GEOG5022 : Introduction to R II

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In this session you will continue to learn about R as a technology for doing data analysis, again using the Brexit result as a case study. This session will be more practical-focussed (and analytically involved) than the last. You will use R to generate insights into the demographics behind the Brexit vote.

By the end of this session you should be able to:

- generate graphical small multiples using `ggplot2`

- make use of more advanced *tidyr* functions, such as `pivot_longer()`, `pivot_wider()`, for preparing R data frames for charting

- calculate summary statistics over your datasets

- perform a linear regression analysis and use graphics to make decisions about model fit

- learn about permutation-based approaches to statistical testing

Task 1. Explore bivariate relationships using correlation

Figure 1: Scatterplots containing varying extents of correlation coefficient.

You finished the last session by plotting maps of the Leave:Remain vote and of different Census

variables. Visually scanning across the maps, you might have observed that variation in the vote by Local Authority (LA) tends to co-vary with variation in the demographic characteristics of LAs. Any systematic co-variation would be interesting given the popular discourse on the Leave:Remain vote — that Leave represented those people and places structurally left behind by economic change.

Any covariation in voting behaviour and demographics can be analysed more directly through correlation analysis. You will have learnt that the *correlation coefficient* can be used to summarise the strength of linear association between two variables. It is a quantity that ranges from perfect negative correlation (-1) to perfect positive correlation (+1) and can be considered a measure of effect size to the extent that it describes how much of something (correlation in this case) exists.

The code below allows the share of Leave vote and demographic characteristics of LAs to be examined using this quantity (correlation coefficient) as well as visually through a scatterplot (created using `ggplot2`).

```r
# Calculate correlation coefficient of share Leave by degree-educated.
data_gb |>
  st_drop_geometry() |>
  summarise(cor(share_leave, degree_educated))

# Generate scatterplot of share Leave by degree-educated.
data_gb |>
  ggplot(aes(x=share_leave, y=degree_educated)) +
  geom_point(colour="#525252",pch=21, alpha=0.8) +
  theme_bw()
```

Instructions	Add the code block to your R script and Run.
Individual coding task	Try exploring the relationship between share of Leave and different Census variables stored in the `data_gb` data frame.

> ℹ️ Type `?cor()` into the R Console. There are different ways in which the correlation statistic can be calculated. You may have learnt earlier in the semester about robust statistics — statistics that are insensitive to outliers. Try calculating correlation coefficients on `share_leave` and `eu_born` but change the correlation statistic calculated from `method="pearson"` to `method="spearman"`. Can you account for this difference? You may find it useful to generate a scatterplot of this correlation structure. If you're really sad, you might also want to explore the effect of outliers further by playing this guess the correlation game — where you must estimate the amount of correlation displayed in a scatterplot.

Task 2. Generate graphical small multiples

Data analysis relies heavily on comparison. You might ask:

- How do current rates of smoking in a small area **compare** to other small areas with similar

population dynamics?

- When **compared** with previous years, does the increase in smoking rates between 2016-2017 represent a significant shift?

Such comparisons can soon become complex and multifaceted.

One visualization solution for supporting such detailed comparison is small multiples — a set of graphics juxtaposed next to one another, ideally in a meaningful order, such that they can be compared. For a deeper overview, check out Nathan Yau's discussion of small multiples.

`ggplot2` and related packages usefully support small multiples with functions such as `facet_wrap()`. A requirement of calls to these various `facet` functions is Tidy data — that is, where just one observation appears per row. Rows in the the data frame are then split and a separate chart is created for each tranche of data.

To generate small multiples of the scatterplots in the previous section — share of Leave against Census variables — we have to collapse our data frame such that a single row is given to each Local Authority (LA) *and* Census variable — basically we need to make our data frame taller and thinner. The *tidyr* package provides methods that allow these types of operations. In the code block below the `pivot_longer()` method is used to collapse multiple columns into rows. Remember you can check the documentation for this function by typing into the R Console `?pivot_longer`.

```
data_gb |>
  st_drop_geometry() |>
  pivot_longer(cols=c(younger_adults:eu_born), names_to= "expl_var",
values_to="la_prop") |>
  ggplot(aes(x=la_prop, y=share_leave))+
  geom_point(colour="#525252",pch=21)+
  facet_wrap(~expl_var, scales="free")+
  theme_bw()
```

Individual coding task	Use the code above to generate small multiple scatterplots and maps similar to those appearing in Figure 2. Notice that the scatterplots are more efficient, data-rich graphics than those in the code provided above. Think about how to engineer the *ggplot2* grammar in order to generate similarly data-dense graphics.

Figure 2: Scatterplots of share of Leave against key explanatory variables accompanied with a summary of the chart grammar.

data	aes	geom	encoding type
proportion census var	x	point	continuous – position in x
share of Leave	y	point	continuous – position in y
region	colour	point	categorical – colour hue
correlation rank	facet	point	ordinal – positional left-to-right, top-to-bottom

> Whilst one form of *untidy* data is observations distributed amongst columns, the reverse is also common — where observations are duplicated amongst rows. *tidyr* provides a helper function (`pivot_wider()`) that has the reverse effect to `pivot_longer()` — this spreads duplicated observations amongst columns, creating new variables and making the data frame wider.

Task 3. Build, explore and test models

Create a univariate linear model

In the previous task you explored variables that not only correlate with the share of Leave vote but also correspond to phenomena that might help explain variation in the vote. We can try to build models that attempt to quantify this — that allow estimates of the *effects* of variables on the Leave vote.

As suggested visually and by its correlation coefficient (*r. -0.76*), there appears to be a strong negative linear association between the Leave vote and proportion of residents in LAs educated to *degree-level* and above. We can *model* for this relationship and talk about the effect of *degree-educated* (explanatory variable) on the Leave vote (outcome) using linear regression. First, a best fit line representing this linear model can be added to the scatterplot with the command: `geom_smooth(method = "lm", se = FALSE)`. We can also generate an object holding this model with

the `lm()` command.

```
# Add OLS regression line to the scatterplot.
data_gb |>
  ggplot(aes(x=degree_educated, y=share_leave))+
  geom_point(colour="#525252",pch=21)+
  geom_smooth(method = "lm", se = FALSE, colour="#525252")+
  theme_bw()

# Generate a univariate linear model object regressing the Leave vote on the
# degree-educated variable. Store object with name "lm_degree_educated".
lm_degree_educated <- lm(share_leave ~ degree_educated, data = data_gb)

summary(lm_degree_educated)
# output
# Call:
# lm(formula = share_leave ~ degree_educated, data = data_gb)
#
# Residuals:
#     Min      1Q   Median      3Q      Max
# -0.26244 -0.01661  0.01646  0.04377  0.13250
#
# Coefficients:
#                 Estimate Std. Error t value Pr(>|t|)
# (Intercept)      0.79723    0.01227   64.95   <2e-16 ***
# degree_educated -0.93703    0.04148  -22.59   <2e-16 ***
# ---
# Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
#
# Residual standard error: 0.06804 on 378 degrees of freedom
# Multiple R-squared:  0.5745,  Adjusted R-squared:  0.5733
# F-statistic: 510.3 on 1 and 378 DF,  p-value: < 2.2e-16
```

Instructions   Run the code in the block above. You can generate a summary of the model output with the following call: `summary(<model-object>)`.

If you're new to regression and the output of the `summary()` function means nothing to you, don't worry. This is a reminder to say that we'll interpret this output together during the session (and below).

Inspect residuals from the univariate model

The regression coefficients that appear after calls to `summary(<model-object>)` simply describe the regression line — and the regression line tells us, on average, what the Leave vote would be if it were entirely dependent on the proportion of the population educated to degree-level. Since there is a strong negative association between Leave and *degree-educated*, the *slope* of the regression line is negative. The coefficient for *degree-educated* (`Estimate Std. -0.937`) can be interpreted as: a one

unit increase in the *degree-educated* population in a LA has the effect of decreasing the Leave vote by c.0.94 units.

But how successful is this model? To what extent is variation in the Leave vote entirely a function of variation in the proportion of people in LAs educated to *degree-level*? It is possible to quantify how well the model fits the data, and importantly *where* it fits the data, by calculating *residuals*. Residuals are simply the difference between an observed value and the value expected by the model. The coefficient of determination (R-squared), a quantity you may have encountered earlier in the term, is simply the sum of squared residuals divided by the squared sum of total residuals (or variance). It tells us how much of the variation in the outcome can be accounted for by the model. In this case 57% of variation in the observed Leave vote can be explained with variation in the *degree-educated* variable (see output screen).

Ideally residuals should follow a normal distribution and distribute randomly around the regression line, with no obvious systematic structure. One means of testing for normality is to simply generate a histogram on the residual variable, as in the block below.

```
# Extract and store model residuals
data_gb$resids_degrees = as_tibble(resid(lm_degree_educated))$value
# Plot histogram of residuals.
data_gb |>
  ggplot(aes(resids_degrees))+
  geom_histogram()
# Calculate maximum residual value to pin to colour scheme.
max_resid <- data_gb |> pull(resids_degrees) |> abs() |> max()

# Scatterplot coloured by residuals.
data_gb |>
    ggplot(aes(x=degree_educated, y=share_leave, fill=resids_degrees))+
    geom_point(colour="#525252",pch=21)+
    geom_smooth(method = "lm", se = FALSE, colour="#525252")+
    scale_fill_distiller(palette="RdBu", direction=1, limits=c(-max_resid,
max_resid))+
    theme_bw()


# Map coloured by residuals implemented in ggplot.
data_gb |>
  ggplot()+
  geom_sf(aes(fill=resids_degrees), size=.03, colour="#525252")+
  # For Region outlines
  geom_sf(
      data=. %>% group_by(Region) %>% summarise(),
      size=.07, fill="transparent", colour="#525252"
  )+
  coord_sf(datum=NA) +
  scale_fill_distiller(palette="RdBu", direction=1, limits=c(-max_resid, max_resid))+
  theme_bw()
```

As can be seen from the histogram, the distribution of residuals is closer to log normal. Inspecting the scatterplot, there is a group of LAs with observed Leave vote shares much lower than expected by our model. Plotting them spatially, we find that they are overwhelmingly concentrated in Scotland. Given the very clear break with Scotland and the rest of the country, there is a strong argument for developing a separate model for England & Wales. Rather than a smooth spatial process, which we sometimes see in maps of residuals, Scotland is categorically distinct.

Figure 3: Residuals and R2 explained.
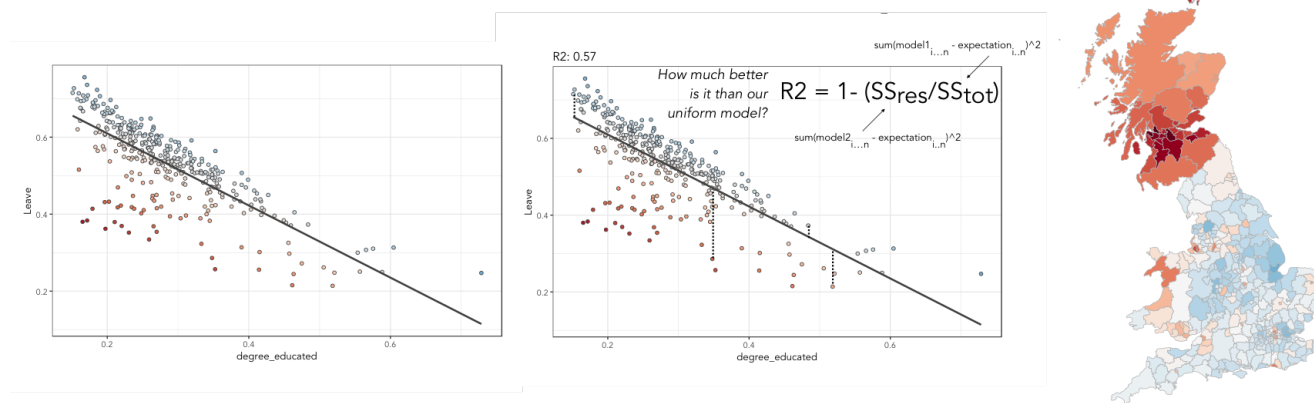
Instructions	Run the code in the block above to generate a scatterplot and map of residuals.
Individual coding task	Generate a new data frame containing data for England & Wales (EW) only. You will need to use the `filter()` function and the `Region` variable to do this. Then create an EW-only linear model regressing *degree-educated* on Leave. Make a note of the R-squared value for the EW-only model. Then generate a map and scatterplot of residuals using a visual grammar similar to that appearing in Figure 3. You may find Task 3 from the previous session useful. How are these residuals distributed around the regression line and across the country?

# Study spatial autocorrelation in residuals

If you successfully completed the *individual coding task* and generated a map and scatterplot of residuals from a linear model regressing *Leave* on *degree-educated*, you will have observed that the residuals distribute reasonably nicely (randomly) around the regression line of the scatterplot. The choropleth map on EW-only data suggests that there may still be spatial structuring to the residuals — patches of red and blue of similar intensities tend to collect together.

Geographers typically test for *spatial autocorrelation* such as this using spatial statistics — you may have already encountered Moran's I, a measure of effect size for spatial autocorrelation. They do so by comparing an observed value of Moran's I against a theoretical distribution that would result under *complete spatial randomness* (CSR) — in this case, this is the assumption that regression residuals distribute around LAs in EW entirely independent of location.

An alternative approach is to perform such a test visually — comparing the observed Choropleth against a set of Choropleths that one might expect to see under CSR (or some other sensible assumption — Beecham et al. 2017). The code below enables such a *graphical inference* test (Wickham et al. 2010).

```r
# Function for generating map line-up test
do_lineup <- function(data) {
  real <- sample(1:9,1)
  for(i in 1:12) {
    if(i==real) {
      data <- cbind(data, data$value)
      colnames(data)[i+1] <- paste("p", i, sep = "")
    }
    else {
      permutation <- sample(data$value,nrow(data))
      data <- cbind(data, permutation)
      colnames(data)[i+1] <- paste("p", i, sep = "")
    }
  }
  # Draw maps
  map <- tm_shape(data) +
    tm_polygons(
      fill=c("p1","p2","p3","p4","p5","p6","p7","p8","p9"),
      fill.scale = tm_scale_continuous(values="brewer.rd_bu"),
      col="gray80",
      lwd=1) +
    tm_layout(legend.show=FALSE, frame=FALSE)
  print(map)
  print(real)
}
# Do line-up on EW model
do_lineup(data_gb |> filter(Region!="Scotland") |> select(geometry,
value=resids_degrees))
```

Figure 4: Map LineUp on residuals from the EW-only model.
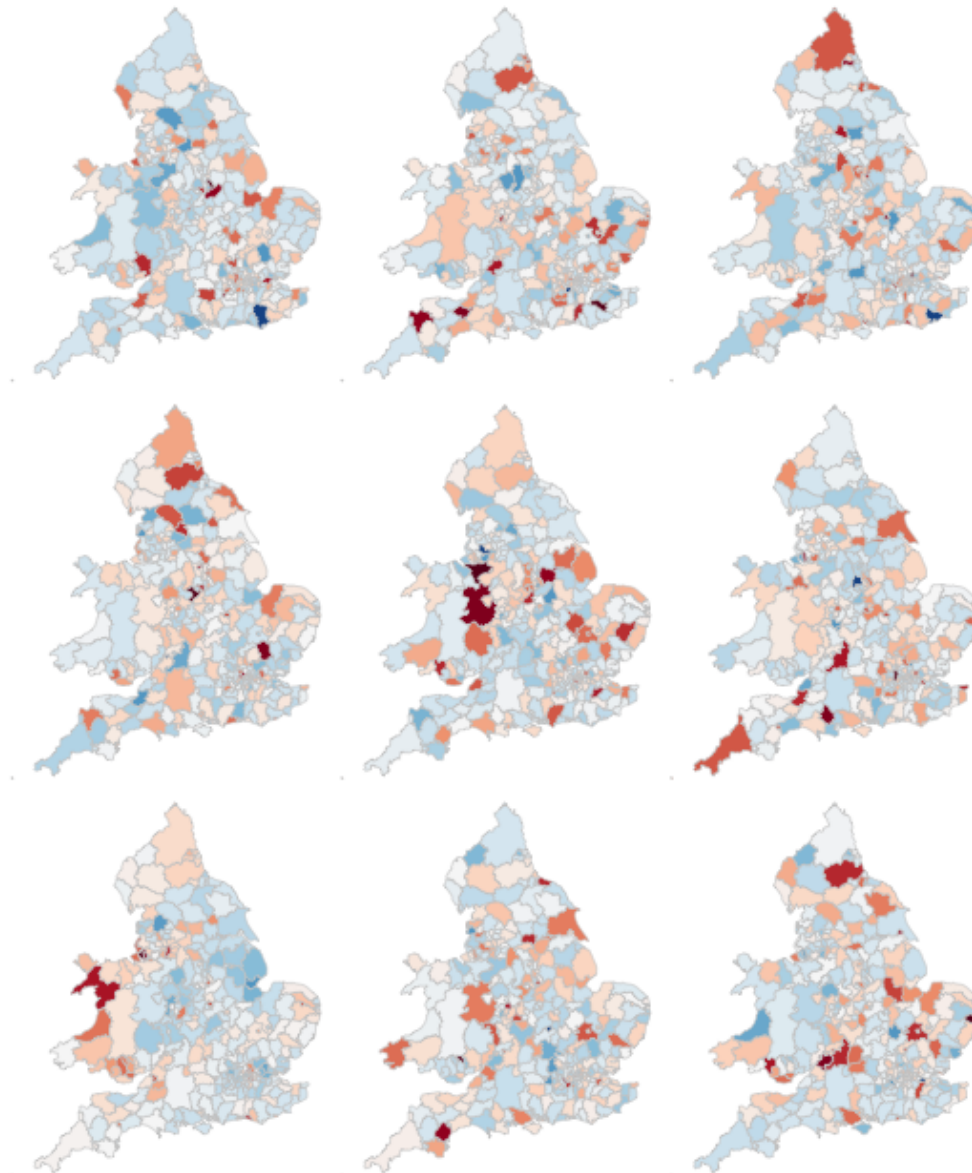
Task 4. Data challenge

Individual coding task
Explore relationships between the Leave vote and the 12 Census variables held in the `data_gb` data frame. You may choose to generate scatterplots showing *share Leave* against these explanatory variables before building separate linear regression models for each Census variable. You may also wish to investigate (perhaps visually initially) wether relationships between *share Leave* and Census variables differ for different parts of the country.

Optional aside for the interested R user

As part of *Task 4* you may have considered fitting univariate models separately for each of the

candidate explanatory variables from the 2011 Census. To help with this, we can use new packages — `purrr` and `broom` — again written under the *tidyverse* design philosophy.

```r
# Generate univariate models separately on each explanatory variable.
univariate_models <- data_gb |>
  st_drop_geometry() |>
  select(c(lad15nm, share_leave), younger_adults:eu_born) |>
  pivot_longer(-c(share_leave, lad15nm), names_to="expl_var", values_to="la_prop") |>
  group_by(expl_var) |>
  nest() %>%
  mutate(model=purrr::map(data, ~lm(share_leave ~ la_prop, data=.)),
         tidy=purrr::map(model, broom::tidy)) |>
  unnest(tidy) |>
  filter(term != "(Intercept)")


# Differentiate sign on regression coefficients when plotting.
b1_sign <- c("#7b3294","#008837")

# Plot regression coefficients from separate univariate models.
univariate_models |>
  mutate(sign=ifelse(estimate>0,"pos","neg")) |>
  ggplot(aes(x=reorder(expl_var,estimate), y=estimate))+
  geom_pointrange(aes(ymin=estimate-2*std.error, ymax = estimate+2*std.error,colour =
factor(sign)),
                  position=position_dodge(.9))+
  geom_hline(aes(yintercept=0))+
  theme_classic()+
  xlab("candidate explanatory variables")+
  ylab("regression coefficient")+
  scale_colour_manual(values=b1_sign)+
  coord_flip()
```

Figure 4: Regression coefficients for univariate models fit separately for candidate explanatory variables.
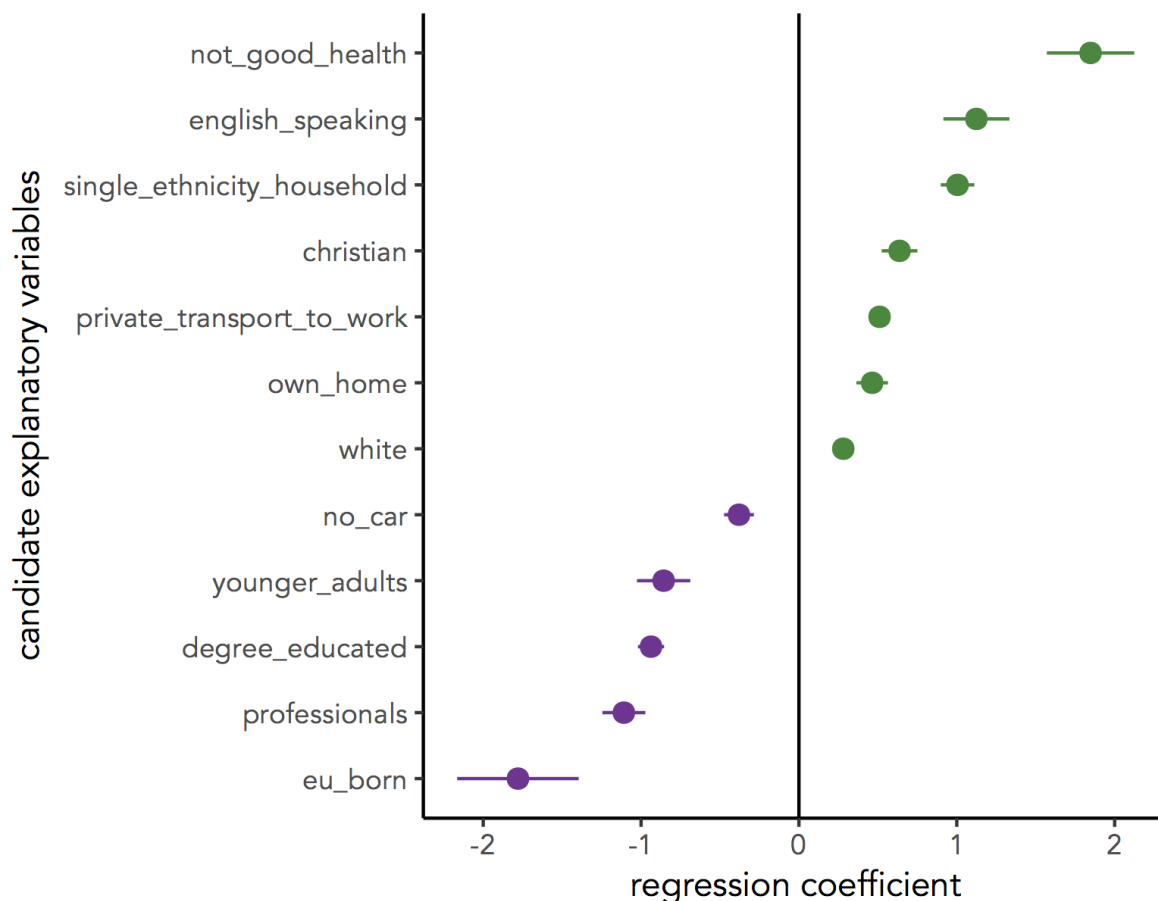
Further reading (non-essential)

- Beecham, R. et al. (2020) Regionally-structured explanations behind area-level populism: An update to recent ecological analyses. PLoS One, 15(3): e0229974. code. doi: 10.1371/journal.pone.0229974.

- Beecham, R. et al. (2018) Locally-varying explanations behind the United Kingdom's vote to leave the United Kingdom. *Journal of Spatial Information Science*, 16: 117-136. code. doi: 10.5311/JOSIS.2018.16.377

- Beecham, R. et al. (2017) Map line-ups: effects of spatial structure on graphical inference. *IEEE Transactions on Visualization & Computer Graphics*, 23(1):391–400. We propose and evaluate through a large crowd-sourced experiment a particular approach to graphical inference testing using maps. Full data analysis code and talk is available at the paper website. doi: 10.1109/TVCG.2016.2598862

- Wickham, H. et al. (2010) Graphical Inference for Infovis. *IEEE Transactions on Visualization and Computer Graphics*, 16(6):973–979. Hadley Wickham's seminal piece on graphical inference — well worth a read, if only for his erudite description of statistical testing and NHST. doi: 10.1109/TVCG.2010.161