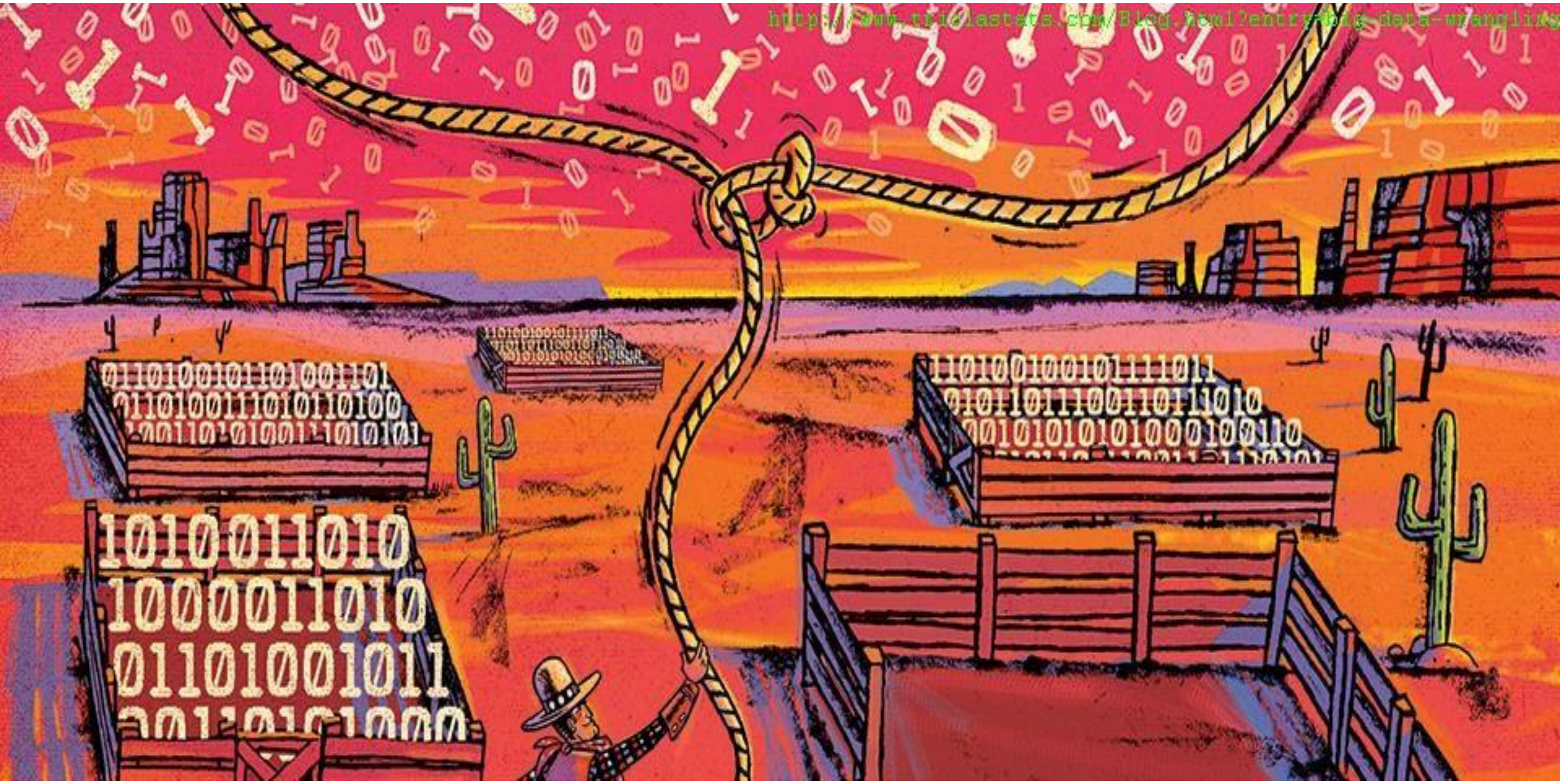
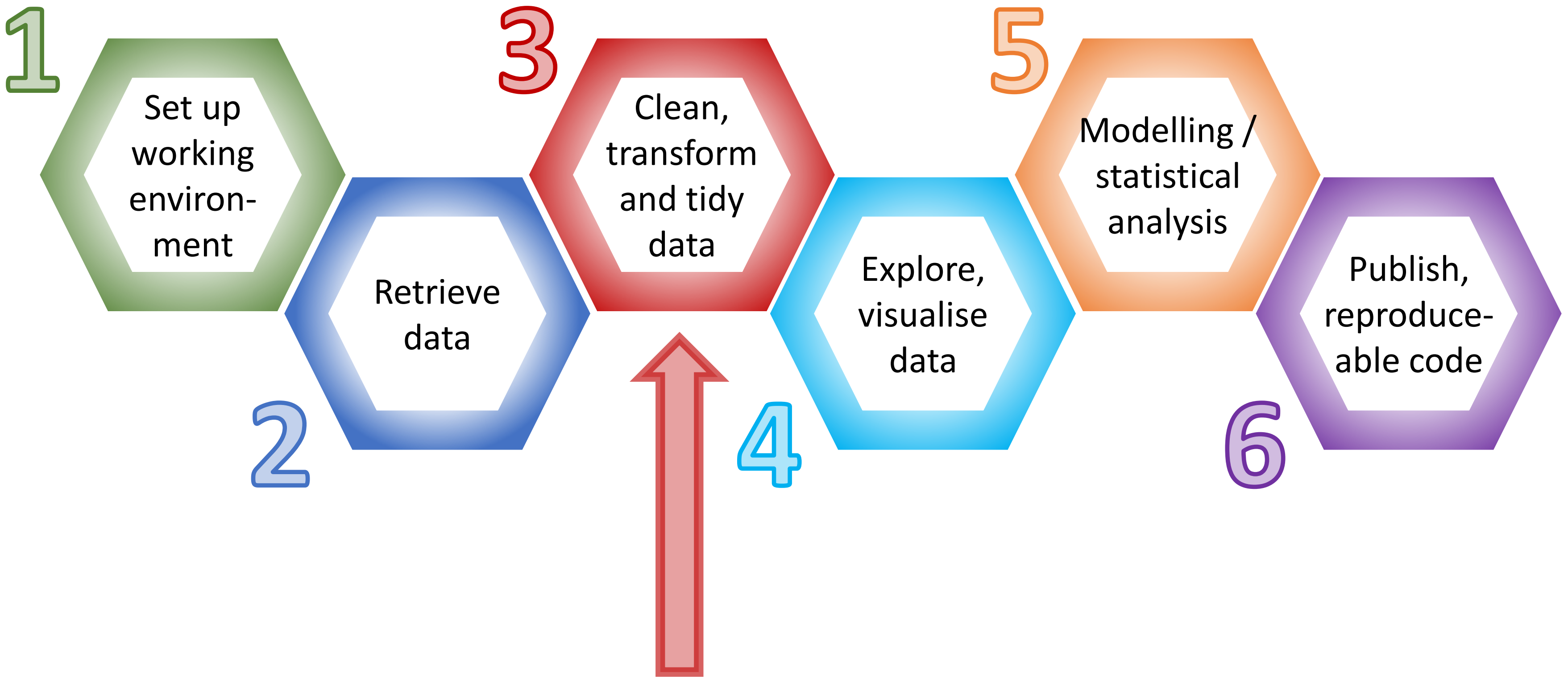
Palaeodata wrangling with the Tidyverse



Steve Juggins

Newcastle University

Palaeodata Workflow


1
Set up working environ-ment
2
Retrieve data
3
Clean, transform and tidy data
4
Explore, visualise data
5
Modelling / statistical analysis
6
Publish, reproduce-able code

Not sexy, not clever, not always straightforward, and can be very time consuming.
Having a good set of tools in R can:

- Increase efficiency
- Reduce errors
- Self-documenting & reproducible

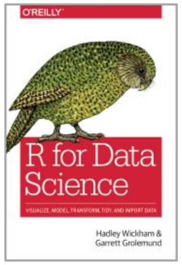
Based on Fig 3, Slater et al. 2019. Using R in hydrology: a review of recent developments and future directions. Hydrology and Earth System Sciences **23:2939-2963.**

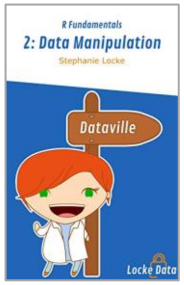
Guiding principles

- Everything is possible in **Base R** but solutions may not be obvious, use a mix functions with different syntax, and require ad-hoc packages: the Wild West that is Base R!
- **Tidyverse** offers a consistent approach to data wrangling, fast, concise & logical syntax, and very flexible.
- Some things may be faster in Base R but speed is rarely a limiting factor.
- Focus on code that is simple, readable and easy to understand (things that promote learning, easier debugging, reproducibility and code sharing).
- Today - Don't get bogged down in the details of individual functions and operations. Focus on the big picture - the details will come with practice.

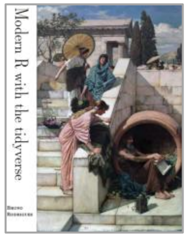
Resources

Whickham & Grolemund, R for Data Science,
free online https://r4ds.had.co.nz/


O'REILLY
R for Data Science
VISUALIZE, MODEL, TRANSFORM, TIDY, AND IMPORT DATA
Hadley Wickham & Garrett Grolemund

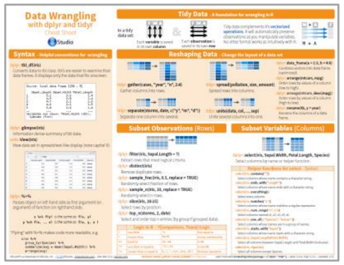


Locke, R Fundamentals 2: Data Manipulation (£11)
https://itsalocke.com/company/books/



Bruno Rodrigues, Modern R with the tidyverse
free online https://b-rodrigues.github.io/modern_R/ or buy pdf for < £10

Murray Logan's website, excellent tutorials & book
https://www.flutterbys.com.au/stats/


Data Wrangling with dplyr and tidyr Cheat Sheet
Tidy Data
Reshaping Data
Subset Observations (Rows)
Subset Variables (Columns)

Rstudio cheatsheets
https://www.rstudio.com/resources/cheatsheets/

stackoverflow + 1001 other websites…

Example: Impact of the Neolithic Agricultural Transition

Contents lists available at SciVerse ScienceDirect

Journal of Archaeological Science

journal homepage: http://www.elsevier.com/locate/jas

ELSEVIER

The impact of the Neolithic agricultural transition in Britain: a comparison of pollen-based land-cover and archaeological ^{14}C date-inferred population change

Jessie Woodbridge[a,*], Ralph M. Fyfe[a], Neil Roberts[a], Sean Downey[b], Kevan Edinborough[b], Stephen Shennan[b]

Jessie Woodbridge, Ralph Fyfe & colleagues

Woodbridge et al. (2014) & Fyfe et al. (2010)

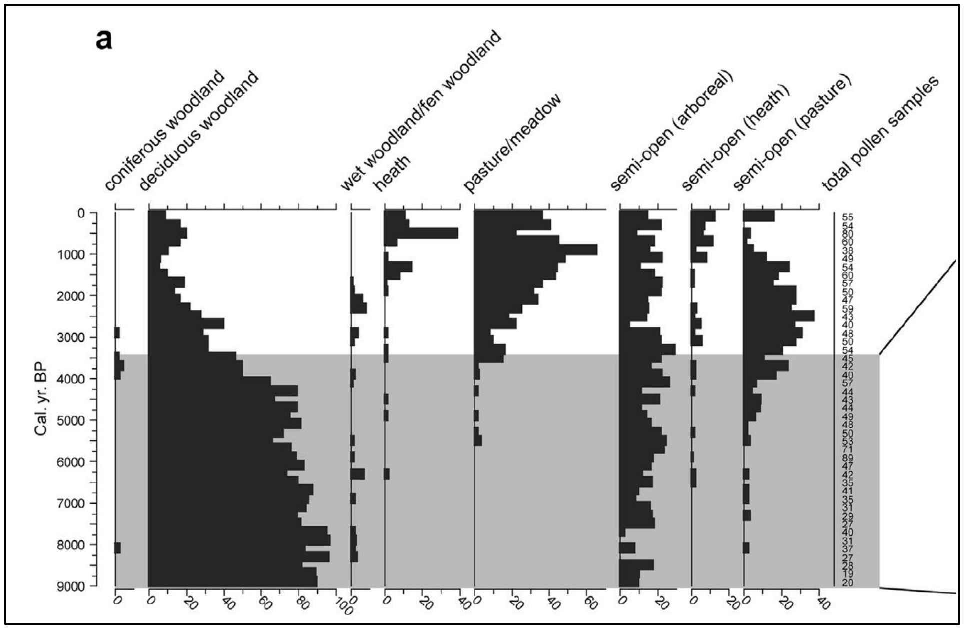
Aim: Reconstruct anthropogenic land-cover change in Britain over the last 9000 years

Fyfe, et al. 2010. A pollen-based pseudobiomisation approach to anthropogenic land-cover change. The Holocene **20:1165-1171.**

Woodbridge, et al. 2014. The impact of the Neolithic agricultural transition in Britain: a comparison of pollen-based land-cover and archaeological 14C date-inferpoll population change. Journal of Archaeological Science **51:216-224.**

Land-cover reconstructions for Britain

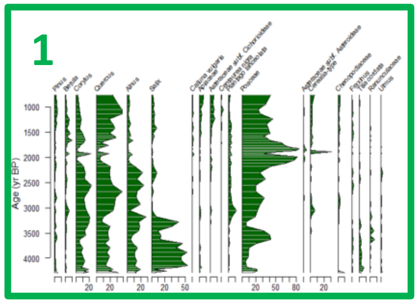
Figure 3 from Woodbridge et al. (2014)



Thanks to Jessie Woodbridge and Ralph Fyfe for sharing their data!

Example: Impact of the Neolithic Agricultural Transition

1. Extract dated pollen profiles from European pollen database (+ other sources), 41 sites in total.



2. Classify each pollen type to a land cover class (LCC)

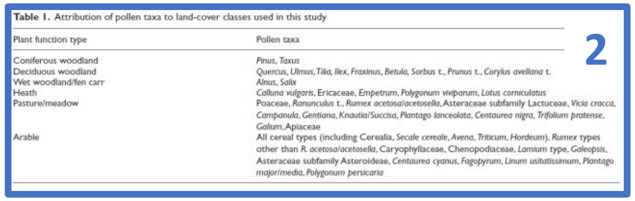
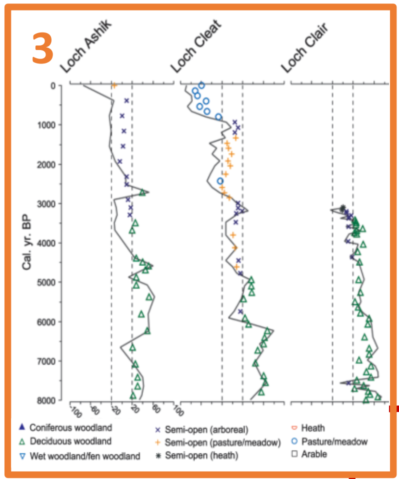


Table 1. Attribution of pollen taxa to land-cover classes used in this study

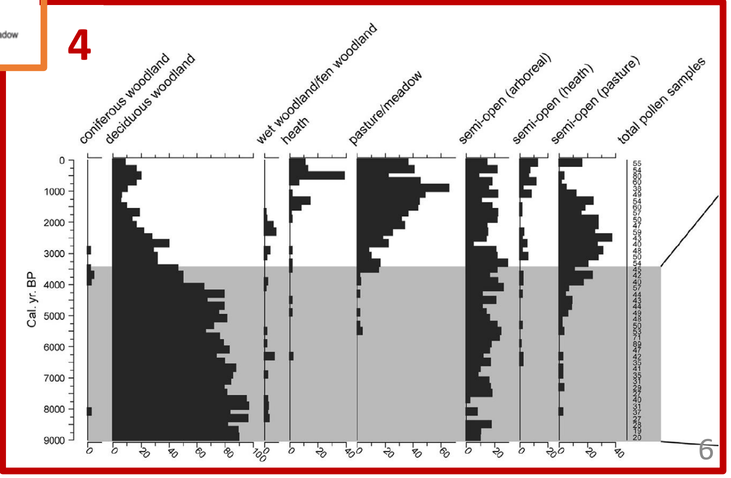
Plant function type	Pollen taxa
Coniferous woodland	*Pinus, Taxus*
Deciduous woodland	*Quercus, Ulmus, Tilia, Ilex, Fraxinus, Betula, Sorbus* t., *Prunus* t., *Corylus avellana* t.
Wet woodland/fen carr	*Alnus, Salix*
Heath	*Calluna vulgaris*, Ericaceae, *Empetrum, Polygonum viviparum, Lotus corniculatus*
Pasture/meadow	Poaceae, *Ranunculus* t., *Rumex acetosa/acetosella*, Asteraceae subfamily Lactuceae, *Vicia cracca, Campanula, Gentiana, Knautia/Succisa, Plantago lanceolata, Centaurea nigra, Trifolium pratense, Galium*, Apiaceae
Arable	All cereal types (including Cerealia, *Secale cereale, Avena, Triticum, Hordeum*), *Rumex* types other than *R. acetosa/acetosella*, Caryophyllaceae, Chenopodiaceae, *Lamium* type, *Galeopsis*, Asteraceae subfamily Asteroideae, *Centaurea cyanus, Fagopyrum, Linum usitatissimum, Plantago major/media, Polygonum persicaria*

3. For each site, transform species data to major vegetation types (land cover class: LCC) and calculate the dominant LCC for each sample.



Fyfe et al. (2010)

4. Sum sample LCCs for all sites in 200 year time slices, convert to % of each LCC & plot.



Day 1 aims

Morning

Aims: To reproduce Woodbridge et al. Figure 3 using Tidyverse methods & do some modelling (richness, rate-of-change).

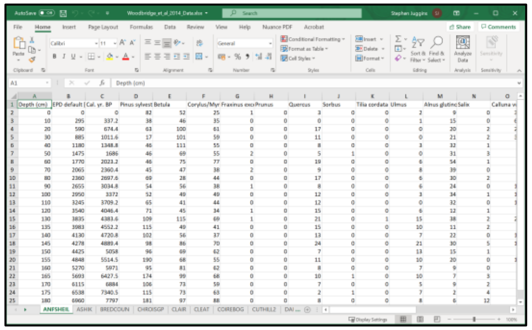
1. Work through analysis of a single site using base R
2. Repeat using Tidyverse
3. Apply to all (41) sites & create synthesis figure
4. Modelling with the Tidyverse

Afternoon

- Work with your own data, ask questions, get help

The data

1. **Woodbridge_et_al_2014_Data.xlsx**: Excel file with pollen counts for 42 sites, each site on a separate tab. Columns for pollen types, Depth and Cal. Age BP + alternative chronologies, sample IDs & and pollen sum.

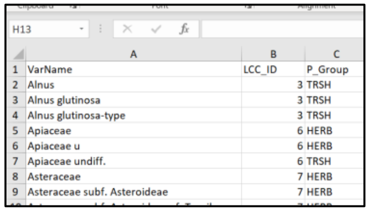


	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
1	Depth (cm)	EPD default (	Cal. yr. BP	Pinus sylvest	Betula	Corylus/Myr	Fraxinus exc	Prunus	Quercus	Sorbus	Tilia cordata	Ulmus	Alnus glutino	Salix	Calluna v
2	0	0	0	82	52	25	1	0	3	0	0	2	9	0	
3	10	295	337.2	38	46	35	0	0	0	0	0	1	15	0	
4	20	590	674.4	63	100	61	0	0	17	0	0	0	20	2	
5	30	885	1011.6	17	101	59	0	0	11	0	0	0	21	2	
6	40	1180	1348.8	46	111	55	0	0	8	0	0	3	32	1	
7	50	1475	1686	46	69	55	2	0	5	1	0	0	31	3	
8	60	1770	2023.2	46	75	77	0	0	19	0	0	6	54	1	
9	70	2065	2360.4	45	47	38	2	0	9	0	0	8	39	0	
10	80	2360	2697.6	69	28	44	0	0	17	0	0	6	30	2	
11	90	2655	3034.8	54	56	38	1	0	8	0	0	6	24	0	
12	100	2950	3372	52	49	49	0	0	12	0	0	3	34	1	
13	110	3245	3709.2	65	41	44	0	0	12	0	0	0	32	0	
14	120	3540	4046.4	71	45	34	1	0	15	0	0	6	12	1	
15	130	3835	4383.6	109	115	69	1	0	21	0	1	15	38	2	
16	135	3983	4552.2	115	49	41	0	0	15	0	0	10	11	2	
17	140	4130	4720.8	102	56	37	0	0	13	0	0	7	22	0	
18	145	4278	4889.4	98	86	70	0	0	24	0	0	21	30	5	
19	150	4425	5058	96	69	62	0	0	7	0	0	13	15	1	
20	155	4848	5514.5	190	68	55	0	0	11	0	0	10	20	0	
21	160	5270	5971	95	81	62	0	0	8	0	0	7	9	0	
22	165	5693	6427.5	174	99	68	0	0	10	1	0	10	7	3	
23	170	6115	6884	106	73	59	0	0	7	0	0	5	9	2	
24	175	6538	7340.5	115	73	63	0	0	2	1	0	7	2	4	
25	180	6960	7797	181	97	88	0	0	8	0	0	8	6	12	

ANFSHEIL ASHIK BREDCOUN CHROISGP CLAIR CLEAT COIREBOG CUTHILL2 DAI ...

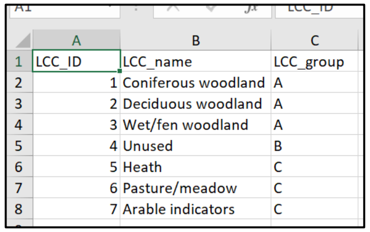
2. **LCC_Info.xlsx**: Excel file with the following worksheets:

LCC_Taxon_List: Lookup table of taxon names and corresponding land cover classification (numeric code, 1-7).



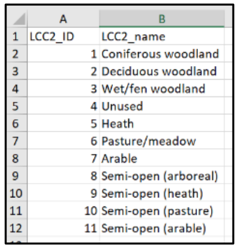
	A	B	C
1	VarName	LCC_ID	P_Group
2	Alnus	3	TRSH
3	Alnus glutinosa	3	TRSH
4	Alnus glutinosa-type	3	TRSH
5	Apiaceae	6	HERB
6	Apiaceae u	6	HERB
7	Apiaceae undiff.	6	TRSH
8	Asteraceae	7	HERB
9	Asteraceae subf. Asteroideae	7	HERB

LCC_Taxon_Classes: Lookup table of LCC taxon class and names (3 woodland, 3 open classes).



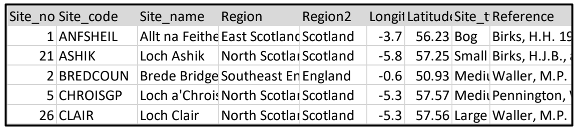
	A	B	C
1	LCC_ID	LCC_name	LCC_group
2	1	Coniferous woodland	A
3	2	Deciduous woodland	A
4	3	Wet/fen woodland	A
5	4	Unused	B
6	5	Heath	C
7	6	Pasture/meadow	C
8	7	Arable indicators	C

LCC2_Assemblage_Classes: Lookup table of LCC2 assemblage classes and names (3 woodland, 3 open, 4 semi-open classes).



	A	B
1	LCC2_ID	LCC2_name
2	1	Coniferous woodland
3	2	Deciduous woodland
4	3	Wet/fen woodland
5	4	Unused
6	5	Heath
7	6	Pasture/meadow
8	7	Arable
9	8	Semi-open (arboreal)
10	9	Semi-open (heath)
11	10	Semi-open (pasture)
12	11	Semi-open (arable)

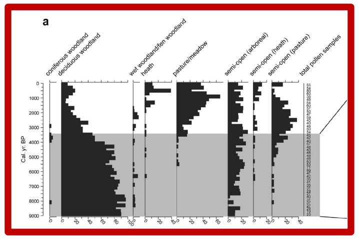
Site_info: Information about each site, incl.Region.



Site_no	Site_code	Site_name	Region	Region2	Longit	Latitud	Site_t	Reference
1	ANFSHEIL	Allt na Feithe	East Scotland	Scotland	-3.7	56.23	Bog	Birks, H.H. 19
21	ASHIK	Loch Ashik	North Scotla	Scotland	-5.8	57.25	Small	Birks, H.J.B.,
2	BREDCOUN	Brede Bridge	Southeast En	England	-0.6	50.93	Mediu	Waller, M.P.
5	CHROISGP	Loch a'Chrois	North Scotla	Scotland	-5.3	57.57	Mediu	Pennington,
26	CLAIR	Loch Clair	North Scotla	Scotland	-5.3	57.56	Large	Waller, M.P.

Land Cover Classification (LCC) method

Step1: Calculate LCC for each site



1. Import data
2. Clean data - remove unwanted columns
3. Convert counts to percentages
4. Allocate each pollen type to an LCC class and sum sqrt-percentages across each class
5. Normalise the sqrt-percent LCC data to 100%
6. Calculate the sum of woodland (A) and open (C) LCC classes
7. Calculate Affinity score as A-C
8. Calculate the LCC class with highest %

Affinity	#	LCC class with max Affinity		#	LCC2_name
Affinity > 20	1	Coniferous woodland	→	1	Coniferous woodland
	2	Deciduous woodland	→	2	Deciduous woodland
	3	Wet/fen woodland	→	3	Wet/fen woodland
	4	Unused		4	Unused
Affinity < 20	5	Heath	→	5	Heath
	6	Pasture/meadow	→	6	Pasture/meadow
	7	Arable indicators	→	7	Arable
Affinity -20 to 20	1	Coniferous woodland	→	8	Semi-open (arboreal)
	2	Deciduous woodland	→	8	Semi-open (arboreal)
	3	Wet/fen woodland	→	8	Semi-open (arboreal)
	5	Heath	→	9	Semi-open (heath)
	6	Pasture/meadow	→	10	Semi-open (pasture)
	7	Arable indicators	→	11	Semi-open (arable)

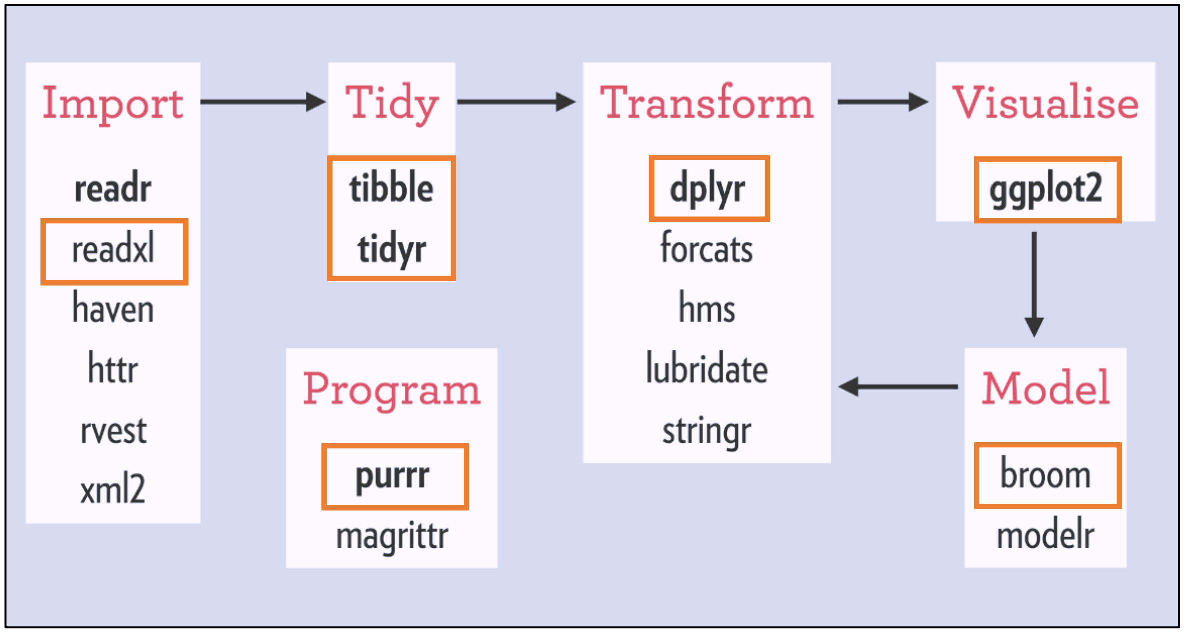
Step2: Aggregate multiple sites

1. Aggregate data from all sites and count the number of levels in each LCC2 class in 200 year time slices (N)
2. Convert N to percentage of each LCC2 class in each time slice

Part 1: Code it in Base R

What is the Tidyverse?

- Collection of R packages designed for data science that share common interface standards, grammar and data structures
- You spend more time on concepts and less sorting out syntax
- Promotes code readability



- Both **general purpose** packages: tibble for data frames, tidyr for tidying, dplyr for transforming and ggplot for visualisation, and **specialised** packages for data import (readxl), dates & time (lubridate, hms), strings (stringr), factors (forcats) plus others.

Core features

1. Uses tibbles rather than data frames
   - refined print method
   - strict about $ subsetting, doesn't like rownames
   - easier to created nested data frames

2. Encourages use of the pipe `%>%`
   - Instead of `summary(lm(y~x, data=df))`
   - Use `df %>% lm(y~x, data=.) %>% summary()`

3. Promotes use of tidy data
   - Every column is a variable
   - Every row is an observation
   - Every cell is a single value

Tidy data

Not tidy !

(because the variable is pollen type and the attributes are taxon and count)

Depth (cm)	Cal. yr. BP	Pinus sylve	Taxus bac	Betula	Betula/Co
132	1514	3	1	40	2
164	1618.5	3	3	33	1
196	1723	3	2	34	2
228	1827.5	4	4	33	1
260	1932	5	3	34	3
268	2143.75	4	3	43	0
276	2355.5	14	2	40	0
284	2567.25	11	1	60	0
292	2779	10	3	54	2

Wide format

Tidy !

(Each column is a variable, pollen counts are described by key/value pairs)

Depth (cm)	Cal. yr. BP	Taxon	Count
132	1514	Pinus sylvestris	3
132	1514	Taxus baccata	1
132	1514	Betula	40
132	1514	Betula/Corylus/Myrica	2
164	1618.5	Pinus sylvestris	3
164	1618.5	Taxus baccata	3
164	1618.5	Betula	33
164	1618.5	Betula/Corylus/Myrica	1
196	1723	Pinus sylvestris	3

Long format

Convert from wide to long with `pivot_longer()`

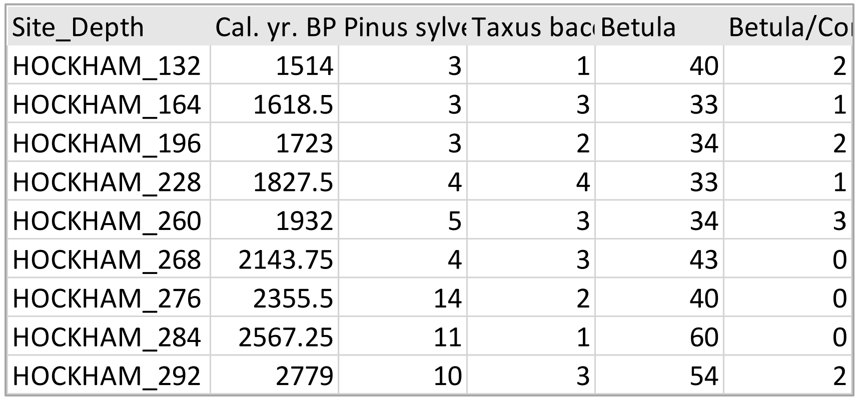
```
df %>% pivot_longer(
   cols=-c(`Depth (cm)`, `Cal. yr. BP`),
   names_to="Taxon", values_to="Count")
```

Convert from long to wide with `pivot_wider()`

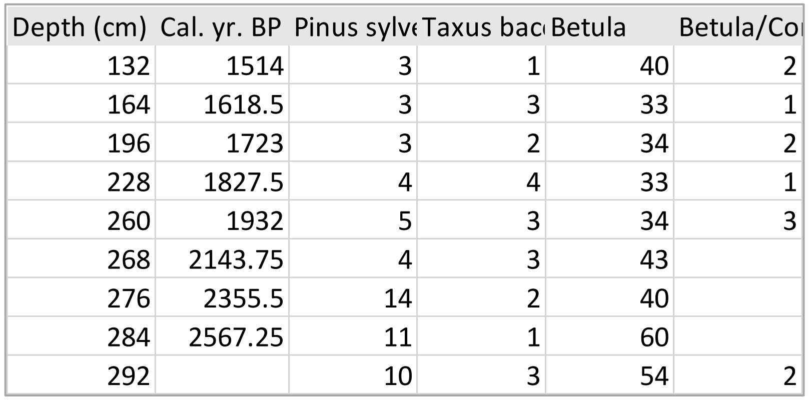
```
df %>% pivot_wider(
   id_cols=c(`Depth (cm)`, `Cal. yr. BP`),
   names_from=Taxon, values_from=Count)
```

In package tidyr

Tidy data?



Site_Depth	Cal. yr. BP	Pinus sylve	Taxus bac	Betula	Betula/Co
HOCKHAM_132	1514	3	1	40	2
HOCKHAM_164	1618.5	3	3	33	1
HOCKHAM_196	1723	3	2	34	2
HOCKHAM_228	1827.5	4	4	33	1
HOCKHAM_260	1932	5	3	34	3
HOCKHAM_268	2143.75	4	3	43	0
HOCKHAM_276	2355.5	14	2	40	0
HOCKHAM_284	2567.25	11	1	60	0
HOCKHAM_292	2779	10	3	54	2



Depth (cm)	Cal. yr. BP	Pinus sylve	Taxus bac	Betula	Betula/Co
132	1514	3	1	40	2
164	1618.5	3	3	33	1
196	1723	3	2	34	2
228	1827.5	4	4	33	1
260	1932	5	3	34	3
268	2143.75	4	3	43	
276	2355.5	14	2	40	
284	2567.25	11	1	60	
292		10	3	54	2

```
df %>% tidyr::separate(Site_Depth,
   into=c("Site_code", "Depth" ))
```

```
# Base R replace in situ
df[is.na(df)] <- 0

# Base R create new df
replace(df, is.na(d), 0)

# Tidy, replace NAs except in cols 1 & 2
df %>% mutate(across(-(1:2),
     ~replace_na(.x, 0)))
```

dplyr functions for data transformation

dplyr function
Base R equivalent

select: select columns (subset)

filter: subsetting rows based on condition (subset)

arrange: sorting (sort, order)

distinct: find unique values (unique)

slice: selecting rows based on position ([])

mutate: create new columns (transform)

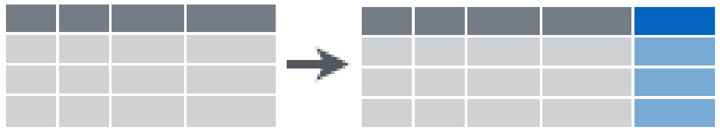
group_by: defining groups of rows to process subsets

summarise: summarise data (optionally by group) (aggregate)

*_join: merging data sets (merge)

bind_rows, bind_cols: combine multiple dfs by row or column (rbind, cbind)

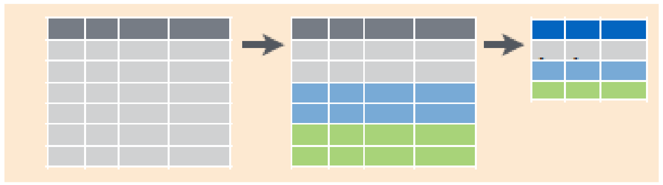
Creating new variables using mutate



Depth (cm)	Cal. yr. BP	Taxon	Count
132	1514	Pinus sylvestris	3
132	1514	Taxus baccata	1
132	1514	Betula	40
132	1514	Betula/Corylus/Myrica	2
164	1618.5	Pinus sylvestris	3
164	1618.5	Taxus baccata	3
164	1618.5	Betula	33
164	1618.5	Betula/Corylus/Myrica	1
196	1723	Pinus sylvestris	3

```
df %>%
   mutate(SQRT_Count=sqrt(Count))
A tibble: 9 x 5
  `Depth (cm)` `Cal. yr. BP` Taxon                 Count SQRT_Count
         <dbl>         <dbl> <chr>                 <dbl>      <dbl>
1          132          1514  Pinus sylvestris          3       1.73
2          132          1514  Taxus baccata             1       1
3          132          1514  Betula                   40       6.32
4          132          1514  Betula/Corylus/Myrica     2       1.41
5          164          1618. Pinus sylvestris          3       1.73
6          164          1618. Taxus baccata             3       1.73
7          164          1618. Betula                   33       5.74
8          164          1618. Betula/Corylus/Myrica     1       1
9          196          1723  Pinus sylvestris          3       1.73
```

Summarising by group



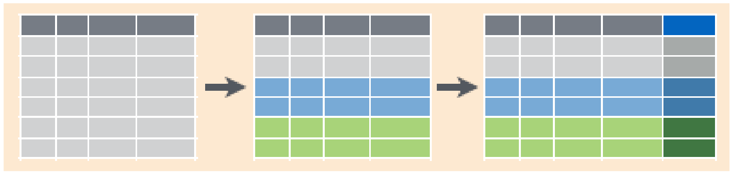
Split -> Apply -> Combine

Depth (cm)	Cal. yr. BP	Taxon	Count
132	1514	Pinus sylvestris	3
132	1514	Taxus baccata	1
132	1514	Betula	40
132	1514	Betula/Corylus/Myrica	2
164	1618.5	Pinus sylvestris	3
164	1618.5	Taxus baccata	3
164	1618.5	Betula	33
164	1618.5	Betula/Corylus/Myrica	1
196	1723	Pinus sylvestris	3

```
df %>% summarise(Total=sum(Count))

          Total
          <dbl>
1            89
```

```
df %>%
  group_by(`Depth (cm)`) %>%
  summarise(Total=sum(Count))

   `Depth (cm)` Total
          <dbl> <dbl>
1           132    46
2           164    40
3           196     3
```

Compute new variables by group



Depth (cm)	Cal. yr. BP	Taxon	Count
132	1514	Pinus sylvestris	3
132	1514	Taxus baccata	1
132	1514	Betula	40
132	1514	Betula/Corylus/Myrica	2
164	1618.5	Pinus sylvestris	3
164	1618.5	Taxus baccata	3
164	1618.5	Betula	33
164	1618.5	Betula/Corylus/Myrica	1
196	1723	Pinus sylvestris	3

```
df %>%
    group_by(`Depth (cm)`) %>%
    mutate(Percent=Count/sum(Count)*100)
```

```
`Depth (cm)` `Cal. yr. BP` Taxon                  Count Percent
        <dbl>         <dbl> <chr>                  <dbl>   <dbl>
1         132          1514  Pinus sylvestris          3    6.52
2         132          1514  Taxus baccata             1    2.17
3         132          1514  Betula                   40   87.0
4         132          1514  Betula/Corylus/Myrica     2    4.35
5         164          1618. Pinus sylvestris          3    7.5
6         164          1618. Taxus baccata             3    7.5
7         164          1618. Betula                   33   82.5
8         164          1618. Betula/Corylus/Myrica     1    2.5
9         196          1723  Pinus sylvestris          3  100
```

Summarising across rows

Lakes	Depth1	Depth2	Depth3
A	30	40	50
B	20	50	40
C	25	10	15
D	45	35	48

```
df %>% mutate(MaxDepth=max(Depth1, Depth2, Depth3))
A tibble: 4 x 5
  Lakes Depth1 Depth2 Depth3 MaxDepth
  <chr>  <dbl>  <dbl>  <dbl>    <dbl>
1 A         30     40     50       50
2 B         20     50     40       50
3 C         25     10     15       50
4 D         45     35     48       50
```

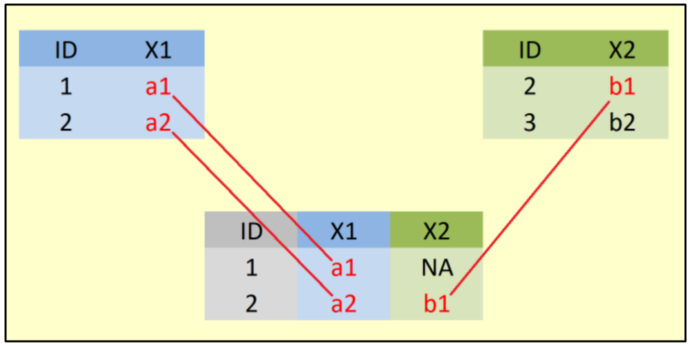
```
df %>%
    rowwise() %>%
    mutate(MaxDepth=max(Depth1, Depth2, Depth3))
# A tibble: 4 x 5
# Rowwise:
  Lakes Depth1 Depth2 Depth3 MaxDepth
  <chr>  <dbl>  <dbl>  <dbl>    <dbl>
1 A         30     40     50       50
2 B         20     50     40       50
3 C         25     10     15       25
4 D         45     35     48       48
```

```
df %>% mutate(MaxDepth = pmax(Depth1, Depth2, Depth3)
```

Merging tables

Join or merge tables using column(s) common to both tables

Left join – all rows from left df, matching rows from right



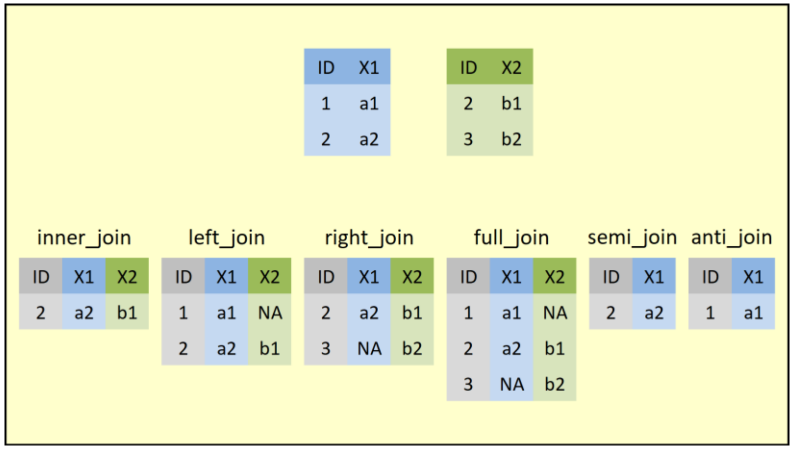
ID	X1
1	a1
2	a2

ID	X2
2	b1
3	b2

ID	X1	X2
1	a1	NA
2	a2	b1

```
Df1 %>% left_join(df2, by='ID')
```

Other join types



ID	X1
1	a1
2	a2

ID	X2
2	b1
3	b2

inner_join

ID	X1	X2
2	a2	b1

left_join

ID	X1	X2
1	a1	NA
2	a2	b1

right_join

ID	X1	X2
2	a2	b1
3	NA	b2

full_join

ID	X1	X2
1	a1	NA
2	a2	b1
3	NA	b2

semi_join

ID	X1
2	a2

anti_join

ID	X1
1	a1

Mutating joins: combine variables from the 2 sources

Filtering joins: use right hand df to filter rows in lh df

R object	Description
Single site data	
poll	original pollen data
poll_long	pollen counts in long format
poll_long_trans	pollen percentages & sqrt in long format
poll_long_LCC	pollen with totals for LCC classes
poll_long_LCC2	pollen with LCC classification for each sample
Combined data (41 sites)	
allpoll_nested	nested list of original pollen data
allpoll_LCC2	pollen with LCC classification for each sample in long format
allpoll_agg	LCC2 classification, aggregated by 200-year time slices
allpoll_rich	palynological richness for all sites / levels, in long format

Part 2: Code it using the Tidyverse

Code comparison: Part 1

Base R

```
del <- colnames(poll) %in% non_pollen
poll <- poll[, !del]
depth_age <- subset(poll, select=c(`Depth (cm)`, `Cal. yr. BP`))
spec <- subset(poll, select=-c(`Depth (cm)`, `Cal. yr. BP`))
colnames(depth_age) <- c("Depth", "Age_BP")
spec_pc <- spec / rowSums(spec) * 100
spec_sqrt <- sqrt(spec_pc)
sel <- match(colnames(spec_sqrt), LCC_taxon_list$VarName)
LCC_code <- LCC_taxon_list$LCC_ID[sel]
spec_LCC <- t (rowsum(t(spec_sqrt), group=LCC_code))
spec_LCC <- data.frame(spec_LCC, check.names=FALSE)
spec_LCC <- spec_LCC / rowSums(spec_LCC) * 100
spec_LCC$A <- rowSums(spec_LCC[, c("1", "2", "3")])
spec_LCC$C <- rowSums(spec_LCC[, c("5", "6", "7")])
spec_LCC$Affinity <- spec_LCC$A - spec_LCC$C
A_nms <- c("1", "2", "3")
C_nms <- c("5", "6", "7")
AC_nms <- c(A_nms, C_nms)
LCC2_ID <- kit::nif(
  spec_LCC$Affinity > 20, as.integer(A_nms[apply(spec_LCC[, A_nms], 1,
                       which.max)]),
  spec_LCC$Affinity < -20, as.integer(C_nms[apply(spec_LCC[, C_nms],
                       1, which.max)]),
  default = ifelse(as.integer(AC_nms[apply(spec_LCC[, AC_nms],
                       1, which.max)]) < 4, 8L,
                 as.integer(AC_nms[apply(spec_LCC[, AC_nms], 1,
                       which.max)]) + 4L)
)
spec_LCC$LCC2_ID <- LCC2_ID
LCC2 <- cbind(depth_age, spec_LCC)
LCC2 <- merge(LCC2, LCC2_assem_classes, by="LCC2_ID",
        all.x=TRUE, sort=FALSE)
LCC2 <- LCC2[order(LCC2$Depth), ]
LCC_names <- LCC_taxon_classes$LCC_name[as.integer(AC_nms)]
```

Tidyverse

```
poll_long <- poll %>%
  rename("Depth"=`Depth (cm)`, "Age_BP"=`Cal. yr. BP`) %>%
  pivot_longer(cols=-c("Depth", "Age_BP"),
               names_to="VarName", values_to="Count") %>%
  filter(Count > 0 & !(VarName %in% non_pollen))

poll_long_trans <- poll_long %>%
  group_by(Depth) %>%
  mutate(Percent = Count / sum(Count) * 100,
         SQRT_PC = sqrt(Percent)) %>%
  ungroup()

poll_long_LCC <- poll_long_trans %>%
  left_join(LCC_taxon_list, by="VarName") %>%
  group_by(Depth, Age_BP, LCC_ID) %>%
  summarise(Percent=sum(Percent),
            SQRT_PC=sum(SQRT_PC),
            .groups="drop_last") %>%
  mutate(Norm_SQRT_PC=SQRT_PC/sum(SQRT_PC)*100) %>%
  ungroup() %>%
  left_join(LCC_taxon_classes, by="LCC_ID")

poll_long_LCC2 <- poll_long_LCC %>%
  group_by(Depth, Age_BP) %>%
  mutate(A=sum(Norm_SQRT_PC[LCC_group=="A"]),
         C=sum(Norm_SQRT_PC[LCC_group=="C"]),
         Affinity=A-C) %>%
  slice_max(Norm_SQRT_PC, n=1, with_ties=FALSE) %>%
  ungroup() %>%
  mutate(LCC2_ID=case_when(
    Affinity >= -20 & Affinity <= 20 & LCC_ID %in% 1:3 ~ 8,
    Affinity >= -20 & Affinity <= 20 & LCC_ID %in% 5:7 ~ LCC_ID + 4,
               TRUE ~ LCC_ID)) %>%
  left_join(LCC2_assem_classes, by="LCC2_ID")
```

Working with multiple datasets – base R

How to apply our LCC code for 1 site to many?

Use a for loop!

```
for (val in sequence) {
    statement
}
```

`sequence` is a vector and **`val`** takes on each of its values during the loop. In each iteration statement is **`evaluated`**.

```
x <- 1:5
for (i in x) {
   print(i)
}
[1] 1
[1] 2
[1] 3
[1] 4
[1] 5
```

Rewriting code as a function

- To apply our LCC function to multiple sites we can use a loop and collate results at each iteration.
- We could include all the LCC code within the loop but this is not good – makes the code more complex, and we should aim to reuse code, not repeat it.
- Encapsulate the code in a function, and call the function from within the loop.

Defining a function:

```
my_fun <- function(arg1, arg2, ...) {
    statements
    return(object)
}
```

Example:

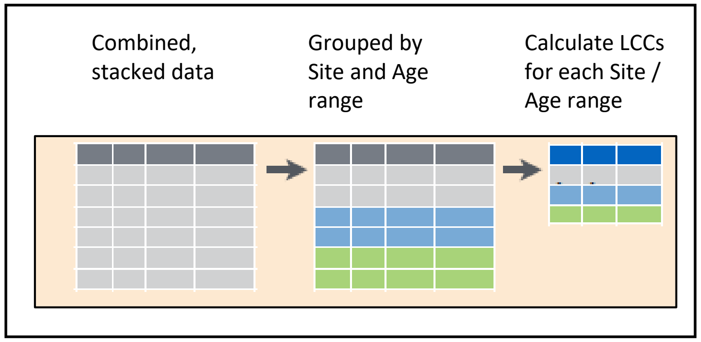
```
my_fun <- function(a, b) {
   c <- a + b
   return(c)
}
my_fun(2, 3)
[1] 5
```

Part 3A: Code to aggregate multiple sites
Base R

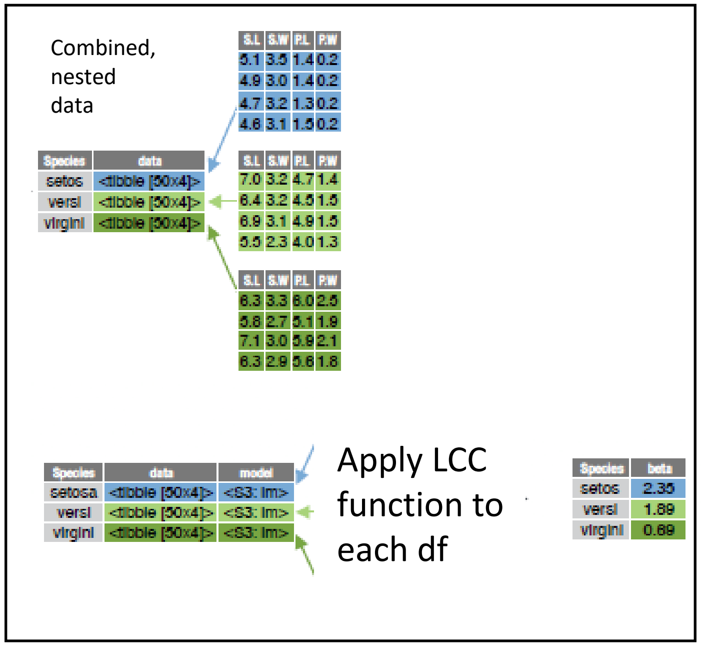
Working with multiple datasets – Tidyverse

Two approaches with Tidy functions that avoid loops and produce more readable, elegant code:

1. Convert each df to long format, and stack, and perform summaries / transformations by grouping of Site and Age/Depth


Combined, stacked data
Grouped by Site and Age range
Calculate LCCs for each Site / Age range

2. Convert to nested data frame that stores data of each site within the cell of a larger organising table. Apply a function to each nested table and collate results.



S.L	S.W	P.L	P.W
5.1	3.5	1.4	0.2
4.9	3.0	1.4	0.2
4.7	3.2	1.3	0.2
4.6	3.1	1.5	0.2

S.L	S.W	P.L	P.W
7.0	3.2	4.7	1.4
6.4	3.2	4.5	1.5
6.9	3.1	4.9	1.5
5.5	2.3	4.0	1.3

S.L	S.W	P.L	P.W
6.3	3.3	6.0	2.5
5.8	2.7	5.1	1.9
7.1	3.0	5.9	2.1
6.3	2.9	5.6	1.8

Species	data
setos	<tibble [50x4]>
versi	<tibble [50x4]>
virgini	<tibble [50x4]>

Species	data	model
setosa	<tibble [50x4]>	<S3: lm>
versi	<tibble [50x4]>	<S3: lm>
virgini	<tibble [50x4]>	<S3: lm>

Species	beta
setos	2.35
versi	1.89
virgini	0.69

Second approach is more flexible as it allows us to apply more complex modelling functions to each nested df.

Figures from tidyverse cheat sheets

Working with nested data using **purrr**

Useful functions:

tidyr::nest(df, cols): creates data frame with cols nested within grouped defined by the non-nesting columns.

tidyr:: unnest(df, cols): unnests a nested column col of a nested data frame.

purrr::map applies a function to each element of a list or vector

Working with nested data frames

Original data frame

```
iris
 A tibble: 150 x 5
   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
          <dbl>       <dbl>        <dbl>       <dbl> <fct>
 1          5.1         3.5          1.4         0.2 setosa
 2          4.9         3            1.4         0.2 setosa
 3          4.7         3.2          1.3         0.2 setosa
 4          4.6         3.1          1.5         0.2 setosa
 5          5           3.6          1.4         0.2 setosa
 6          5.4         3.9          1.7         0.4 setosa
 7          4.6         3.4          1.4         0.3 setosa
 8          5           3.4          1.5         0.2 setosa
 9          4.4         2.9          1.4         0.2 setosa
10          4.9         3.1          1.5         0.1 setosa
```

Nested data frame

```
n_iris <- iris %>% nest(data = -Species)
n_iris
 A tibble: 3 x 2
  Species    data
  <fct>      <list>
1 setosa     <tibble [50 x 4]>
2 versicolor <tibble [50 x 4]>
3 virginica  <tibble [50 x 4]>
```

List-column named "data"

Use map to apply function summary to each nested table

```
n_iris$data %>% map(summary)
[[1]]
  Sepal.Length    Sepal.Width     Petal.Length    Petal.Width
 Min.   :4.300   Min.   :2.300   Min.   :1.000   Min.   :0.100
 1st Qu.:4.800   1st Qu.:3.200   1st Qu.:1.400   1st Qu.:0.200
 Median :5.000   Median :3.400   Median :1.500   Median :0.200
 Mean   :5.006   Mean   :3.428   Mean   :1.462   Mean   :0.246
 3rd Qu.:5.200   3rd Qu.:3.675   3rd Qu.:1.575   3rd Qu.:0.300
 Max.   :5.800   Max.   :4.400   Max.   :1.900   Max.   :0.600
[[2]]
 Sepal.Length    Sepal.Width     Petal.Length   Petal.Width
 Min.   :4.900   Min.   :2.000   Min.   :3.00   Min.   :1.000
```

Working with nested data frames

Apply base R function **summary** to each nested table and add results to original nested df

```
n_iris %>% mutate(summary = map(data, summary))
 A tibble: 3 x 3
  Species    data              summary
  <fct>      <list>            <list>
1 setosa     <tibble [50 x 4]> <table [6 x 4]>
2 versicolor <tibble [50 x 4]> <table [6 x 4]>
3 virginica  <tibble [50 x 4]> <table [6 x 4]>
```

Use formula version to supply arguments to function (in this case **lm**)

```
n_iris %>% mutate(model = map(data, ~lm(Sepal.Width~Sepal.Length, data=.)))
 A tibble: 3 x 3
  Species    data              model
  <fct>      <list>            <list>
1 setosa     <tibble [50 x 4]> <lm>
2 versicolor <tibble [50 x 4]> <lm>
3 virginica  <tibble [50 x 4]> <lm>
```

Use "." to pass the df to the mapped function

Part 3B: Code to aggregate multiple sites using Tidyverse

Code comparison: Part 2

Base R

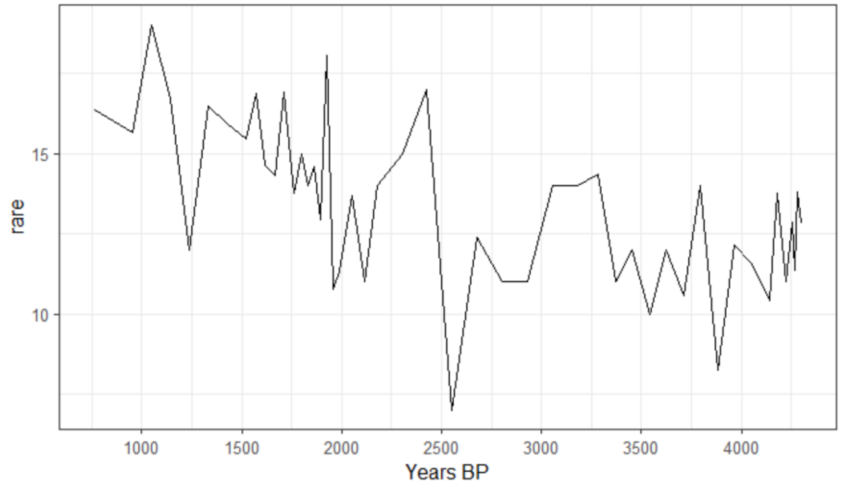
```
LCC2 <- NULL
for (i in sites) {
  print(i)
  d <- read_excel("Woodbridge_et_al_2014_Data.xlsx", sheet=i)
  tmp <- fun_LCC2_base(d, LCC_taxon_list=LCC_taxon_list,
                          LCC_taxon_classes=LCC_taxon_classes)
  tmp <- data.frame(Site_code=i, tmp)
  LCC2 <- rbind(LCC2, tmp)
}

cuts <- seq(0, 20000, by=200)
Age2 <- cut(LCC2$Age_BP, breaks=cuts, labels=FALSE,
        include.lowest=TRUE) * 200 - 200
LCC2_count <- with(LCC2, table(Age2, LCC2_ID))
LCC2_percent <- LCC2_count[, -1] /
        rowSums(LCC2_count[, -1]) * 100
LCC2_percent <- as.data.frame.matrix(LCC2_percent)
LCC2_percent <- data.frame(Age2=as.integer(
               rownames(LCC2_count)),
               LCC2_percent, check.names=FALSE)
LCC2_percent <- subset(LCC2_percent, Age2 <= 9000)
LCC2_names <- LCC2_assem_classes$LCC2_name[
               as.integer(colnames(LCC2_percent)[-1])]
```

Tidyverse

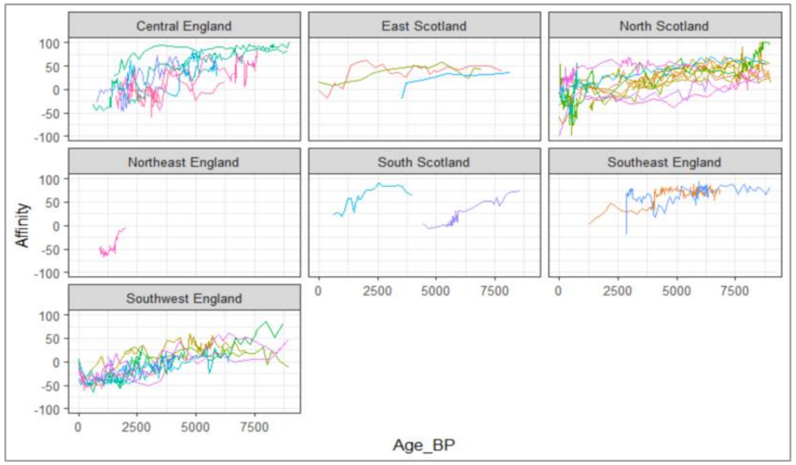
```
allpoll_nested <- tibble(Site_code=names(allpoll_list),
               data=allpoll_list)

allpoll_LCC2 <- allpoll_nested %>%
  mutate(data, data=map(data, ~fun_long_tidy(.x,
        non_pollen=non_pollen))) %>%
  mutate(data, data=map(data, ~fun_LCC2_tidy(.x,
        LCC_taxon_list=LCC_taxon_list,
        LCC_taxon_classes=LCC_taxon_classes,
        LCC2_assem_classes=LCC2_assem_classes))) %>%
  unnest(data)

allpoll_agg <- allpoll_LCC2 %>%
  filter(Age_BP <= 9000) %>%
  mutate(Age2=cut_width(Age_BP, boundary=0, width=200,
        labels=FALSE) * 200 - 200) %>%
  group_by(Age2, LCC2_ID) %>%
  summarise(N=n(), .groups="drop_last") %>%
  mutate(PC=N/sum(N)*100) %>%
  pivot_wider(id_cols=c(Age2), names_from=LCC2_ID, values_from=PC,
        values_fill=0) %>%
  pivot_longer(cols=-c(Age2), names_to="LCC2_ID", values_to="PC") %>%
  mutate(LCC2_ID=as.integer(LCC2_ID)) %>%
  left_join(LCC2_assem_classes, by="LCC2_ID")
```

Modelling with the Tidyverse

Part 1: Calculated palynological richness using rarefaction



Part 2: Calculated affinity scores for each site using purrr::map
(100 = dominated by arboral taxa
-100 = dominated by open taxa)



Very simple question:
How do richness and affinity covary?

Part 4A: Modelling with the Tidyverse

broom for tidying model output

The problem

$$\begin{tikzcd}\boxed{\text{Tidy(ish) data}} \arrow[r] & \boxed{\text{Model}} \arrow[r] & \boxed{\begin{array}{l}\text{Not tidy!}\\ \text{No common format}\end{array}}\end{tikzcd}$$

The broom solution

$$\begin{tikzcd}\boxed{\text{Model}} \arrow[r] & \boxed{\begin{array}{l}\text{Convert to tidy with consistent output format}\\ \text{for multiple model types (currently >130}\\ \text{included, easy to add your own).}\end{array}}\end{tikzcd}$$

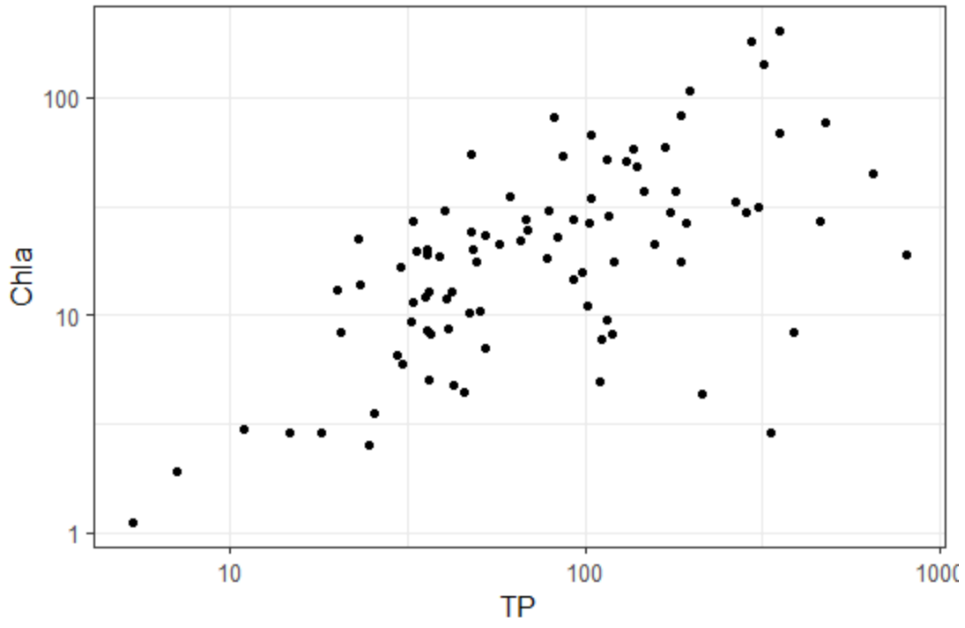
tidy:	tibble that summarises model findings (e.g. coefficients, p-values)
glance:	concise one-row summary (e.g. r-squared, degf)
augment:	columns original data was modelled on (e.g. predictions, residuals)

Part 4B: Modelling with the Tidyverse

UK Lakes water chemistry

Total phosphorus (TP), Chlorophyll-*a* (Chla) and maximum depth (MaxDepth) measurements for 90 UK lakes.

What is the relationship between Chla & TP?



Does this relationship vary with lake depth?

Part 4: Modelling with the Tidyverse

Your turn!