1 | Ind\_ID | Unique identifier for each termite genotypes |
| 2 | Mound\_ID | Unique identifier for the termite mound from which the termite was collected |
| 3 | Date\_collected | Collection date |
| 4 | Caste | Soldier, worker, or alate |

**Mean\_mound\_Fij.csv**

Mean inter-individual genetic distance (Fij) for each pair of mounds within 60m distance.

|  |  |  |
| --- | --- | --- |
| Column | Heading | Description |
| 1 | Mound\_ID\_1 | Unique identifier for mound 1 |
| 2 | Mound\_ID\_2 | Unique identifier for mound 2 |
| 3 | Mean\_Fij | Mean inter-individual genetic distance (Fij) |
| 4 | Glade\_Colony\_Factor | A factor indicating whether the two mounds are the same (Mound), different mounds on the same glade (Glade), or different mounds not on a glade (0 – 60 m). |
| 5 | Distance | Geographic distance between the two mounds, in meters. |

**Mound\_metadata.csv**

|  |  |  |
| --- | --- | --- |
| Column | Heading | Description |
| 1 | Mound\_ID | Unique identifier for each mound |
| 2 | Easting | X coordinate in WGS84 UTM Zone 37N |
| 3 | Northing | Y coordinate in WGS84 UTM Zone 37N |
| 4 | Mound\_Diameter | Mound diameter in meters |
| 5 | Glade\_Distance | Distance to the nearest glade, in meters |
| 6 | Sequence | GenBank accession number for the 16S sequence. |
| 7 | Species | Scientific name. |
| 8 | Dung\_density | Dung density in number of discrete piles per square meter |
| 9 | NDVI | Mean NDVI on the mound |
| 10 | Off\_mound\_NDVI | Mean NDVI for an annulus equal to the mound diameter plus seven meters, with a hole equal to the mound diameter plus two meters |

**Fig2A\_data.csv**

Distances between neighboring mounds

|  |  |  |
| --- | --- | --- |
| Column | Heading | Description |
| 1 | Mound\_ID\_1 | Unique identifier for mound 1 |
| 2 | Mound\_ID\_2 | Unique identifier for mound 2 |
| 3 | DIST | Distance between neighboring mounds in meters |
| 4 | Glade\_Factor | Factor indicating whether both mounds are on a glade (2), one mound on and one mound off (1), or no mounds on the glade (0). |

**Fig2BCD\_data.csv**

Data for mound distance regressions.

|  |  |  |
| --- | --- | --- |
| Column | Heading | Description |
| 1 | Mound\_ID | Unique identifier for each mound |
| 2 | n\_neighbors | Number of first neighbors |
| 3 | mean\_neighbor\_dist | Mean distance to all first neighbors in meters |
| 4 | Glade\_Dist | Distance to nearest glade in meters |
| 5 | mound\_size | Mound diameter in meters |
| 6 | mean\_neighbor\_size | Mean neighbor diameter in meters |
| 7 | mean\_mound\_size | Mean mound size of focal mound (col. 1) plus all neighbors |

**Glade\_NDVI\_data.csv**

NDVI data for each glade

|  |  |  |
| --- | --- | --- |
| Column | Heading | Description |
| 1 | Glade\_ID | Unique identifier for each glade |
| 2 | Glade\_Dist | Distance from the glade edge in meters |
| 3 | NDVI\_mean | Mean NDVI calculated from all raster cells within 1 meter of that distance from the glade edge |
| 4 | NDVI\_sd | Standard deviation of the NDVI values used to calculate the mean |

**FigS2.Rdata**

R data file containing two objects:

Mean\_mound\_Fij. See description above

Mound\_dists. Data frame containing genetic and geographic distances among termite mounds

|  |  |  |
| --- | --- | --- |
| Column | Heading | Description |
| 1 | pop1 | Unique identifier for each mound. |
| 2 | pop2 | Unique identifier for each mound. |
| 3 | geodist | Geographic distance in meters |
| 4 | neighbors | Factor indicating whether mounds are neighbors |
| 5 | glade | Factor indicating whether mounds are on glades |
| 6 | D | Genetic distance (Nei’s D) |
| 7 | Dist\_Factor | Factor indicating the distance class for each pair of mounds |