

wingen:

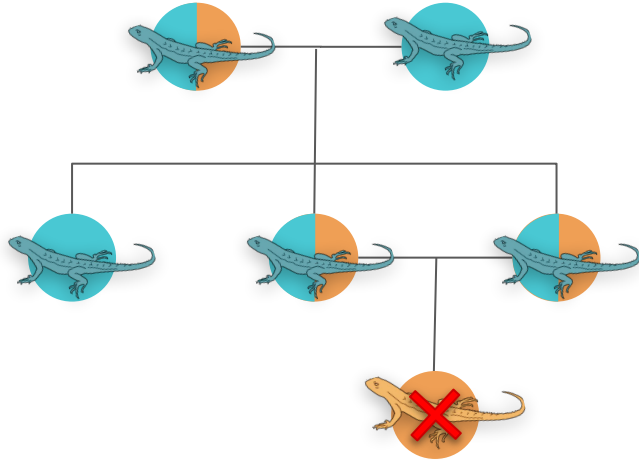
Mapping genetic diversity

Anusha Bishop & Anne Chambers (2024)

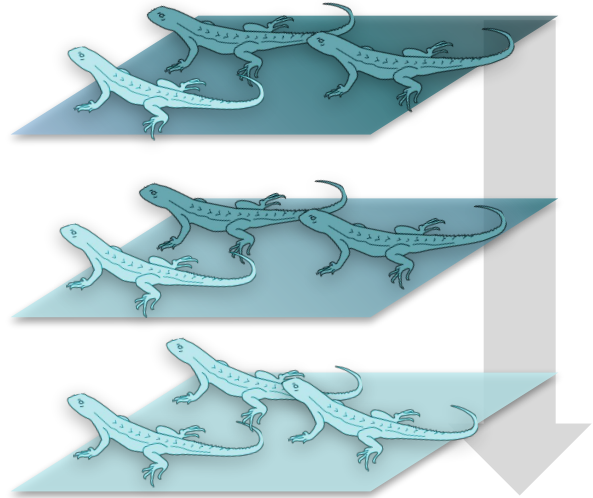


The importance of genetic diversity

Population Viability



Evolutionary Potential



THE LOST GENOMES in Science

doi: 10.1126/science.abn5642



Genetic diversity loss in the Anthropocene

MOISES EXPOSITO-ALONSO , TOM R. BOOKER , LUCAS CZECH , LAUREN GILLESPIE , SHANNON HATLEY , CHRISTOPHER C. KYRIAKOPOULOS , PATRICIA L. M. LANG , LAURA LEVENTHAL , DAVID NOGUES-BRAVO , VERONICA PAGOWSKI , MEGAN RUFFLEY , JEFFREY P. SPENCE , SEBASTIAN E. TORO ARANA , CLEMENS  [Info & Affiliations](#)

SCIENCE • 22 Sep 2022 • Vol 377, Issue 6612 • DOI: 10.1126/science.abc.1234567

↓ 8,682 13

**“We estimate that
more than 10% of
genetic diversity
may already be lost
for many threatened and
nonthreatened species...”**

- Exposito-Alonso et al. (2022)

Declining genetic diversity

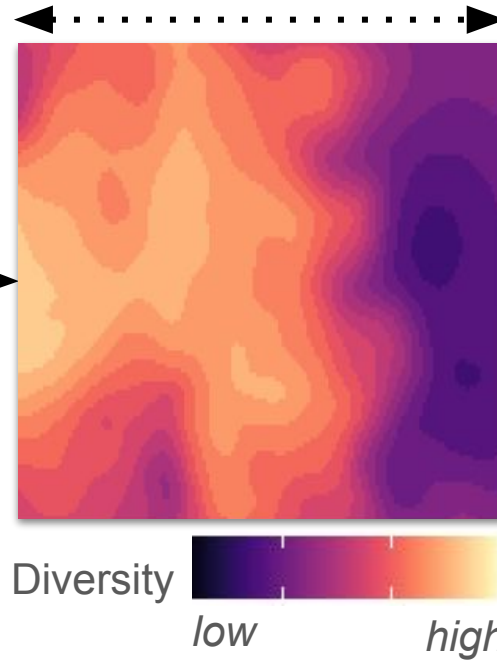
Habitat loss is one of the major drivers of species extinctions and declines of species richness at local scales. Smaller areas of remnant habitat also harbor smaller populations and lower genetic diversity, which restrict potential adaptation to environmental change. Exposito-Alonso *et al.* developed a framework to predict decreases in naturally occurring mutations, and thus genetic diversity, with habitat loss (see the Perspective by Ruegg and Turbek). Georeferenced genomic data from across the native ranges of the small mustard plant *Arabidopsis thaliana* and 20 other species suggest that the mutation-area relationship follows a power law. This relationship predicts that many species have already experienced sub-

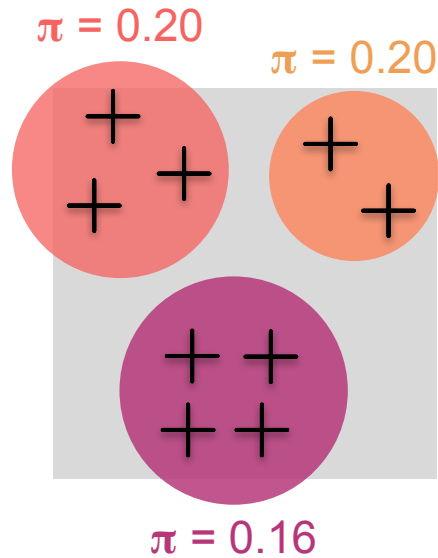
Understanding genetic diversity across landscapes

Determine **drivers of genetic diversity** patterns

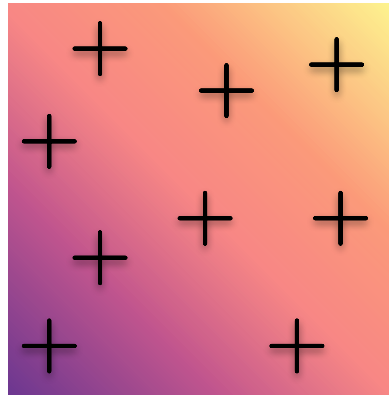
Protect valuable areas
of **high genetic diversity**

Identify vulnerable areas of
low genetic diversity

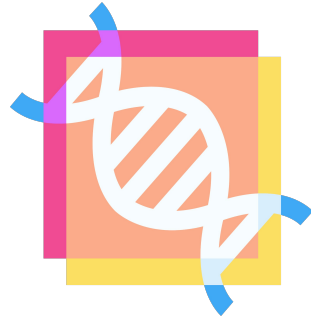




Traditional:
calculating genetic
diversity by
population

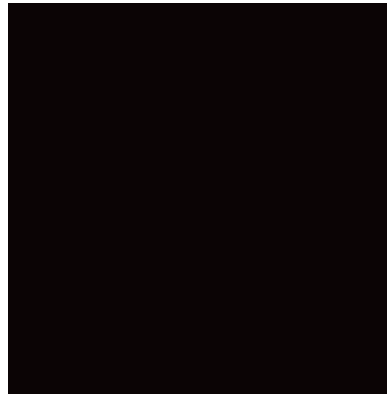
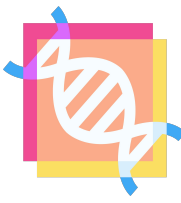


New:
calculating genetic
diversity continuously

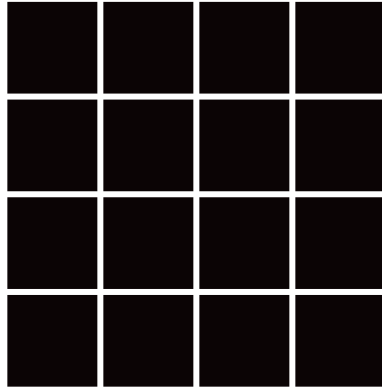


wingen

*Continuous mapping of genetic
diversity using moving windows*



**Example
Landscape**



**Example
Landscape**

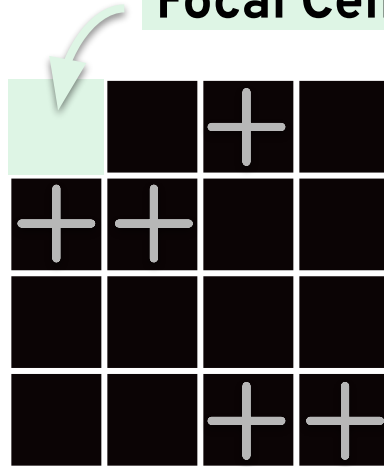


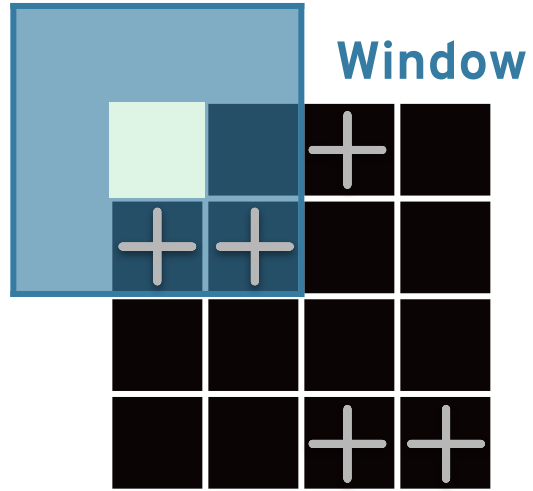
		+	
+	+		
		+	+

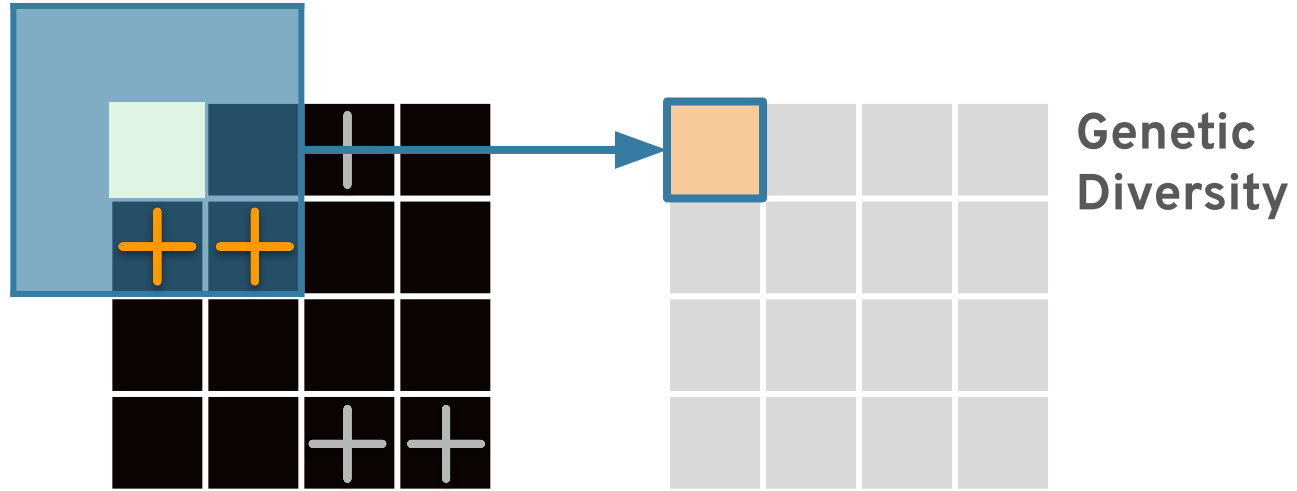
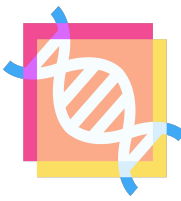
← Samples

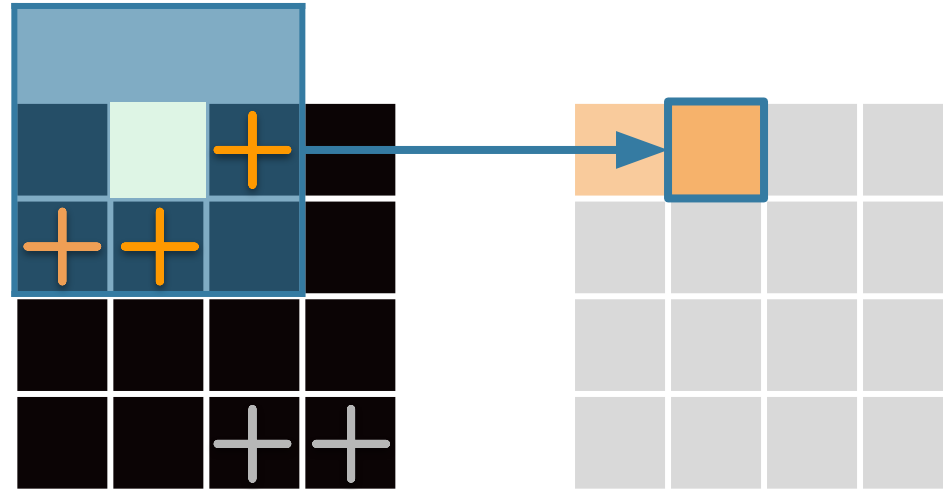


Focal Cell

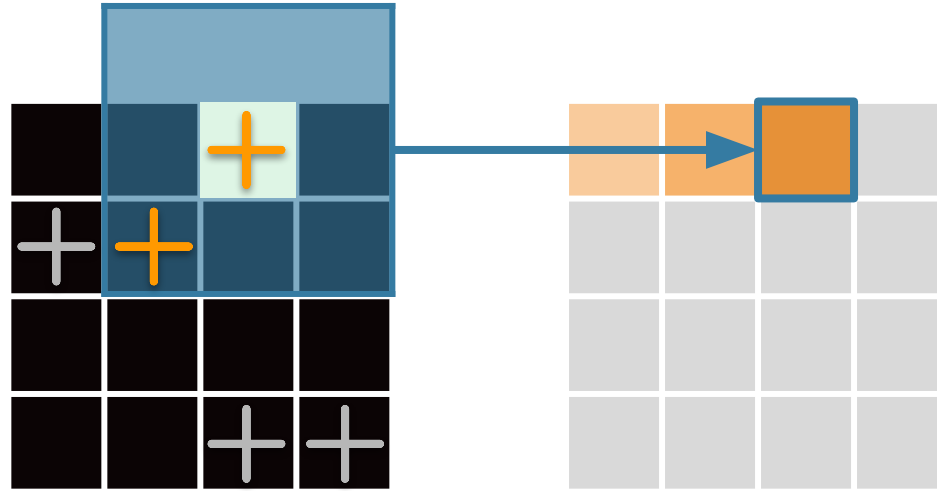








**Genetic
Diversity**



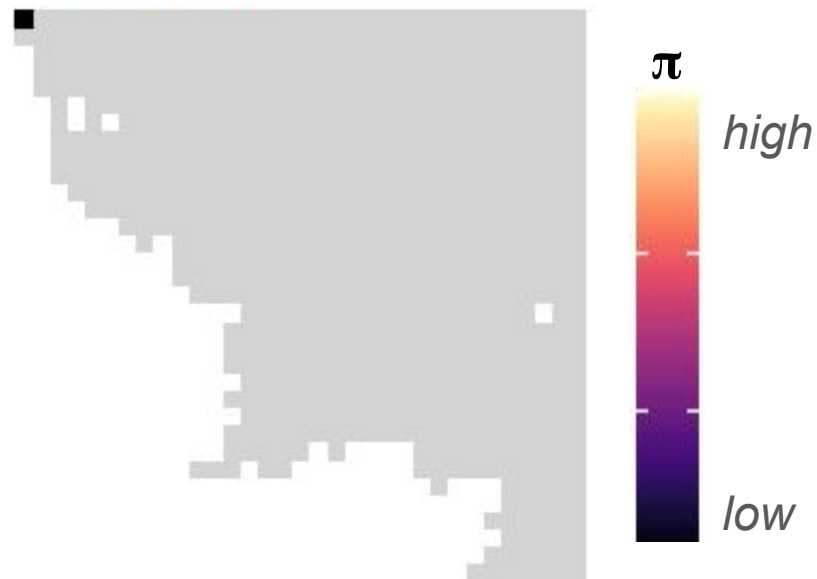
**Genetic
Diversity**

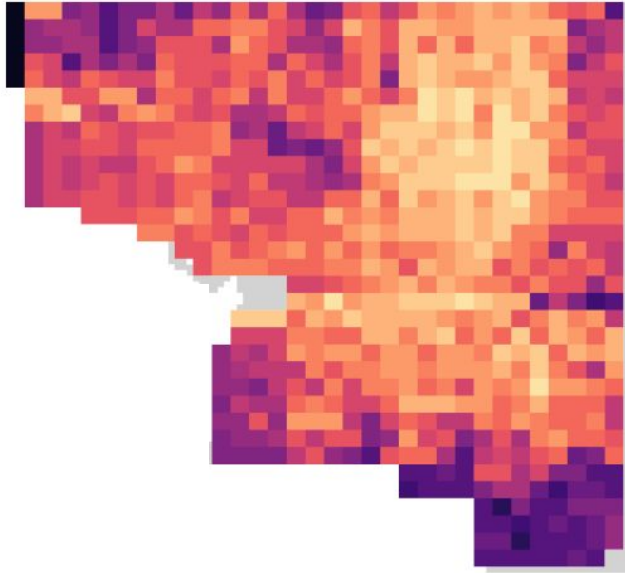
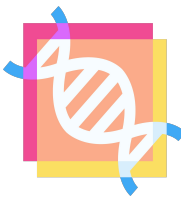


Landscape

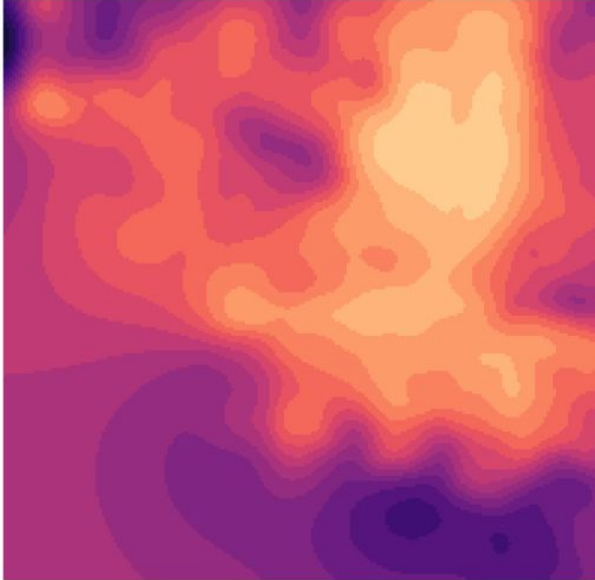


Genetic Diversity

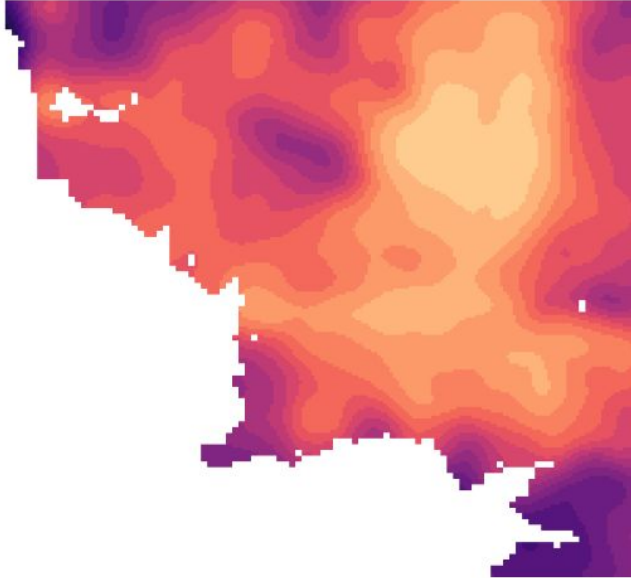




Moving window
maps of π ,
allelic richness,
heterozygosity,
and more...

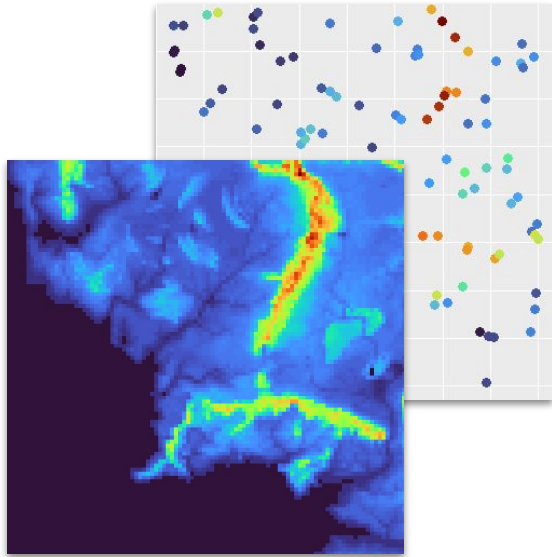


Kriging to produce
interpolated maps
of genetic diversity



Masking to exclude
undersampled regions

Generalized window functions



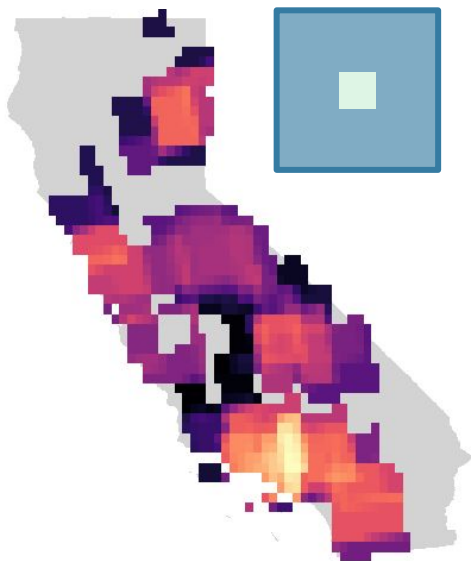
Input non-genomic data and use custom statistics:

- ✓ Phenotypic data
- ✓ Environmental data
- ✓ Anything else that can be formatted as a matrix or dataframe...

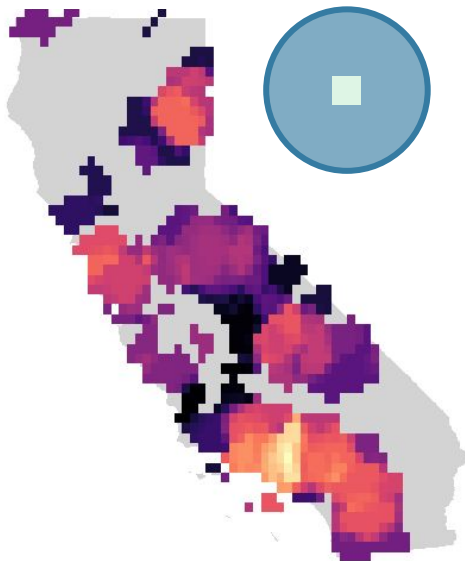
Window options

original

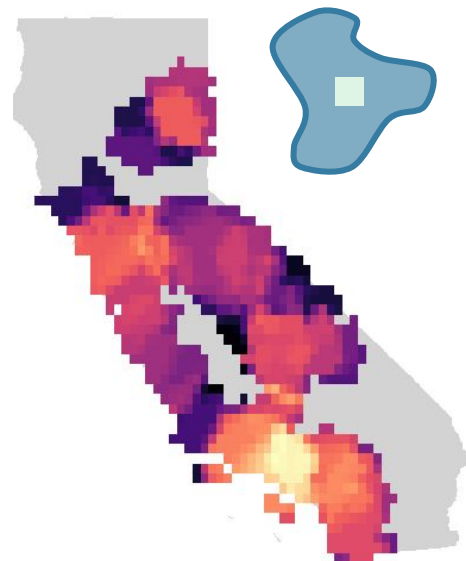
Rectangular



Circular



Resistance



EXERCISES

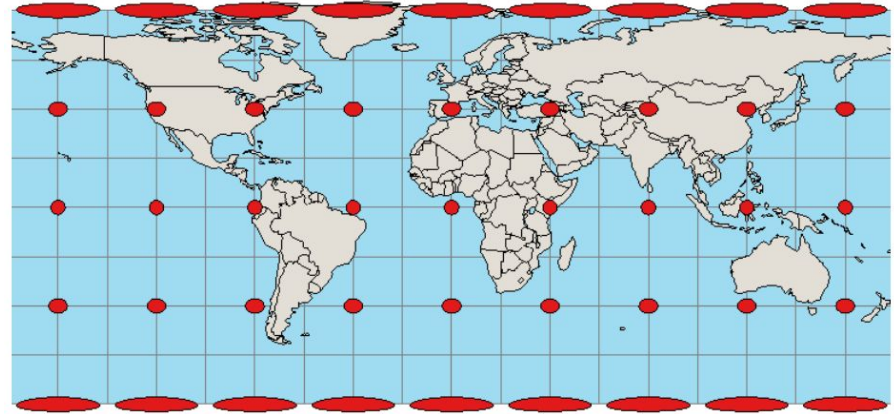
Crash course: coordinate projections

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

Problem for our windows:

Longitudes are closer together the further you move away → the size of the window will change based where we are in globe

One latitude unit does not equal one longitude unit → the window will be rectangular when we want it to be square



Unprojected Latitude and Longitude
(EPSG 4326)

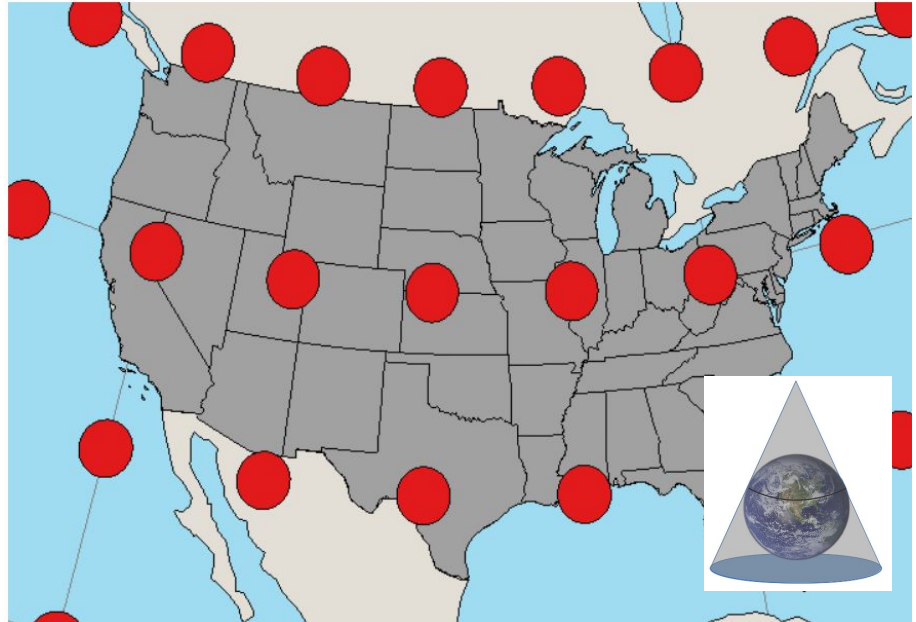
Crash course: coordinate projections

Equal-area projections

The size of any area is in proportion to the size on the earth

No projections are perfect, all have a some kind of distortion:

1. Conformal - preserve angles (shape), distort areas and distances
2. Equal area - preserve area, distort angles (shape)
3. Equidistant - preserve distances, but only from certain points/lines



North America Albers Equal Area
Conic Projection (ESRI 102008)

1. Reprojecting coordinates

***st_as_sf()**
converts our
coordinates into a sf
(spatial) object*

liz_coords

```
> head(liz_coords)
      x      y
1 -120.3972 41.56120
3 -116.8923 34.16940
5 -124.0408 40.90450
```

coords = the
names of the
columns with x/y
coordinates

Try running:
plot(coords_longlat)
plot(coords_proj)

crs = the original CRS
(longitude/latitude)

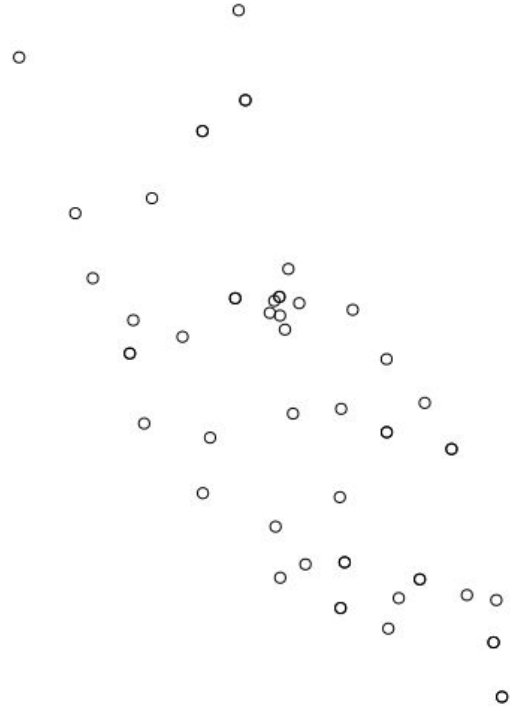
```
1 # First, we reformat our dataframe of coordinates into sf coordinates
2 coords_longlat <- st_as_sf(liz_coords, coords = c("x", "y"), crs = "+proj=longlat")
3
4 # Next, the coordinates and raster can be projected to an equal area projection, in
  this case NAD83 / California Albers (EPSG 3310)
5 coords_proj <- st_transform(coords_longlat, crs = 3310)
```

***st_transform()** projects our coordinates to a new CRS*

crs = the new CRS

Output: sf object

```
> coords_proj
Simple feature collection with 53 features and 0 fields
Geometry type: POINT
Dimension: XY
Bounding box: xmin: -340513.1 ymin: -564863.1 xmax: 335547.8 ymax: 393840.3
Projected CRS: NAD83 / California Albers
First 10 features:
  geometry
1  POINT (-33176.1 393840.3)
2  POINT (286436.8 -422680)
3  POINT (-340513.1 328157.9)
4  POINT (126514.8 -24393.74)
5  POINT (24696.91 -32481.12)
6  POINT (-165504.3 -183124.2)
7  POINT (18481.19 -327140.6)
8  POINT (10469.52 -28638.13)
9  POINT (-83306.63 -280435.5)
10 POINT (191003.6 -426930.1)
```



2. Creating raster from coordinates

See what happens when you change the value of **res**

***coords_to_raster()**
creates a raster from our
projected coordinates*

our projected
coordinates

buffer = the number of cells to add
around the coordinates as a buffer

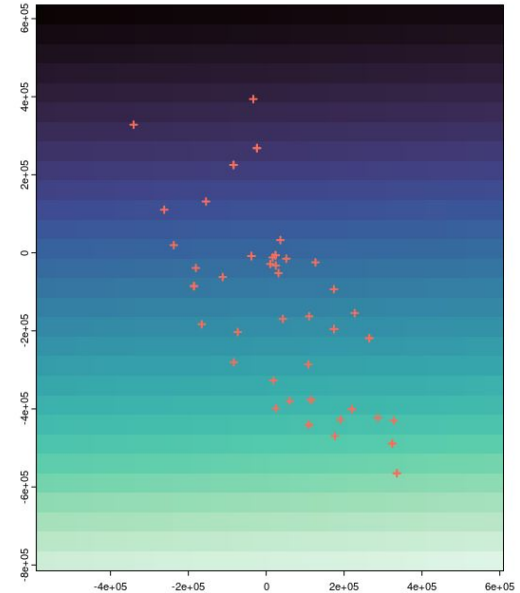
```
1 liz_lyr <- coords_to_raster(coords_proj, res = 50000, buffer = 5, plot = TRUE)
```

res = desired resolution for the output
raster (the units are based on the
coordinates; in this case it is in meters)

plot = whether to plot
the resulting raster

Output: SpatRaster

```
> liz_lyr
class      : SpatRaster
dimensions : 29, 24, 1  (nrow, ncol, nlyr)
resolution : 50000, 50000  (x, y)
extent     : -590513.1, 609486.9, -814863.1, 635136.9  (xmin, xmax, ymin, ymax)
coord. ref.: NAD83 / California Albers (EPSG:3310)
source(s)  : memory
name       : lyr.1
min value  : 1
max value  : 696
```



Previewing window

See what happens when you change the value of **wdim** and **fact**

fact = aggregation factor for the raster (0 = no aggregation)

preview_gd() previews the moving window and sampling counts

raster

coordinates

wdim = window dimensions in cells

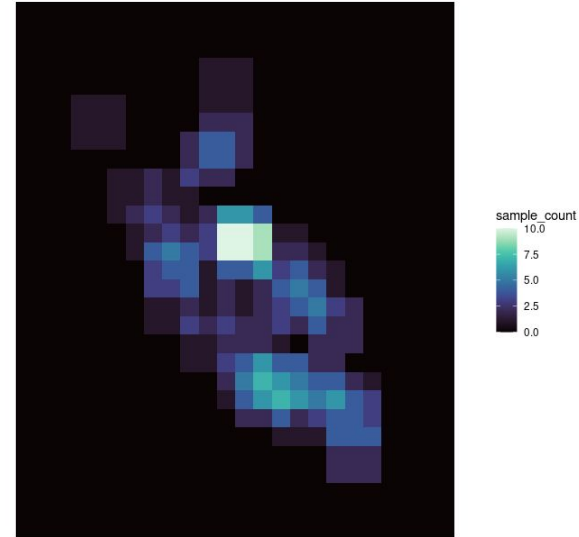
```
1 sample_count <- preview_gd(liz_lyr, coords_proj, wdim = 3, fact = 0)
2
3 # Visualize the sample count layer
4 ggplot_count(sample_count)
```

raster where values are sample counts in the window

ggplot_count() plots the sample count rasters (you can also use *plot_count()* or *just plot()*)

Output: SpatRaster

```
> sample_count
class       : SpatRaster
dimensions  : 29, 24, 1  (nrow, ncol, nlyr)
resolution  : 50000, 50000  (x, y)
extent      : -590513.1, 609486.9, -814863.1, 635136.9  (xmin, xmax, ymin, ymax)
coord. ref. : NAD83 / California Albers (EPSG:3310)
source(s)   : memory
name        : sample_count
min value    : 0
max value    : 10
```



Run the moving window

window_gd() runs the moving window analysis

```
1  wgd <- window_gd(liz_vcf, ← VCF
2  coords_proj, ← Coordinates
3  liz_lyr, ← Raster
4  stat = "pi", ← stat = statistic to calculate
5  wdim = 3,
6  fact = 0
7  )
```

*Checkout other arguments you can change by running **?window_gd***

See what happens when you change the value of **wdim**, **fact**, and **min_n** (min # of samples in a window).

Output: SpatRaster

```
> wgd
class      : SpatRaster
dimensions : 29, 24, 2  (nrow, ncol, nlyr)
resolution : 50000, 50000  (x, y)
extent      : -590513.1, 609486.9, -814863.1, 635136.9  (xmin, xmax, ymin, ymax)
coord. ref. : NAD83 / California Albers (EPSG:3310)
source(s)   : memory
names       :      pi, sample_count
min values  : 0.02683333,      0
max values  : 0.11301645,     10
```


Plot results

ggplot_gd() plots the moving window raster

Raster

bkg = raster or other spatial object to use for background

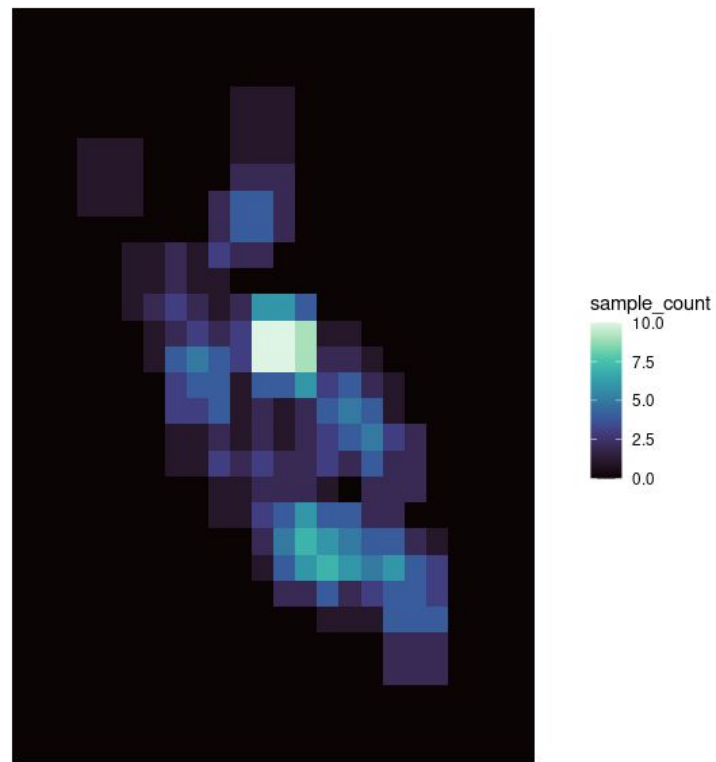
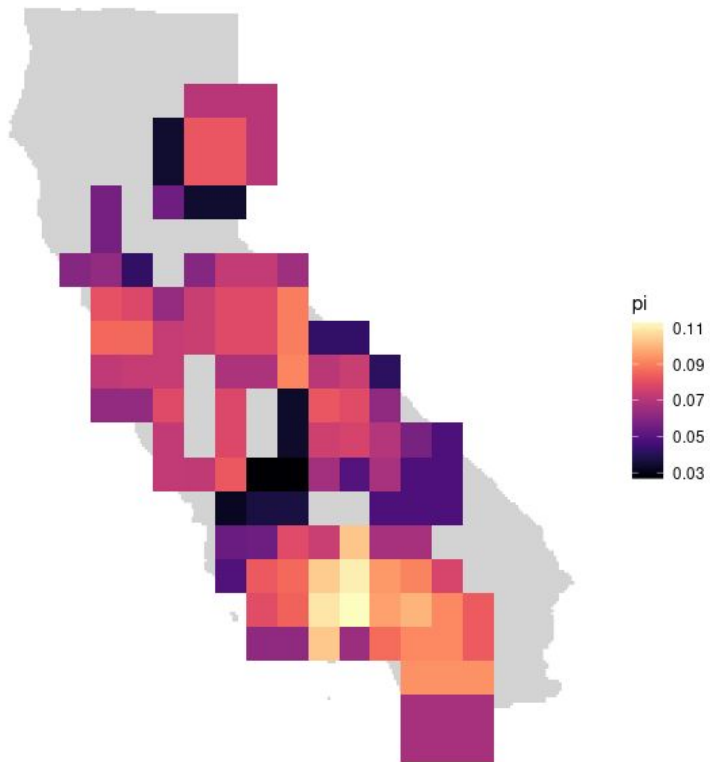
This plot can be modified using **ggplot2** functions

```
1 # Plot map of pi
2 ggplot_gd(wgd, bkg = envlayer) + ggtitle("Moving window pi")
3
4 # Plot sample count map
5 ggplot_count(wgd) + ggtitle("Sample count")
```

ggplot_count() plots the sample count layer window raster

Try changing the color scheme by running **ggplot_gd() + scale_fill_viridis_c(option = "inferno")** (other options to try are "turbo", "viridis", "plasma", "rocket", etc.)

Output: ggplots



Krige results

index = which raster layers to krig (here we use the first (diversity) and the second (sample count) layers)

Moving window raster

Raster to interpolate across

```
1 kgd <- krig_gd(wgd, index = 1:2, liz_lyr, disagg_grd = 5)
```

***krig_gd()** produce a spatially interpolated (smoothed) map*

See what happens when you change **disagg_grd**

disagg_grd = factor by which to disaggregate the raster used for interpolation (**liz_lyr**). This increases the resolution of the smoothed layer.

Output: SpatRaster

```
> kgd
class      : SpatRaster
dimensions : 145, 120, 2  (nrow, ncol, nlyr)
resolution : 10000, 10000 (x, y)
extent      : -590513.1, 609486.9, -814863.1, 635136.9 (xmin, xmax, ymin, ymax)
coord. ref. : NAD83 / California Albers (EPSG:3310)
source(s)   : memory
names       :          pi, sample_count
min values  : 0.02683333,          0
max values  : 0.11301645,          10
```

Mask results

Moving window or
kriged raster to mask

Raster to mask with

minval = minimum
value of the masking
raster, below which
values are replaced with
NA (masked)

```
1 mgd_1 <- mask_gd(kgd, kgd[["sample_count"]], minval = 1)
```

mask_gd() mask the moving
window or kriged rasters using
another raster or spatial object

You can also use a
spatial object (e.g.
a vector/polygon)
for masking

If no minval is provided,
areas of the masking
raster that are NA will be
masked

See what happens when you change **minval** or
use **wgd[["sample_count"]]** instead

Exercises

1. Load the example dataset
2. Create inputs
 - a. Project coordinates
 - b. Create a raster layer from your coordinates using `coords_to_raster()`
3. Preview moving window map using `preview_gd()`
4. Create moving window map using `window_gd()`
5. Krige moving window map using `krig_gd()`
6. Mask moving window map using `mask_gd()`