

A Landscape Genomics Analysis Toolkit in R (`algatr`): Workshop

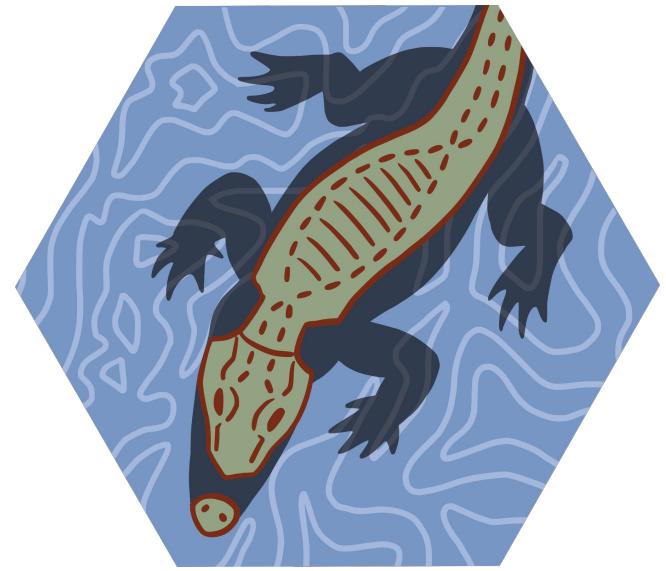
E. Anne Chambers: eachambers@berkeley.edu

Anusha Bishop: anusha.bishop@berkeley.edu

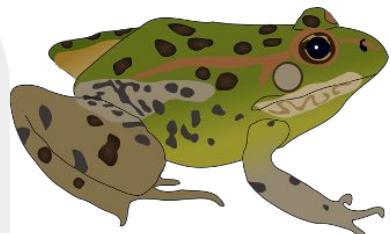
Install algatr on your computer:

```
# Install and load algatr
devtools::install_github("TheWangLab/algatr")
library(algatr)

# Install all of the algatr packages
alazygatr_packages()
```



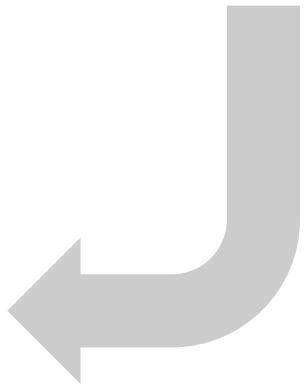
Conservation genomics



R. spectabilis



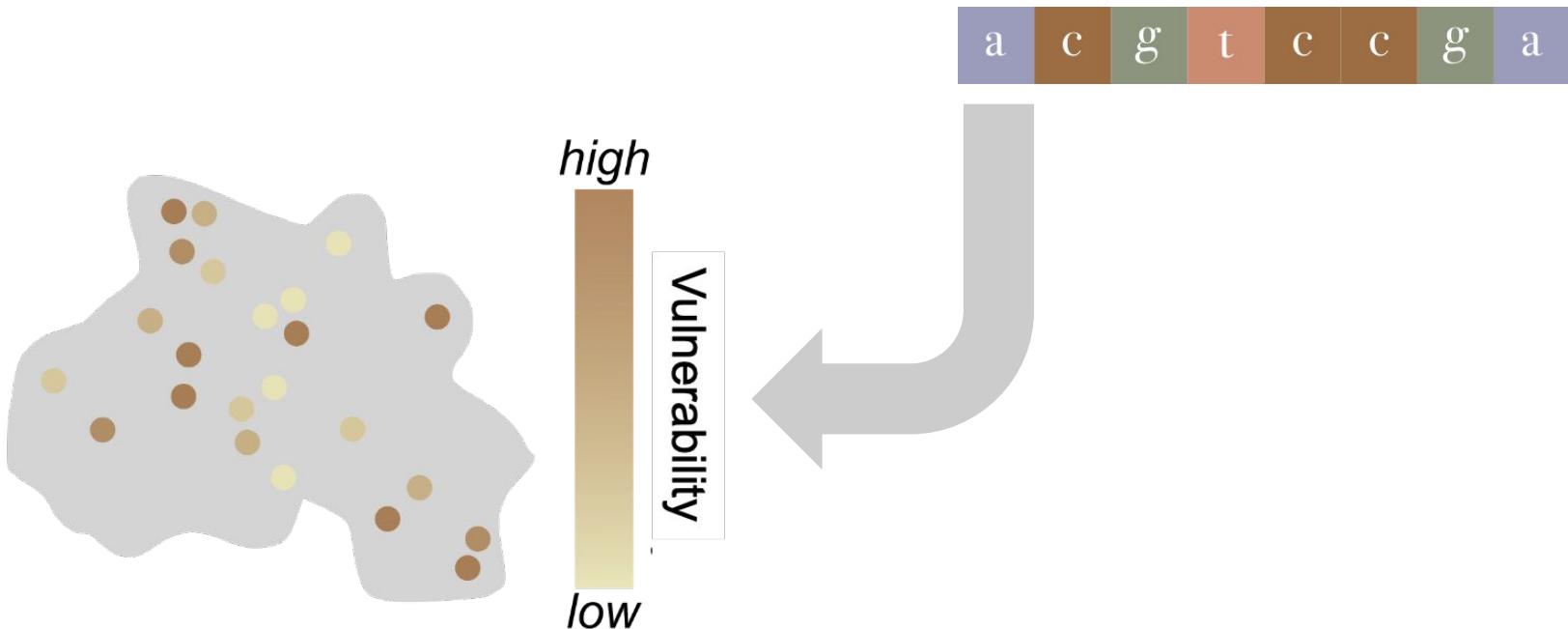
R. tlahoci



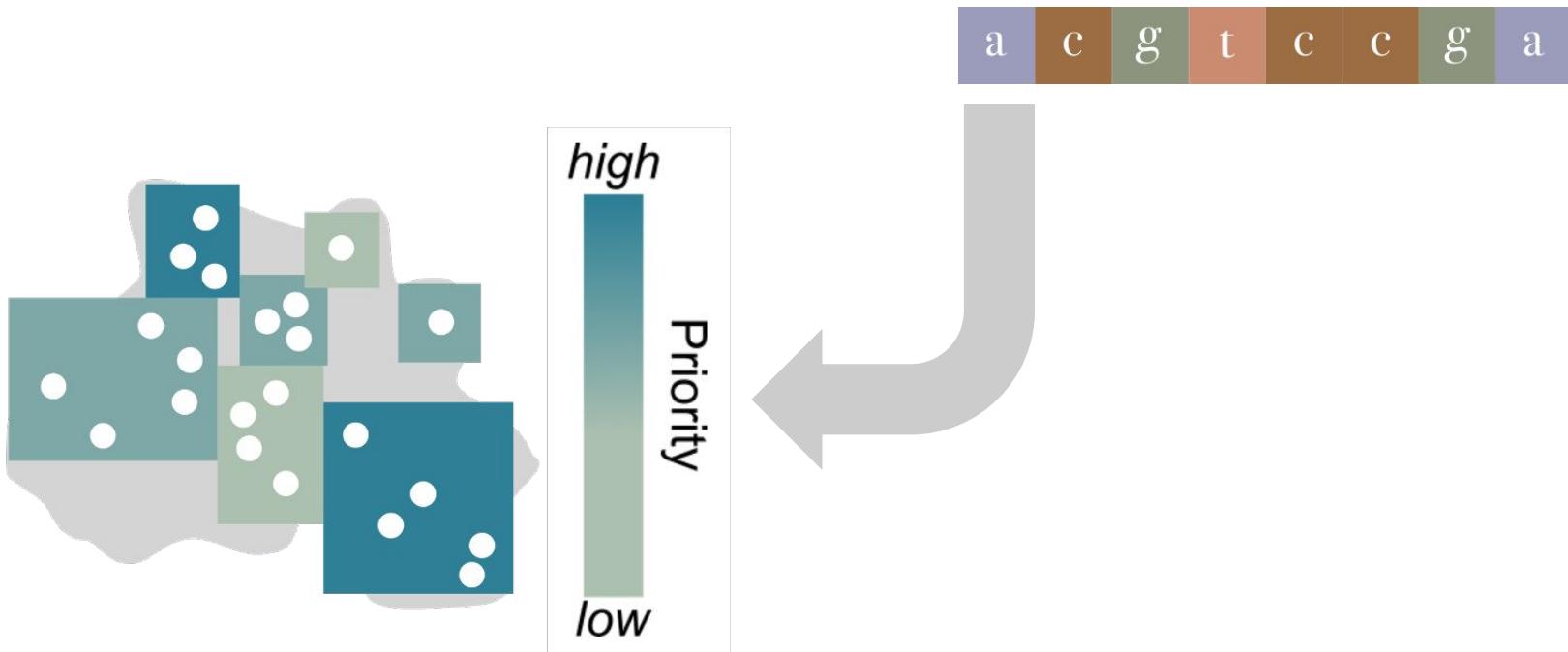
a c g t c c g a

A sequence of eight colored squares, each containing a letter. The colors of the squares are: purple (a), brown (c), green (g), orange (t), brown (c), purple (c), green (g), and purple (a). This likely represents a DNA sequence or a specific genomic region being compared.

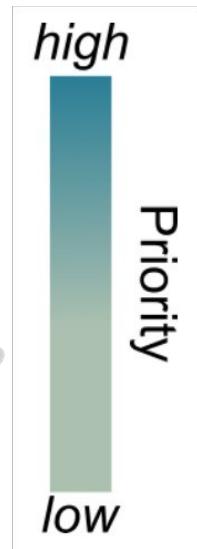
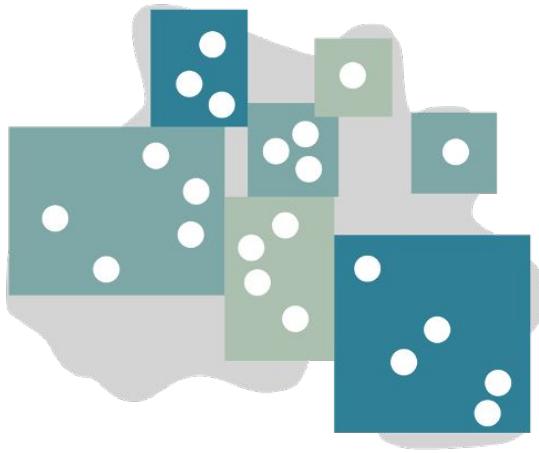
Conservation genomics



Conservation genomics



Biological conservation has become an inherently spatial problem.

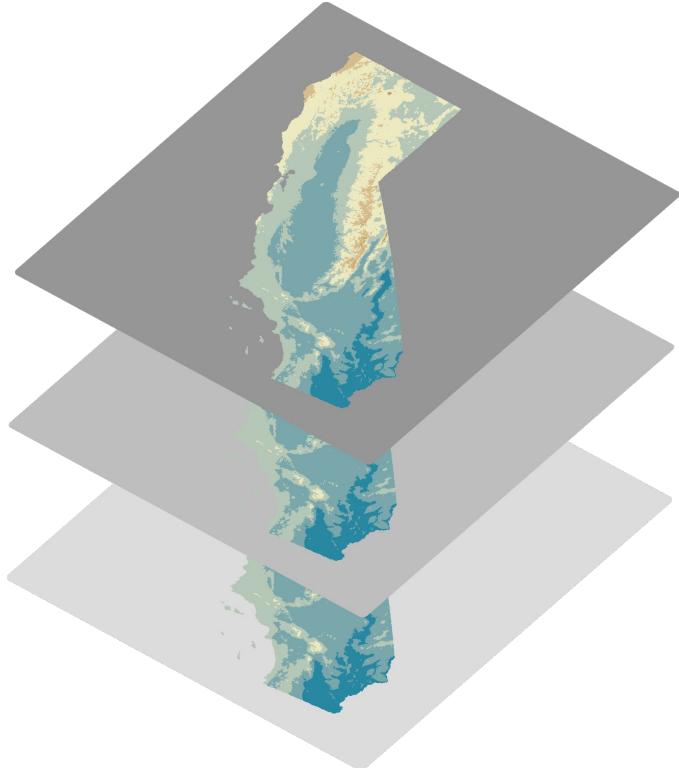
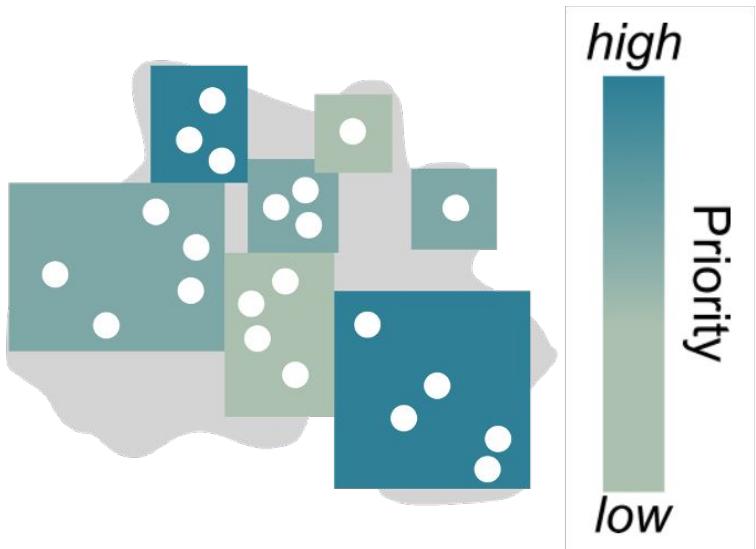


Landscape ecology

+

Population genetics

Landscape genomics



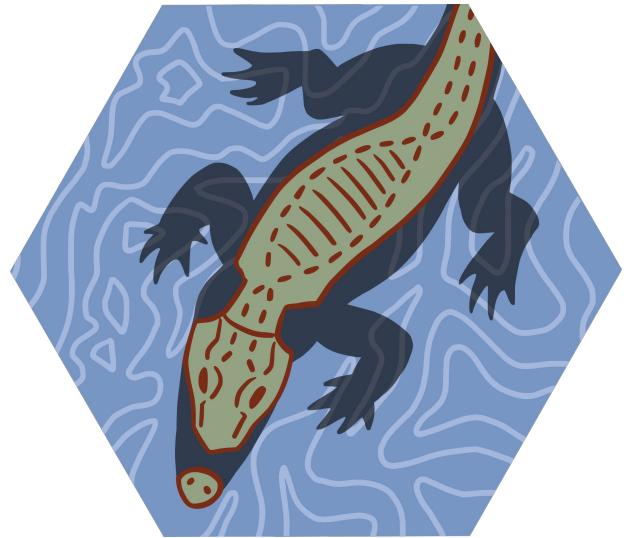
California Conservation Genomics Project

Goal: to produce the most comprehensive genomic dataset ever assembled for conserving biodiversity

Who we are: 100+ scientists and officials from across the UC campuses, government agencies and NGOs

What we are doing: sequencing and analyzing genomic data from 230+ species to inform conservation across California





algatr

<https://github.com/TheWangLab/algatr>

Chambers, Bishop, & Wang (2024) *Mol. Ecol. Res.*

How is genetic diversity distributed?

How do we delineate population units for management?

How can we identify and protect adaptive genetic variation?

How can we conserve areas that protect critical population processes?



algatr

<https://github.com/TheWangLab/algatr>

Chambers, Bishop, & Wang (2024) *Mol. Ecol. Res.*

Population structure

TESS

Genetic diversity

wingen

Adaptive genetic variation

LFMM

RDA

IBD and IBE

MMRR

GDM

Welcome!

https://github.com/TheWangLab/algatr_workshop

Structure of this workshop

In this course, we provide brief lectures summarizing each of algatr's **six** landscape genomics methods. Exercises will refer to each of the algatr vignettes. Relevant materials are as follows:

Lecture topic	Exercise materials	Relevant references
Welcome		Chambers et al. 2024
Population structure	TESS vignette	Caye et al. (2015)
Genetic diversity	wingen vignette	Bishop et al. (2023)
Genotype-environment associations	RDA vignette	Capblancq & Forester (2021)
	LFMM vignette	Caye et al. (2019)
MMRR	MMRR vignette	Wang (2013)
GDM	GDM vignette	Ferrier et al. (2007)

algatr website & vignettes

algatr 1.0.0 Reference Manual [Vignettes ▾](#)

algatr

Genetic data processing
Environmental data processing
Masking
Genetic distances
TESS
MMRR
GDM
RDA
LFMM
Wingen
Alazygatr

  DOI [10.5281/zenodo.720011](https://doi.org/10.5281/zenodo.720011)

A Landscape Genomic Analysis Toolkit
step-by-step, start-to-finish pipeline to analyze genomic data with their data.

Citation



Please cite our paper if you use this package:

Chambers, E.A., Bishop, A.P., & Wang, I.J. (2023). Individual-based landscape genomics for conservation: An analysis pipeline. *Molecular Ecology Resources*.<https://doi.org/10.1111/1755-0998.13884>.

Because algatr makes use of existing software, please also be sure to cite the papers for the relevant corresponding method:

wingen Bishop et al. (2023) DOI: [10.1111/2041-210X.14090](https://doi.org/10.1111/2041-210X.14090)

TESS Caye et al. (2016) DOI: [10.1111/1755-0998.12471](https://doi.org/10.1111/1755-0998.12471)

MMRR Wang (2013) DOI: [10.1111/evo.12134](https://doi.org/10.1111/evo.12134)

GDM Ferrier et al. (2007) DOI: [10.1111/j.1472-4642.2007.00341.x](https://doi.org/10.1111/j.1472-4642.2007.00341.x)

Fitzpatrick et al. (2022) gdm: Generalized Dissimilarity Modeling. R package version 1.5.0-9.1.

algatr website & vignettes

algatr 1.0.0 Reference Manual

Vignettes ▾

algatr

 license MIT DOI 10.5281/72

A Landscape Genomic Analysis Toolkit
step-by-step, start-to-finish pipeline
with their data.

Citation

Please cite our paper if you use this package:

Chambers, E.A., Bishop, A.P., & Wang, I.J. (2023). Individual-based landscape genomics for conservation: An analysis pipeline. *Molecular Ecology Resources*. <https://doi.org/10.1111/1755-0998.13884>.

Because algatr makes use of existing software, please also be sure to cite the papers for the relevant corresponding method:

wingen Bishop et DOI: [10.1111/2041-210X.14090](https://doi.org/10.1111/2041-210X.14090)
al. (2023)

TESS Caye et al. (2016) DOI: [10.1111/1755-0998.12471](https://doi.org/10.1111/1755-0998.12471)

MMRR Wang (2013) DOI: [10.1111/evo.12134](https://doi.org/10.1111/evo.12134)

GDM Ferrier et DOI: [10.1111/j.1472-4642.2007.00341.x](https://doi.org/10.1111/j.1472-4642.2007.00341.x)
al. (2007)

Fitzpatrick et gdm: Generalized Dissimilarity Modeling. R package version
al. (2022) 1.5.0-9.1.



algatr 1.0.0 Reference Manual Vignettes ▾

For additional information on the original development and implementation of the algorithm used by TESS, see [François et al. 2006](#) and [Chen et al. 2007](#). Finally, our code primarily uses the tess3r package (see [here](#) for documentation).

Read in and process input data

Running TESS3 requires three data files: a genotype dosage matrix (the `gen` argument), coordinates for samples (the `coords` argument), and environmental layers (the `envlayers` argument). We can use a vcf and the `vcf_to_dosage()` function to convert a vcf to a dosage matrix.

```
load_algatr_example()  
#>  
#> ----- example dataset -----  
#>  
#> Objects loaded:  
#> *liz_vcf* vcfR object (1000 loci x 53 samples)  
#> *liz_gendist* genetic distance matrix (Plink Distance)  
#> *liz_coords* data frame with x and y coordinates  
#> *CA_env* RasterStack with example environmental layers  
#>  
#> -----  
#>  
#>  
#> Our code assumes that the first column is longitude and second is latitude; check  
head(liz_coords)  
#>           x         y  
#> 1 -120.3972 41.56120  
#> 3 -116.8923 34.16940  
#> 5 -124.0408 40.90450  
#> 7 -118.5614 37.78830  
#> 8 -119.7194 37.72386  
#> 9 -121.8467 36.35440  
#>  
#> Also, our code assumes that sample IDs from gendist and coords are the same order
```

On this page

- Read in and process input data
- Process environmental data
- K selection
- Extracting TESS results
- Krige Q values
- Visualizing TESS results
- Plotting with default tess3r package functions
- Running TESS with `tess_do_everything()`
- Additional documentation and citations

Set-up on your own computer

The screenshot shows a GitHub repository page for 'TheWangLab / algatr_workshop'. The repository is public and has 1 branch and 0 tags. A message indicates it is 20 commits ahead of 'TheWangLab/algatr:main'. The 'Code' dropdown menu is open, showing options for cloning the repository via HTTPS, SSH, or GitHub CLI. A yellow arrow points to the 'Download ZIP' button at the bottom of the clone menu. The repository details include an 'About' section describing it as a 'Workshop for running A Landscape Genomic Analysis Toolkit in R (algatr)' and a link to 'thewanglab.github.io/algatr'. The 'Releases' section shows no releases published.

TheWangLab / algatr_workshop Public

forked from [TheWangLab/algatr](#)

Code Pull requests Actions Projects Wiki Security Insights Settings

alatr_workshop Public

main 1 Branch 0 Tags

This branch is 20 commits ahead of [TheWangLab/algatr:main](#).

AnushaPB Delete Dockerfile

.devcontainer Update setup.sh

figures add logo

renv add back renv

slides Update README.md

vignettes remove unnecessary

.gitignore ignore DS_Store files 2 minutes ago

README.Rmd Update main README 7 hours ago

Go to file Add file Code

Local Codespaces

Clone

HTTPS SSH GitHub CLI

https://github.com/TheWangLab/algatr_workshop.git

Clone using the web URL.

Open with GitHub Desktop

Download ZIP

About

Workshop for running A Landscape Genomic Analysis Toolkit in R (algatr)

[thewanglab.github.io/algatr](#)

Readme

Activity

Custom properties

0 stars

0 watching

0 forks

Report repository

Releases

No releases published

Create a new release

Set-up project from template on Posit Cloud

algatr
University of California, Merced

Content Data Members Usage About

All Content (0) New Project

Your Content

Templates

Archive

Trash

New Project

New Project from Template

New RStudio Project

New Jupyter Project

New Project from Git Repository

All Content (0)

no content

TYPE * ACCESS * SORT AZ

New Project from Template

Templates

From: algatr

algatr_workshop

From: Posit Cloud

tidyverse

Machine Learning in R with tidymodels

quarto

R Markdown

Data Analysis in R with the tidyverse

Machine Learning in R with tidymodels

Quarto Document Publishing with RStudio

R Markdown Document Publishing with RStudio

algatr_workshop

Type: RStudio Project

From: algatr

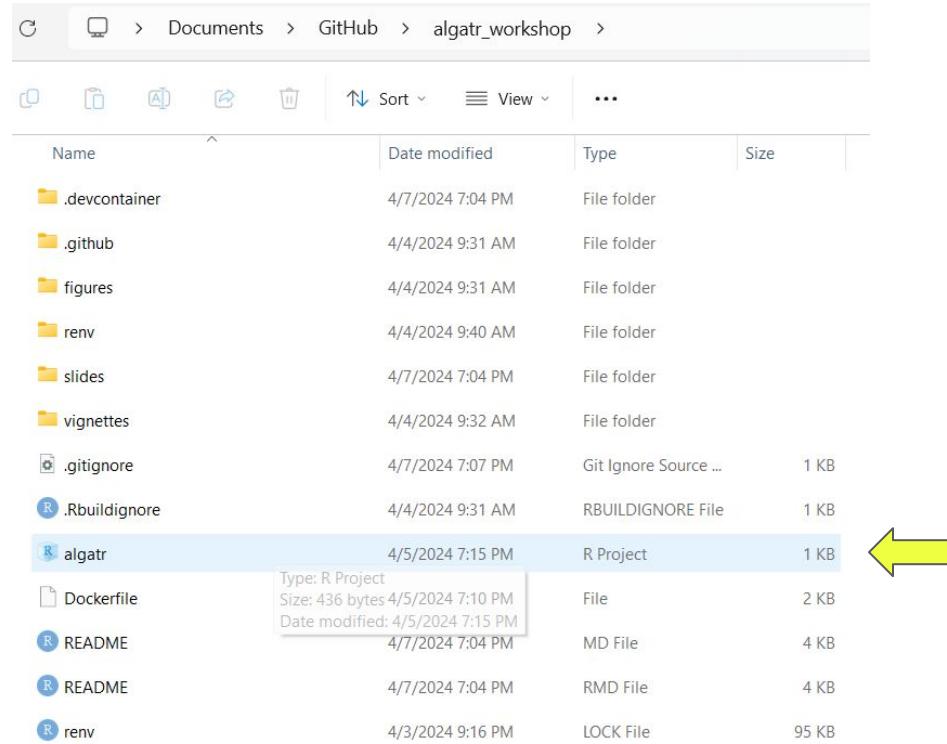
Updated: Apr 5, 2024 7:56 PM

Access: Public

OK

The screenshot illustrates the process of setting up a new project from a template on the Posit Cloud platform. It shows the main dashboard with navigation tabs (Content, Data, Members, Usage, About) and user information (algatr, University of California, Merced, Anusha Bishop). On the left, a sidebar provides quick access to 'Your Content', 'Templates', 'Archive', and 'Trash', along with a 'New Project' button. A secondary 'New Project' button is also visible in the top right of the main content area. The main content area is titled 'All Content (0)' and includes search and filter options (TYPE, ACCESS, SORT). A message 'no content' is displayed. A modal window titled 'New Project from Template' is open, listing templates from 'algatr' and 'Posit Cloud'. The 'algatr_workshop' template is selected. The modal includes details about the template (Type: RStudio Project, From: algatr, Updated: Apr 5, 2024 7:56 PM, Access: Public) and an 'OK' button at the bottom right.

Set-up on your own computer



Name	Date modified	Type	Size
.devcontainer	4/7/2024 7:04 PM	File folder	
.github	4/4/2024 9:31 AM	File folder	
figures	4/4/2024 9:31 AM	File folder	
renv	4/4/2024 9:40 AM	File folder	
slides	4/7/2024 7:04 PM	File folder	
vignettes	4/4/2024 9:32 AM	File folder	
.gitignore	4/7/2024 7:07 PM	Git Ignore Source ...	1 KB
.Rbuildignore	4/4/2024 9:31 AM	RBUILDIGNORE File	1 KB
algatr	4/5/2024 7:15 PM	R Project	1 KB
Dockerfile	Type: R Project Size: 436 bytes Date modified: 4/5/2024 7:15 PM	File	2 KB
README	4/7/2024 7:04 PM	MD File	4 KB
README	4/7/2024 7:04 PM	RMD File	4 KB
renv	4/3/2024 9:16 PM	LOCK File	95 KB

Vignettes

The screenshot shows the posit Cloud interface for an 'Algatr / Untitled Project'. The left sidebar includes links for Spaces, Learn, Help, and Info. The main area displays R code execution results:

```
R version 4.3.3 (2024-02-29) -- "Angel Food Cake"
Copyright (C) 2024 The R Foundation for Statistical Computing
Platform: x86_64-pc-linux-gnu (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'licence()' or 'licence()' for distribution details.

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> library(algatr)
> load_algatr_example()

----- example dataset -----

Objects loaded:
* `liz_vcf` vcfR object (1000 loci x 53 samples)
* `liz_gendist` genetic distance matrix (Plink Distance)
* `liz_coords` dataframe with x and y coordinates
* `CA_env` RasterStack with example environmental layers

----- 

> ?vcf_to_dosage
> ?mmrr_run
>
```

The right side of the interface shows the R environment pane with variables like CA_env, liz_coords, and liz_gendist. A context menu is open over a file named 'file_to_download.R' in the 'Cloud > project' folder, with the 'Export...' option highlighted by a yellow arrow.

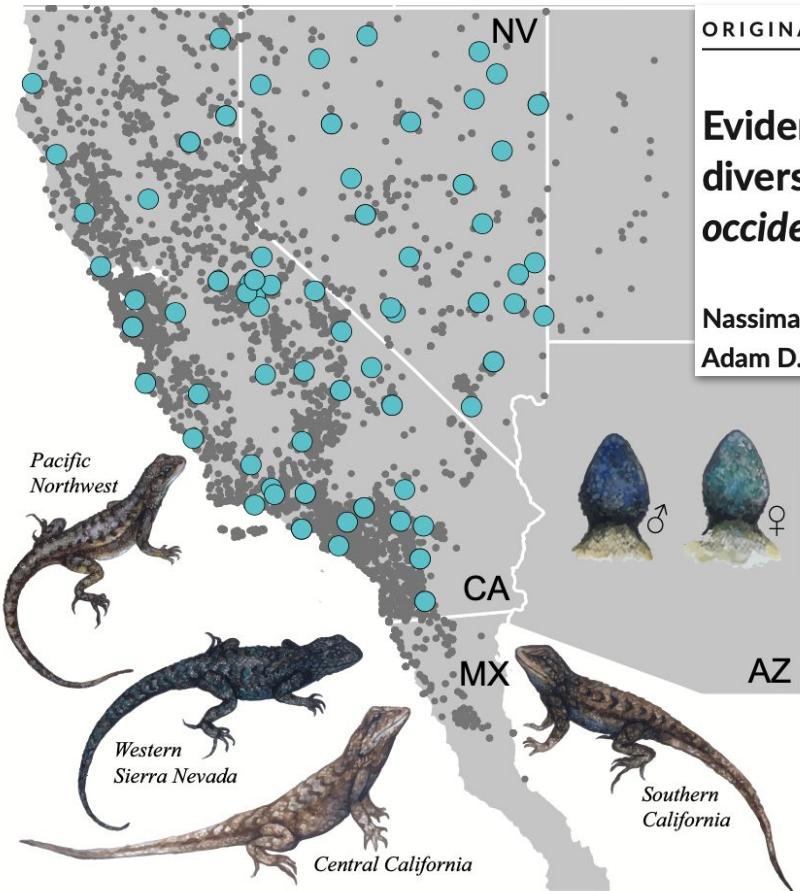
Exporting from posit:

- Copy...
- Copy To...
- Move...
- Copy Folder Path to Clipboard :11 PM
- Open Selected in Source Pane :11 PM
- Open Each File in New Columns :11 PM
- Export...** AM
- Set As Working Directory
- Go To Working Directory
- Synchronize Working Directory :42 PM
- Open New Terminal Here
- Show Hidden Files :11 PM

10 B Apr 6, 2024, 12:06 PM

Getting Started

Example dataset: Bouzid et al. (2022)



ORIGINAL ARTICLE

MOLECULAR ECOLOGY WILEY

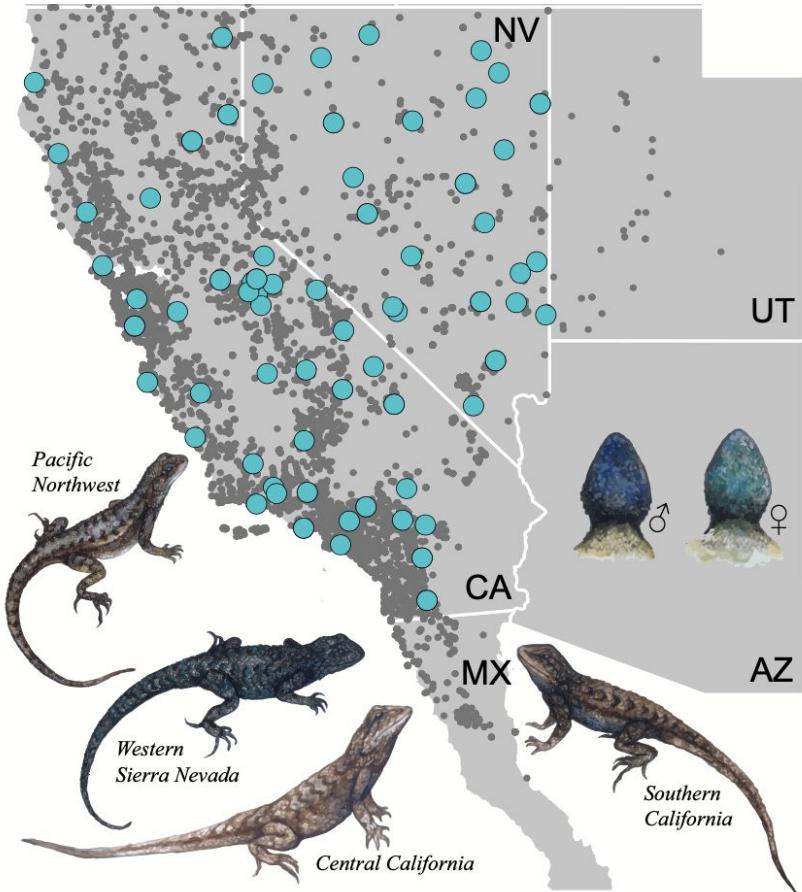
Evidence for ephemeral ring species formation during the diversification history of western fence lizards (*Sceloporus occidentalis*)

Nassima M. Bouzid¹ | James W. Archie² | Roger A. Anderson³ | Jared A. Grummer⁴ | Adam D. Leaché¹



nathistoc.bio.uci.edu

Example dataset: Bouzid et al. (2022)



Genetic data:

53 individuals (53 localities)
Individual-based sampling
1,000 SNPs (ddRAD data)

algatr example dataset

```
> library(algatr)
> load_algatr_example()
```

```
----- example dataset -----
```

```
Objects loaded:
```

```
*liz_vcf* vcfR object (1000 loci x 53 samples)
*liz_gendist* genetic distance matrix (Plink Distance)
*liz_coords* data frame with x and y coordinates
*CA_env* RasterStack with example environmental layers
```

Genetic data:

1. **liz_vcf** - Variant Call Format (VCF) file
2. **liz_gendist** - genetic distances between individuals

liz_coords - Longitude (x) and latitude (y) for each individual

CA_env - environmental data in the form of **raster** layers

Genetic data: the variant call format (VCF) file

```
##fileformat=VCFv4.0
##fileDate=2021/09/28
##source=ipyrad_v.0.9.81
##reference=file://ccgp-workflow-results/68-Strix/results/GCA_030819815.1/data/genome/GCA_030819815.1.fna
##phasing=unphased
##INFO=<ID=NS,Number=1>Type=Integer,Description="Number of Samples With Data">
##INFO=<ID=DP,Number=1>Type=Integer,Description="Total Depth">
##FORMAT=<ID=GT,Number=1>Type=String,Description="Genotype">
##FORMAT=<ID=DP,Number=1>Type=Integer,Description="Read Depth">
##FORMAT=<ID=CATG,Number=1>Type=String,Description="Base Counts (CATG)">
```

Meta information lines (##)

Genetic data: the variant call format (VCF) file

```
##fileformat=VCFv4.0
##fileDate=2021/09/28
##source=ipyrad_v.0.9.81
##reference=file:///ccgp-workflow-results/68-Strix/results/GCA_030819815.1/data/genome/GCA_030819815.1.fna
##phasing=unphased
##INFO=<ID=NS,Number=1,Type=Integer,Description="Number of Samples With Data">
##INFO=<ID=DP,Number=1,Type=Integer,Description="Total Depth">
##FORMAT=<ID=GT,Number=1,Type=String,Description="Genotype">
##FORMAT=<ID=DP,Number=1,Type=Integer,Description="Read Depth">
##FORMAT=<ID=CATG,Number=1,Type=String,Description="Base Counts (CATG)">
#CHROM    POS     ID      REF     ALT     QUAL    FILTER    INFO      FORMAT    IND1
```

Header line (#)

Genetic data: the variant call format (VCF) file

```
##fileformat=VCFv4.0
##fileDate=2021/09/28
##source=ipyrad_v.0.9.81
##reference=file:///ccgp-workflow-results/68-Strix/results/GCA_030819815.1/data/genome/GCA_030819815.1.fna
##phasing=unphased
##INFO=<ID=NS,Number=1>Type=Integer,Description="Number of Samples With Data">
##INFO=<ID=DP,Number=1>Type=Integer,Description="Total Depth">
##FORMAT=<ID=GT,Number=1>Type=String,Description="Genotype">
##FORMAT=<ID=DP,Number=1>Type=Integer,Description="Read Depth">
##FORMAT=<ID=CATG,Number=1>Type=String,Description="Base Counts (CATG)">
#CHROM POS ID REF ALT QUAL FILTER INFO FORMAT IND1
RAD_0 12 loc0_pos11 G A 13 PASS NS=113;DP=4086 GT:DP:CATG 0/0:19:0,0,0,19
RAD_0 15 loc0_pos14 T A 13 PASS NS=112;DP=4086 GT:DP:CATG 0/1:19:0,10,9,0
RAD_0 23 loc0_pos22 T A 13 PASS NS=114;DP=4086 GT:DP:CATG 1/1:19:0,0,19,0
RAD_0 55 loc0_pos54 A T 13 PASS NS=114;DP=4086 GT:DP:CATG ./.:19:0,0,19,0
```

Data lines

Genetic data: the variant call format (VCF) file

```
##fileformat=VCFv4.0
##fileDate=2021/09/28
##source=ipyrad_v.0.9.81
##reference=file:///ccgp-workflow-results/68-Strix/results/GCA_030819815.1/data/genome/GCA_030819815.1.fna
##phasing=unphased
##INFO=<ID=NS,Number=1,Type=Integer,Description="Number of Samples With Data">
##INFO=<ID=DP,Number=1,Type=Integer,Description="Total Depth">
##FORMAT=<ID=GT,Number=1,Type=String,Description="Genotype">
##FORMAT=<ID=DP,Number=1,Type=Integer,Description="Read Depth">
##FORMAT=<ID=CATG,Number=1,Type=String,Description="Base Counts (CATG)">
#CHROM POS ID REF ALT QUAL FILTER INFO FORMAT IND1
RAD_0 12 loc0_pos11 G A 13 PASS NS=113;DP=4086 GT:DP:CATG 0/0:19:0,0,0,19
RAD_0 15 loc0_pos14 T A 13 PASS NS=112;DP=4086 GT:DP:CATG 0/1:19:0,10,9,0
RAD_0 23 loc0_pos22 T A 13 PASS NS=114;DP=4086 GT:DP:CATG 1/1:19:0,0,19,0
RAD_0 55 loc0_pos54 A T 13 PASS NS=114;DP=4086 GT:DP:CATG ./.:19:0,0,19,0
```



Each row is a variant



Individuals are
in columns

Genetic data: the variant call format (VCF) file

#CHROM	POS	ID	REF	ALT	QUAL	FILTER	INFO	FORMAT	IND1
RAD_0	12	loc0_pos11	G	A	13	PASS	NS=113;DP=4086	GT:DP:CATG	0/0:19:0,0,0,19
RAD_0	15	loc0_pos14	T	A	13	PASS	NS=112;DP=4086	GT:DP:CATG	0/1:19:0,10,9,0
RAD_0	23	loc0_pos22	T	A	13	PASS	NS=114;DP=4086	GT:DP:CATG	1/1:19:0,0,19,0
RAD_0	55	loc0_pos54	A	T	13	PASS	NS=114;DP=4086	GT:DP:CATG	./.:19:0,0,19,0

Genetic data: the variant call format (VCF) file

Variant	IND1
loc0_pos11	GG
loc0_pos14	TA
loc0_pos22	TT
loc0_pos54	NA

#CHROM	POS	ID	REF	ALT	QUAL	FILTER	INFO	FORMAT	IND1
RAD_0	12	loc0_pos11	G	A	13	PASS	NS=113;DP=4086	GT:DP:CATG	0/0:19:0,0,0,19
RAD_0	15	loc0_pos14	T	A	13	PASS	NS=112;DP=4086	GT:DP:CATG	0/1:19:0,10,9,0
RAD_0	23	loc0_pos22	T	A	13	PASS	NS=114;DP=4086	GT:DP:CATG	1/1:19:0,0,19,0
RAD_0	55	loc0_pos54	A	T	13	PASS	NS=114;DP=4086	GT:DP:CATG	./.:19:0,0,19,0

Genetic data: genotype dosage matrix

VCF file (*inds are cols, SNPs are rows*)

Genotype	VCF
Homozygous reference	0/0
Heterozygous	0/1
Homozygous alternate	1/1
Missing	./.

Variant	REF	ALT	IND1
loc0_pos11	G	A	0/0
loc0_pos14	T	A	0/1
loc0_pos22	T	A	1/1
loc0_pos54	A	T	./.

Genetic data: genotype dosage matrix

Genotype	VCF	Dosage
Homozygous reference	0/0	0
Heterozygous	0/1	1
Homozygous alternate	1/1	2
Missing	./.	NA

VCF file (*inds* are *cols*, *SNPs* are *rows*)

Variant	REF	ALT	IND1
loc0_pos11	G	A	0/0
loc0_pos14	T	A	0/1
loc0_pos22	T	A	1/1
loc0_pos54	A	T	./.

Dosage matrix (*inds* are *rows*, *SNPs* are *cols*)

IND	loc0_pos11	loc0_pos14	loc0_pos22	loc0_pos54
IND1	0	1	2	NA

VCFs in R

`vcfR::read.vcf()`

`View(liz_vcf)`

liz_vcf	S4 [1000 x 8 x 54] (vcfR::vcfR	S4 object of class vcfR
meta	character [6]	'##fileformat=VCFv4.2' '##fileDate=20220927' '##source=PLINKv1.90' '##contig=...
fix	character [1000 x 8]	'0' '0' '0' '0' '0' '10' '15' '22' '28' '32' '35' 'Locus_10' 'Locus_15' 'Loc ...
gt	character [1000 x 54]	'GT' 'GT' 'GT' 'GT' 'GT' 'GT' '0/0' '0/0' '0/0' '0/0' '0/0' NA '0/0' '0/0' '0/0' ...

VCFs in R

`vcfR::read.vcf()`

`View(liz_vcf)`

liz_vcf	S4 [1000 x 8 x 54] (vcfR::vcfR	S4 object of class vcfR
meta	character [6]	'##fileformat=VCFv4.2' '##fileDate=20220927' '##source=PLINKv1.90' '##contig=...
fix	character [1000 x 8]	'0' '0' '0' '0' '0' '10' '15' '22' '28' '32' '35' 'Locus_10' 'Locus_15' 'Loc ...
gt	character [1000 x 54]	'GT' 'GT' 'GT' 'GT' 'GT' 'GT' '0/0' '0/0' '0/0' '0/0' NA '0/0' '0/0' '0/0' ...

```
> liz_vcf@gt
  FORMAT ALT3  BAR360 BLL5  BNT5  BOF1
[1,] "GT"   "0/0"  "0/0"  "0/0"  "0/0"  "0/0"
[2,] "GT"   "0/0"  "0/0"  NA     "0/0"  NA
[3,] "GT"   "0/0"  "0/0"  "0/0"  NA     NA
[4,] "GT"   "0/0"  NA     "0/0"  NA     NA
[5,] "GT"   "0/0"  "0/0"  NA     "0/0"  NA
[6,] "GT"   NA     "0/0"  "0/0"  "0/0"  NA
[7,] "GT"   NA     "0/0"  "0/0"  NA     "0/0"
[8,] "GT"   "1/1"  "1/1"  "0/1"  "0/0"  "0/0"
[9,] "GT"   "0/0"  "0/0"  NA     "0/0"  NA
[10,] "GT"  "0/0"  "0/0"  "0/0"  "0/0"  "0/0"
```

Querying package functions in R

?vcf_to_dosage

vcf_to_dosage {algatr} R Documentation

Convert a vcf to a dosage matrix

Description

Convert a vcf to a dosage matrix

Usage

```
vcf_to_dosage(x)
```

Arguments

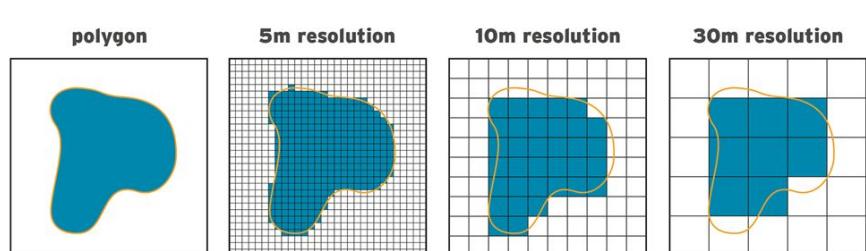
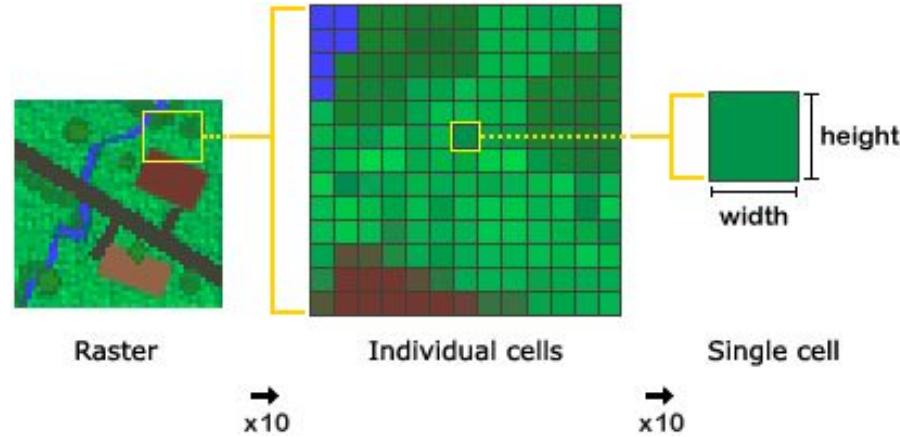
`x` can either be an object of class 'vcfR' or a path to a .vcf file

Rasters

Raster - a grid of rectangular cells where each cell has a value

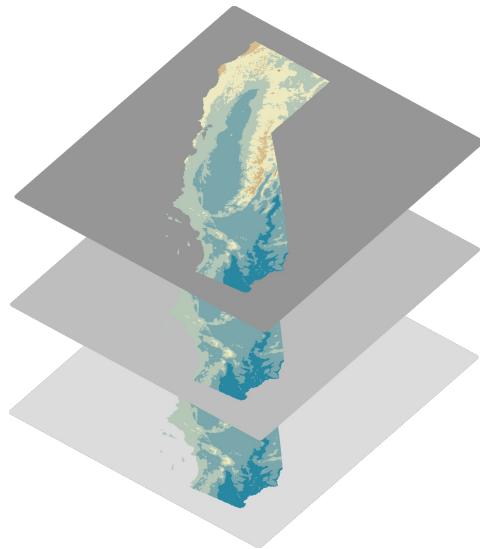
Components of spatial scale:

1. Resolution - raster cell size
2. Extent - the total space covered by the raster (usually referred to based on the corner coordinates of the raster)

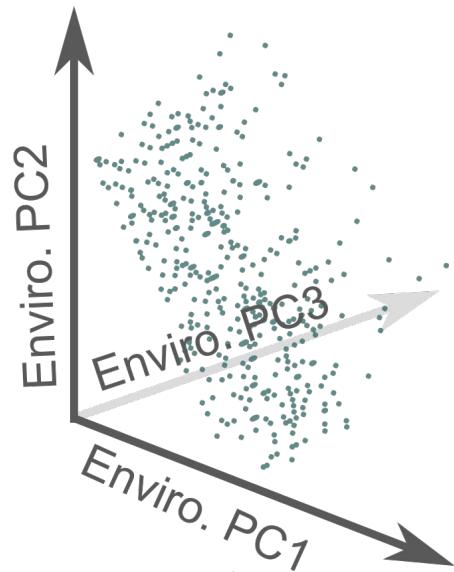


Some words you'll hear: raster, raster layer, raster stack (multiple raster layers), SpatRaster/RasterLayer/RasterStack (raster objects in R)

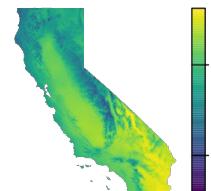
CA_env



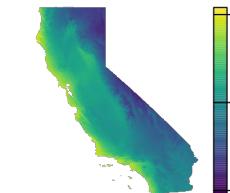
Enviro data layers



Enviro. PC1



Enviro. PC2



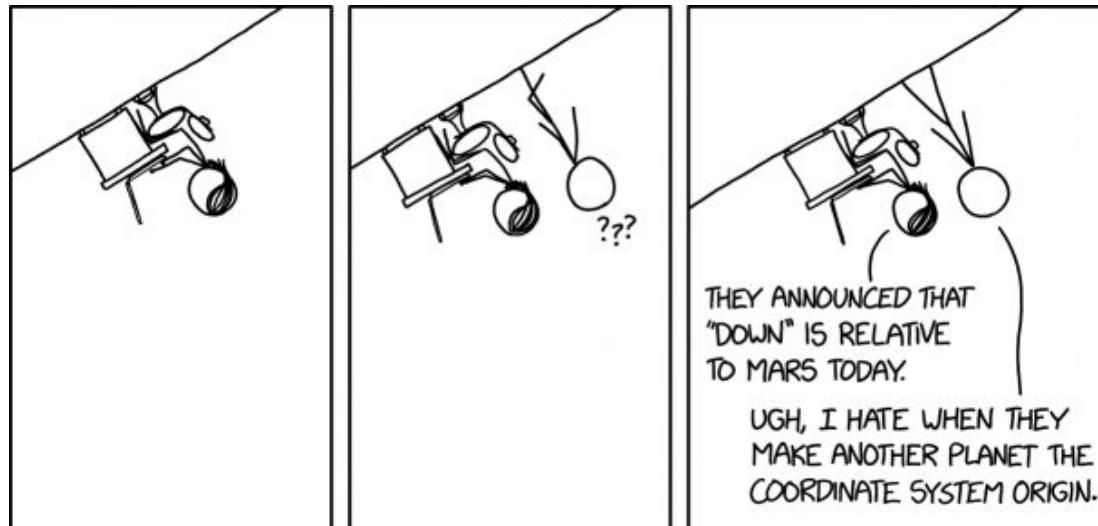
Enviro. PC3



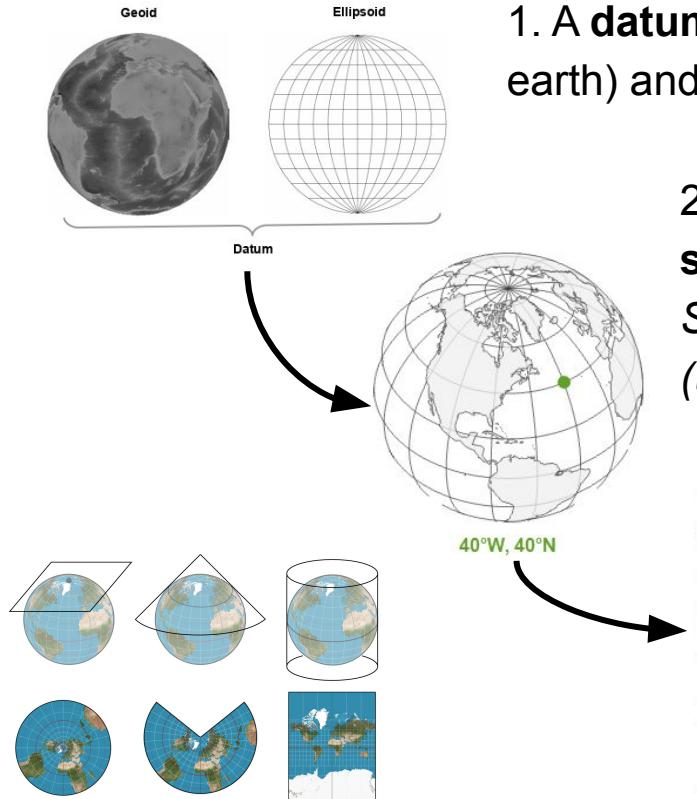
Crash course: coordinate projections

Coordinate systems - a way to measure and communicate location

Projection - transformations applied to represent the 3D world in 2D



Crash course: coordinate projections



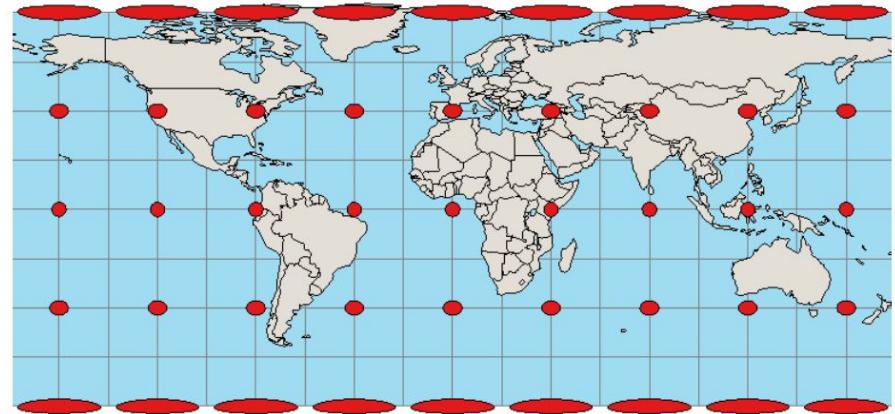
1. A **datum** is created from a **geoid** (reference surface for the earth) and a smooth **spheroid/ellipsoid**
2. The datum defines the **coordinate reference system** for latitude and longitude → *World Geodetic System from 1984 (WGS 84) is the most common (used by the Global Positioning System; GPS)*
3. The 3D latitudes and longitudes are transformed into 2D X and Y coordinates using a **projected coordinate system**

Crash course: coordinate projections

Why can't we just use unprojected longitude/latitude?

Longitudes are closer together the further you move away

One latitude unit does not equal one longitude unit



*Unprojected Latitude and Longitude
(EPSG 4326)*