

CSSS 569 Visualizing Data and Models

Lab 7: Visualizing Network/Relational Data

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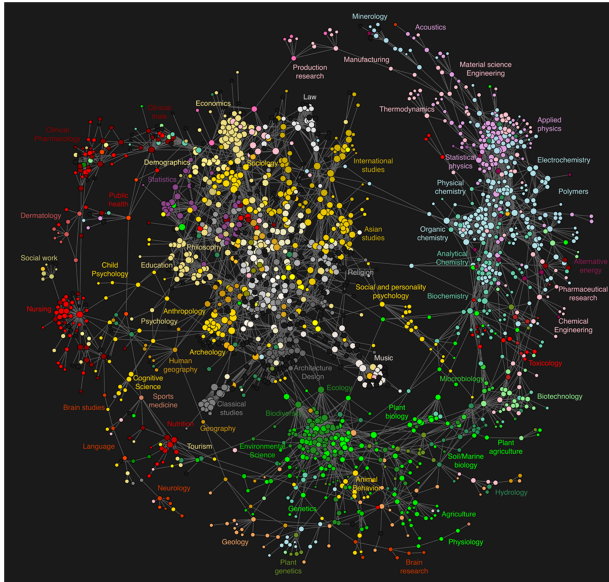
Prerequisite

- ▶ The following packages are required for this lab:

```
packages <- c("tidygraph", "ggraph", "reshape2", "cluster", "circlize")  
install.packages(packages)
```

Introduction: Relational data

- Map of sciences (Bollen et al. 2009)



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- ▶ Network data create many challenges for visualization

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- ▶ Network data create many challenges for visualization
 - ▶ Cursed by high dimensionality

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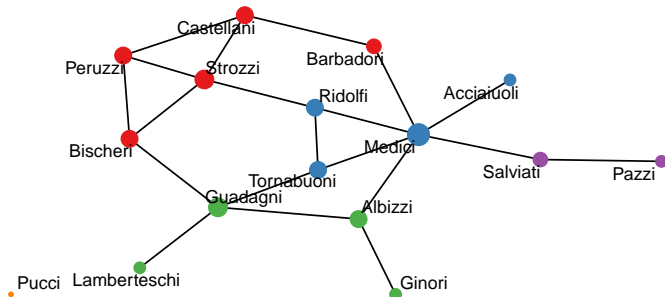
- ▶ Network data create many challenges for visualization
 - ▶ Cursed by high dimensionality
 - ▶ Network diagrams usually result in hairballs or spaghetti balls. . .

Introduction: Relational data

- ▶ Network data create many challenges for visualization
 - ▶ Cursed by high dimensionality
 - ▶ Network diagrams usually result in hairballs or spaghetti balls. . .
 - ▶ The main takeaway of this lab is actually to seek alternative visualization methods whenever possible

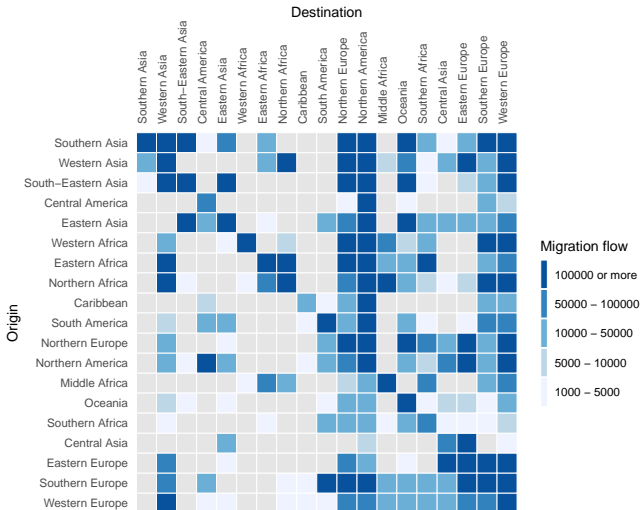
Examples in today's lab

- Florentine families and the rise of Medici: network diagram



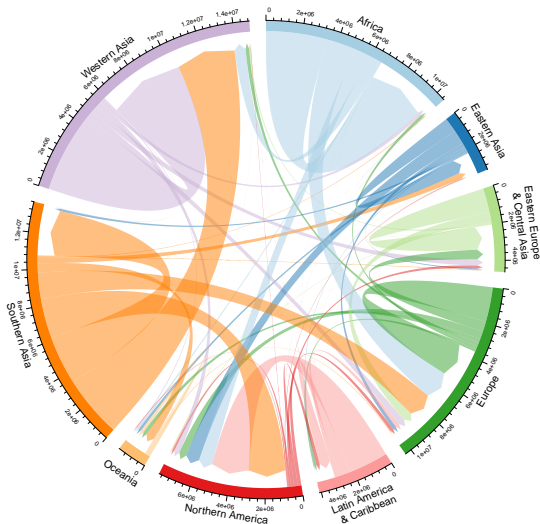
Examples in today's lab

- ▶ Global migration data: heat map
 - ▶ Additional tricks: making NAs explicit; cluster analysis



Examples in today's lab

- Global migration data: chord diagram



Introduction: Relational data

- ▶ The science of networks is incredibly interdisciplinary:

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 - ▶ More specifically, any data whose unit of observation is *dyadic*

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- ▶ In this lab, I want you to think more generically about *relational data*
 - ▶ More specifically, any data whose unit of observation is *dyadic*
 - ▶ Examples: Migration flow data, or import/export data, between countries. . .

Introduction: Relational data

- ▶ Two basic elements:

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 - ▶ Nodes (or vertices)

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 - ▶ Matrix (or adjacency matrix)

Introduction: Relational data

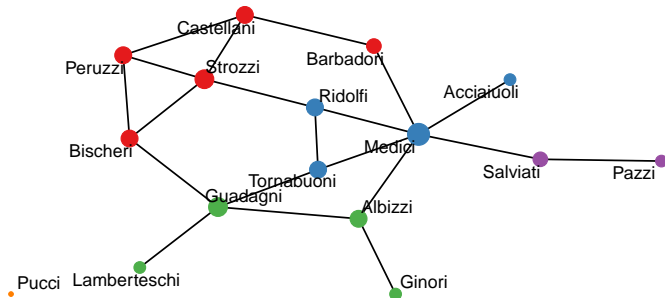
- ▶ Two basic elements:
 - ▶ Nodes (or vertices)
 - ▶ Links (or edges)
- ▶ Two ways to represent relational data:
 - ▶ Matrix (or adjacency matrix)
 - ▶ Long data frame(or edge list)

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- ▶ Two basic elements:
 - ▶ Nodes (or vertices)
 - ▶ Links (or edges)
- ▶ Two ways to represent relational data:
 - ▶ Matrix (or adjacency matrix)
 - ▶ Long data frame(or edge list)
- ▶ Example with the marriage network of Florentine families

Example 1: Florentine families and the rise of Medici

- ▶ Marriage ties between Florentine families in early 15th century
 - ▶ From Padget & Ansell (1993)



Example 1: Florentine families and the rise of Medici

- Represent relational data with matrix (or adjacency matrix)

##	Acciaiuoli	Albizzi	Barbadori	Bischeri	Castellani	Ginori	Guadagni
## Acciaiuoli	0	0	0	0	0	0	0
## Albizzi	0	0	0	0	0	1	1
## Barbadori	0	0	0	0	1	0	0
## Bischeri	0	0	0	0	0	0	1
## Castellani	0	0	1	0	0	0	0
## Ginori	0	1	0	0	0	0	0
## Guadagni	0	1	0	1	0	0	0
## Lamberteschi	0	0	0	0	0	0	1
## Medici	1	1	1	0	0	0	0
## Pazzi	0	0	0	0	0	0	0
## Peruzzi	0	0	0	1	1	0	0
## Pucci	0	0	0	0	0	0	0
## Ridolfi	0	0	0	0	0	0	0
## Salviati	0	0	0	0	0	0	0
## Strozzi	0	0	0	1	1	0	0
## Tornabuoni	0	0	0	0	0	0	1

Example 1: Florentine families and the rise of Medici

- Represent relational data with long data frame(or edge list)

```
##      [,1]      [,2]
## [1,] "Acciaiuoli" "Medici"
## [2,] "Albizzi"   "Ginori"
## [3,] "Albizzi"   "Guadagni"
## [4,] "Albizzi"   "Medici"
## [5,] "Barbadori" "Castellani"
## [6,] "Barbadori" "Medici"
## [7,] "Bischeri"  "Guadagni"
## [8,] "Bischeri"  "Peruzzi"
## [9,] "Bischeri"  "Strozzi"
## [10,] "Castellani" "Peruzzi"
## [11,] "Castellani" "Strozzi"
## [12,] "Guadagni"  "Lamberteschi"
## [13,] "Guadagni"  "Tornabuoni"
## [14,] "Medici"     "Ridolfi"
## [15,] "Medici"     "Salviati"
## [16,] "Medici"     "Tornabuoni"
## [17,] "Pazzi"      "Salviati"
## [18,] "Peruzzi"    "Strozzi"
## [19,] "Ridolfi"    "Strozzi"
## [20,] "Ridolfi"    "Tornabuoni"
```

Example 1: Florentine families and the rise of Medici

```
# install.packages(c("tidygraph", "ggraph"))
library(tidyverse)
library(tidygraph)
library(ggraph)

# Load data (from Chris's website::lab section)
medici <- read.table("data/medici.txt")
medici <- as.matrix(medici)
```


Example 1: Florentine families and the rise of Medici

- First, we have to turn our matrix into a tidygraph object

```
medici_graph <- as_tbl_graph(medici, directed = FALSE)
```

Example 1: Florentine families and the rise of Medici

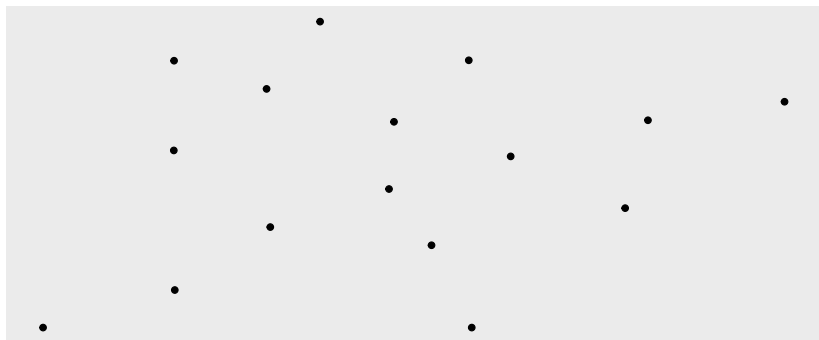
- First, we have to turn our matrix into a tidygraph object

```
## # A tbl_graph: 16 nodes and 20 edges
## #
## # An undirected simple graph with 2 components
## #
## # Node Data: 16 x 1 (active)
##   name
##   <chr>
## 1 Acciaiuoli
## 2 Albizzi
## 3 Barbadori
## 4 Bischeri
## 5 Castellani
## 6 Ginori
## # ... with 10 more rows
## #
## # Edge Data: 20 x 3
##   from    to weight
##   <int> <int> <dbl>
## 1     1     9     1
## 2     2     6     1
## 3     2     7     1
## # ... with 17 more rows
```

Example 1: Florentine families and the rise of Medici

- Visualize network data using ggraph package

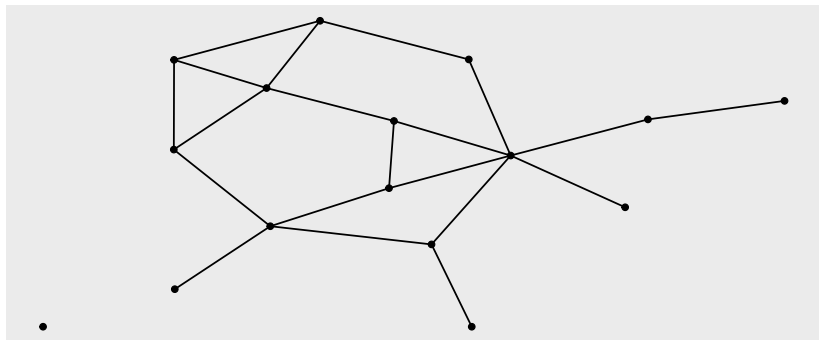
```
ggraph(medici_graph) +  
  geom_node_point()
```



Example 1: Florentine families and the rise of Medici

► Visualize network data using ggraph package

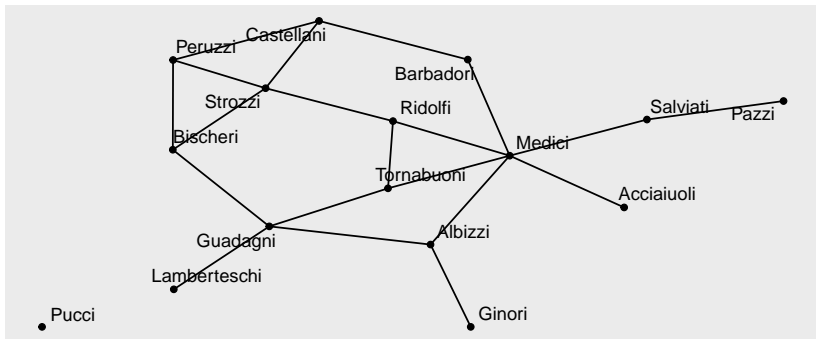
```
ggraph(medici_graph) +  
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  geom_edge_link()
```



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► Visualize network data using ggraph package

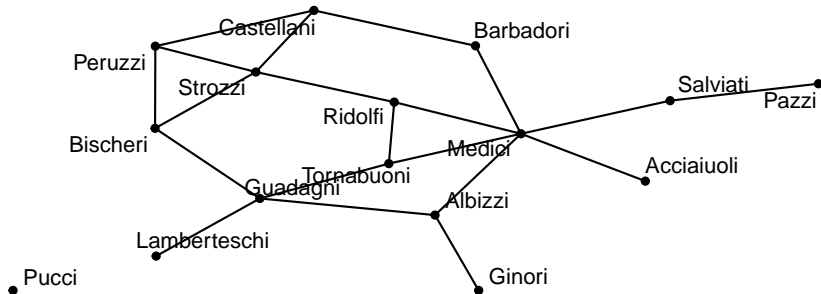
```
ggraph(medici_graph) +  
  geom_node_point() +  
  geom_edge_link() +  
  geom_node_text(aes(label = name), repel = TRUE)
```



Example 1: Florentine families and the rise of Medici

► Visualize network data using ggraph package

```
ggraph(medici_graph) +  
  geom_node_point() +  
  geom_edge_link() +  
  geom_node_text(aes(label = name), repel = TRUE) +  
  theme_graph()
```



Example 1: Florentine families and the rise of Medici

► Create new network measures using tidygraph

```
medici_graph <-  
  medici_graph %>%  
  mutate(  
    # Calculate degree centrality  
    degree = centrality_degree(),  
    # Implement community-detection algorithm  
    community = group_edge_betweenness()  
  )
```

Example 1: Florentine families and the rise of Medici

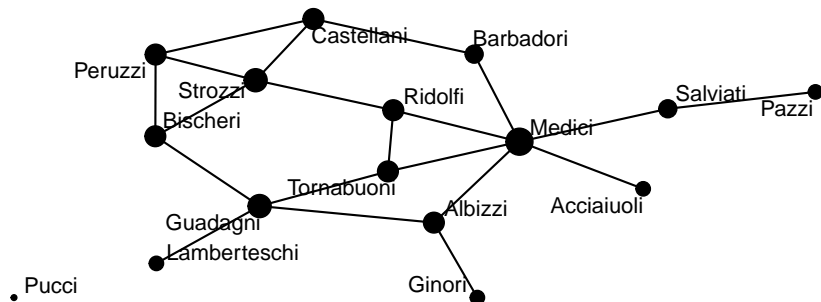
► Create new network measures using tidygraph

```
## # A tbl_graph: 16 nodes and 20 edges
## #
## # An undirected simple graph with 2 components
## #
## # Node Data: 16 x 3 (active)
##   name      degree community
##   <chr>      <dbl>    <int>
## 1 Acciaiuoli      1         2
## 2 Albizzi         3         3
## 3 Barbadori       2         1
## 4 Bischeri        3         1
## 5 Castellani      3         1
## 6 Ginori          1         3
## # ... with 10 more rows
## #
## # Edge Data: 20 x 3
##   from    to weight
##   <int> <int> <dbl>
## 1     1     9     1
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## 3     2     7     1
## # ... with 17 more rows
```


Example 1: Florentine families and the rise of Medici

- Incorporate new network measures into our visualization

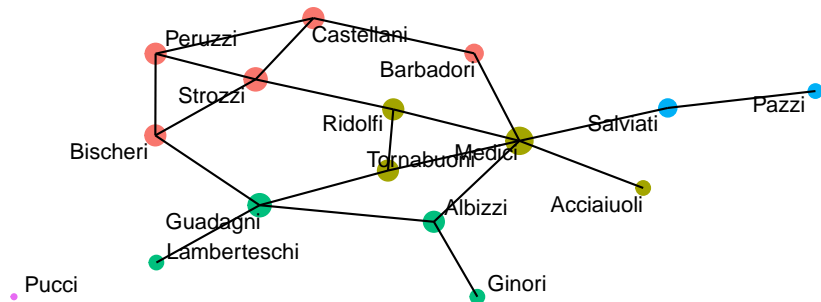
```
ggraph(medici_graph) +  
  geom_node_point(aes(size = degree), show.legend = FALSE) +  
  geom_edge_link() +  
  geom_node_text(aes(label = name), repel = TRUE) +  
  theme_graph()
```



Example 1: Florentine families and the rise of Medici

- Incorporate new network measures into our visualization

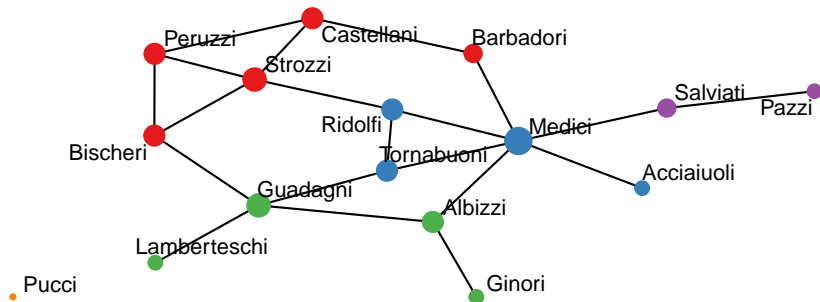
```
ggraph(medici_graph) +  
  geom_node_point(aes(size = degree, color = factor(community)),  
    show.legend = FALSE) +  
  geom_edge_link() +  
  geom_node_text(aes(label = name), repel = TRUE) +  
  theme_graph()
```



Example 1: Florentine families and the rise of Medici

- Incorporate new network measures into our visualization

```
ggraph(medici_graph) +  
  geom_edge_link() +  
  geom_node_point(aes(size = degree, color = factor(community)),  
    show.legend = FALSE) +  
  geom_node_text(aes(label = name), repel = TRUE) +  
  scale_color_brewer(palette = "Set1") +  
  theme_graph()
```



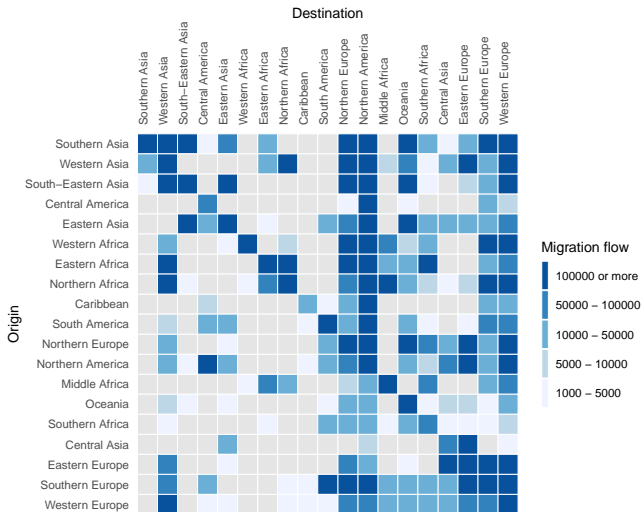
Example 1: Florentine families and the rise of Medici

► Save the output

```
width = 7  
ggsave("output/medici.pdf", width = width, height = width/2)
```

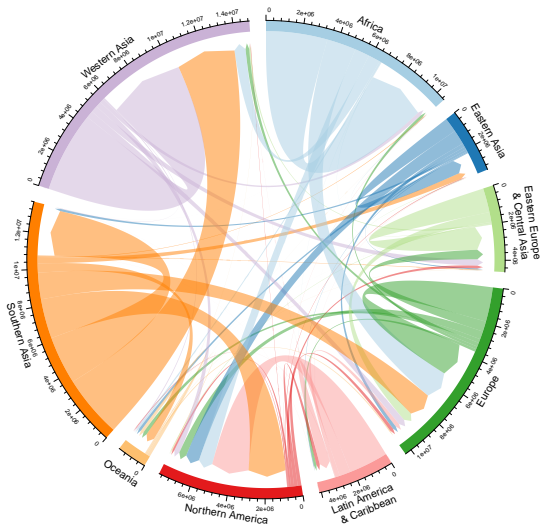
Example 2: Global migration flow data

- ▶ Heat map



Example 2: Global migration flow data

► Chord diagram



Example 2: Global migration flow data

► Original data are from Abel (2018)

```
migrat2010 <- read_csv("data/migrat2010.csv")
```

```
head(migrat2010)
```

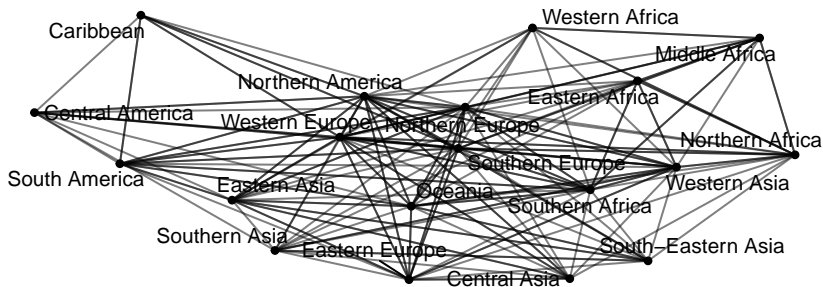
```
## # A tibble: 6 x 3
##   origRegion destRegion      flow
##   <chr>      <chr>      <dbl>
## 1 Caribbean Caribbean    40506
## 2 Caribbean Central America    8183
## 3 Caribbean Northern America 533052
## 4 Caribbean Northern Europe   15584
## 5 Caribbean South America    3264
## 6 Caribbean Southern Europe  21711
```

Example 2: Global migration flow data

- Network diagram doesn't work well here...

```
migrat2010_graph <- as_tbl_graph(migrat2010)
```

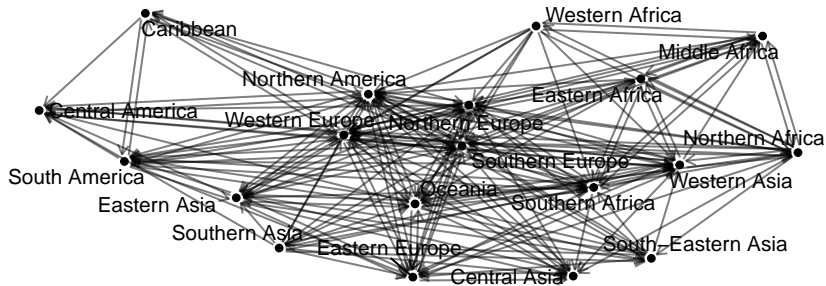
```
ggraph(migrat2010_graph)+  
  geom_edge_link(alpha = 0.5) +  
  geom_node_point() +  
  geom_node_text(aes(label = name), repel = TRUE) +  
  theme_graph()
```



Example 2: Global migration flow data

- Worse still, the data is actually bidirectional, which means you need to visualize **two edges** for each dyadic pair

```
ggraph(migrat2010_graph)+  
  geom_edge_parallel(start_cap = circle(1.25, 'mm'),  
                    end_cap = circle(1.25, 'mm'),  
                    arrow = arrow(length = unit(2, 'mm')),  
                    sep = unit(1.25, 'mm'), alpha = 0.5) +  
  geom_node_point() +  
  geom_node_text(aes(label = name), repel = TRUE) +  
  theme_graph()
```



Example 2: Global migration flow data

- ▶ Two alternative visualization methods:

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- ▶ Two alternative visualization methods:
 - ▶ Heatmap

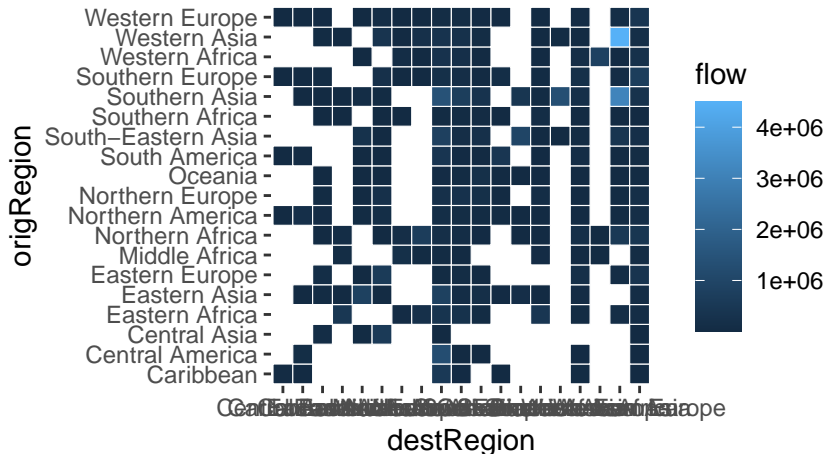
Example 2: Global migration flow data

- ▶ Two alternative visualization methods:
 - ▶ Heatmap
 - ▶ Chord diagram

Example 2: Global migration flow data :: Heatmap

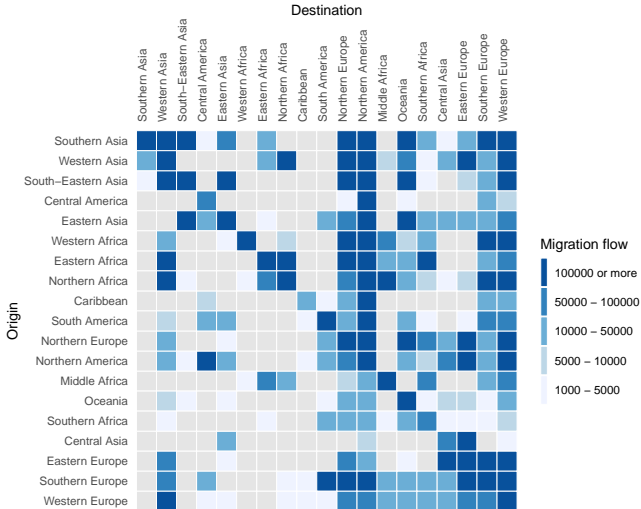
- Like what we did in lab 4 using `geom_tile()`

```
migrat2010 %>%  
  ggplot(aes(y = origRegion, x = destRegion, fill = flow)) +  
  geom_tile(color = "white", size = 0.2) +  
  coord_equal() +  
  theme(panel.background = element_blank())
```



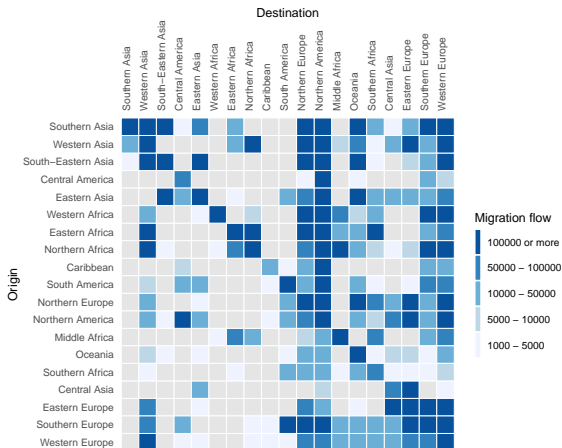
Example 2: Global migration flow data :: Heatmap

- ▶ How can we improve the heat map?
 - ▶ Try to replicate the following example:



Example 2: Global migration flow data :: Heatmap

- ▶ Main tasks:
 - ▶ Make NA values explicit
 - ▶ Turn flow into a categorical variable
 - ▶ Cluster analysis and sorting



Example 2: Global migration flow data :: Heatmap

- ▶ To make NA values explicit, use `expand()` and `left_join()` from `tidyverse`

```
migrat2010 %>%  
  expand(origRegion, destRegion) %>%  
  head()
```

```
## # A tibble: 6 x 2  
##   origRegion destRegion  
##   <chr>      <chr>  
## 1 Caribbean Caribbean  
## 2 Caribbean Central America  
## 3 Caribbean Central Asia  
## 4 Caribbean Eastern Africa  
## 5 Caribbean Eastern Asia  
## 6 Caribbean Eastern Europe
```


Example 2: Global migration flow data :: Heatmap

- ▶ To make NA values explicit, use `expand()` and `left_join()` from `tidyverse`
 - ▶ `expand()` creates all unique combinations of two (or more) variables

```
migrat2010 %>%  
  expand(origRegion, destRegion) %>%  
  head()
```

```
## # A tibble: 6 x 2  
##   origRegion destRegion  
##   <chr>      <chr>  
## 1 Caribbean Caribbean  
## 2 Caribbean Central America  
## 3 Caribbean Central Asia  
## 4 Caribbean Eastern Africa  
## 5 Caribbean Eastern Asia  
## 6 Caribbean Eastern Europe
```

Example 2: Global migration flow data :: Heatmap

- To make NA values explicit, use `expand()` and `left_join()` from `tidyverse`

```
migrat2010 <-  
  migrat2010 %>%  
    expand(origRegion, destRegion) %>%  
    left_join(migrat2010, by = c("origRegion", "destRegion"))  
  
head(migrat2010)
```

```
## # A tibble: 6 x 3  
##   origRegion destRegion      flow  
##   <chr>      <chr>      <dbl>  
## 1 Caribbean Caribbean    40506  
## 2 Caribbean Central America  8183  
## 3 Caribbean Central Asia      NA  
## 4 Caribbean Eastern Africa    NA  
## 5 Caribbean Eastern Asia      NA  
## 6 Caribbean Eastern Europe    NA
```

Example 2: Global migration flow data :: Heatmap

- ▶ To make NA values explicit, use `expand()` and `left_join()` from `tidyverse`
 - ▶ Use the result from `expand()` as a template for `left_join()`

```
migrat2010 <-  
  migrat2010 %>%  
    expand(origRegion, destRegion) %>%  
    left_join(migrat2010, by = c("origRegion", "destRegion"))  
  
head(migrat2010)
```

```
## # A tibble: 6 x 3  
##   origRegion destRegion      flow  
##   <chr>      <chr>      <dbl>  
## 1 Caribbean Caribbean    40506  
## 2 Caribbean Central America  8183  
## 3 Caribbean Central Asia      NA  
## 4 Caribbean Eastern Africa    NA  
## 5 Caribbean Eastern Asia      NA  
## 6 Caribbean Eastern Europe    NA
```

Example 2: Global migration flow data :: Heatmap

► Turn flow into a categorical variable

```
quantile(migrat2010$flow, na.rm = TRUE)
```

```
##           0%           25%           50%           75%          100%  
##    1058.00    9147.75   36104.00  153035.50 4497527.00
```

```
# Create breaks and labels
```

```
breaks <- c(1000, 5000, 10000, 50000, 100000, Inf)  
labels <- c("1000-5000", "5000-10000", "10000-50000",  
           "50000-100000", ">100000")
```

```
# Create a new variable `flowCat`
```

```
migrat2010 <-  
  migrat2010 %>%  
  mutate(flowCat = cut(flow, breaks, labels))
```

Example 2: Global migration flow data :: Heatmap

- Turn flow into a categorical variable

```
head(migrat2010)
```

```
## # A tibble: 6 x 4
##   origRegion destRegion      flow flowCat
##   <chr>      <chr>      <dbl> <fct>
## 1 Caribbean Caribbean  40506 10000-50000
## 2 Caribbean Central America  8183 5000-10000
## 3 Caribbean Central Asia      NA <NA>
## 4 Caribbean Eastern Africa      NA <NA>
## 5 Caribbean Eastern Asia      NA <NA>
## 6 Caribbean Eastern Europe      NA <NA>
```

Example 2: Global migration flow data :: Heatmap

► Clustering analysis and sorting

```
# Load packages
library(reshape2)
library(cluster)

# Convert long data frame into a full matrix
migrat2010_matrix <-
  migrat2010 %>%
  reshape2::acast(origRegion ~ destRegion, value.var = "flow", fill = 0)
```

Example 2: Global migration flow data :: Heatmap

► Clustering analysis and sorting

```
# Convert long data frame into a full matrix
```

```
print(migrat2010_matrix[1:4, 1:4])
```

##	Caribbean	Central America	Central Asia	Eastern Africa
## Caribbean	40506	8183	0	0
## Central America	0	99171	0	0
## Central Asia	0	0	77252	0
## Eastern Africa	0	0	0	444352

Example 2: Global migration flow data :: Heatmap

► Cluster analysis and sorting

```
migrat2010_hclust <-  
  dist(migrat2010_matrix) %>%  
  hclust(method = "ward.D") # Several other methods are available  
  
countryOrder <- migrat2010_hclust$order  
print(countryOrder)
```

```
## [1] 15 18 13 2 5 17 4 8 1 12 10 9 7 11 14 3 6 16 19
```


Example 2: Global migration flow data :: Heatmap

► Clustering analysis and sorting

```
# Sort the countries using the order produced by cluster analysis
```

```
countryLevels <- row.names(migrat2010_matrix)[countryOrder]
```

```
print(countryLevels)
```

```
## [1] "Southern Asia"      "Western Asia"      "South-Eastern Asia"  
## [4] "Central America"   "Eastern Asia"      "Western Africa"  
## [7] "Eastern Africa"    "Northern Africa"   "Caribbean"  
## [10] "South America"     "Northern Europe"   "Northern America"  
## [13] "Middle Africa"     "Oceania"           "Southern Africa"  
## [16] "Central Asia"      "Eastern Europe"    "Southern Europe"  
## [19] "Western Europe"
```

Example 2: Global migration flow data :: Heatmap

► Clustering analysis and sorting

```
# Re-level `origRegion` and `destRegion` according to the level  
migrat2010 <- migrat2010 %>%  
  mutate(  
    origRegion = factor(origRegion, levels = rev(countryLevels)),  
    destRegion = factor(destRegion, levels = countryLevels)  
  )
```

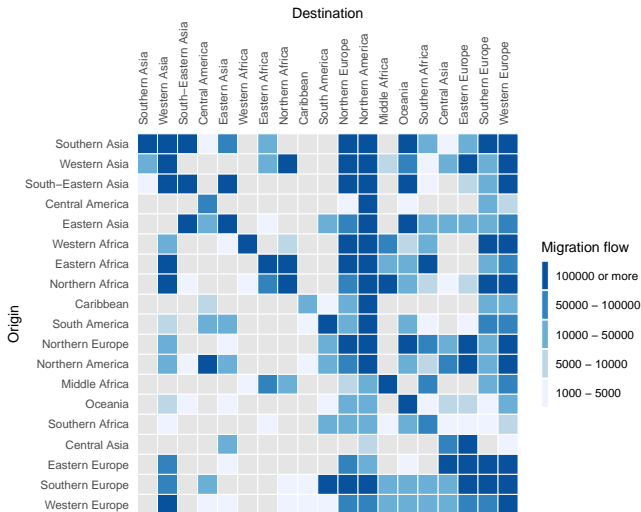
Example 2: Global migration flow data :: Heatmap

► Visualize the heat map again:

```
migrat2010 %>%  
  ggplot(aes(y = origRegion, x = destRegion, fill = flowCat)) +  
  geom_tile(color = "white", size = 0.2) +  
  # Scale fill values with "Blues" palette and "grey90" for NAs  
  scale_fill_brewer(palette = "Blues", na.value = "grey90",  
                    breaks = rev(labels)) +  
  # Put x-axis labels on top  
  scale_x_discrete(position = "top") +  
  coord_equal() +  
  theme(panel.background = element_blank(),  
        axis.ticks.x = element_blank(),  
        axis.ticks.y = element_blank(),  
        # Rotate and align x-axis labels  
        axis.text.x.top = element_text(angle = 90, hjust = 0),  
        legend.key.height = grid::unit(0.8, "cm"),  
        legend.key.width = grid::unit(0.2, "cm")  
  ) +  
  guides(fill = guide_legend(title = "Migration flow")) +  
  labs(y = "Origin", x = "Destination")
```

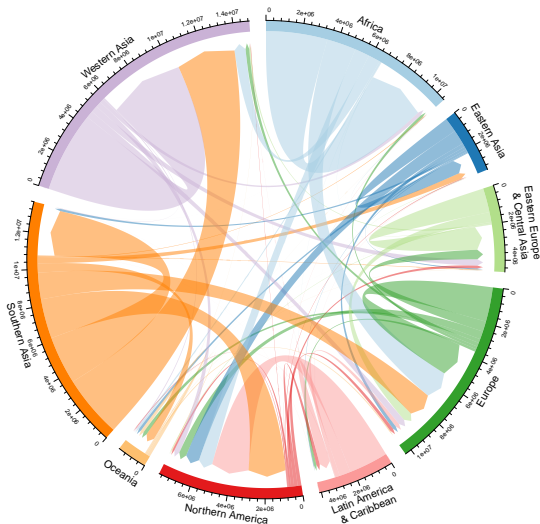
Example 2: Global migration flow data :: Heatmap

- Visualize the heat map again:



Example 2: Global migration flow data :: Chord diagram

- ▶ Chord diagram has become growingly popular



Example 2: Global migration flow data :: Chord diagram

- ▶ We'll use the `circlize` package: full documentation [here](#)

```
library(circlize)
```

Example 2: Global migration flow data :: Chord diagram

- ▶ But first, we have to aggregate regions and further reduce the dimensionality

```
# Create vectors of countries to be aggregated
Europe <- c("Southern Europe", "Western Europe", "Northern Europe")
EECA <- c("Eastern Europe", "Central Asia")
Africa <- c("Eastern Africa", "Middle Africa", "Northern Africa",
            "Southern Africa", "Western Africa")
LACarib <- c("Central America", "South America", "Caribbean")
SAsia <- c("South-Eastern Asia", "Southern Asia")

# Use mutate() and across() to recode
# `origRegion` and `destRegion` simultaneously
migrat2010 <-
  migrat2010 %>%
    mutate(across(c(origRegion, destRegion),
      ~ case_when(
        .x %in% Europe ~ "Europe",
        .x %in% EECA ~ "Eastern Europe \n& Central Asia",
        .x %in% Africa ~ "Africa",
        .x %in% LACarib ~ "Latin America \n& Caribbean",
        .x %in% SAsia ~ "Southern Asia",
        TRUE ~ as.character(.x)
      )
    )
  )
```

Example 2: Global migration flow data :: Chord diagram

- But first, we have to aggregate regions and further reduce the dimensionality

```
# Collapse (sum) flow values according by newly aggregated regions
```

```
migrat2010 <- migrat2010 %>%  
  group_by(origRegion, destRegion) %>%  
  summarize(flowTotal = sum(flow, na.rm = TRUE)) %>%  
  ungroup()
```

```
## `summarise()` has grouped output by 'origRegion'. You can override using the
```

```
head(migrat2010)
```

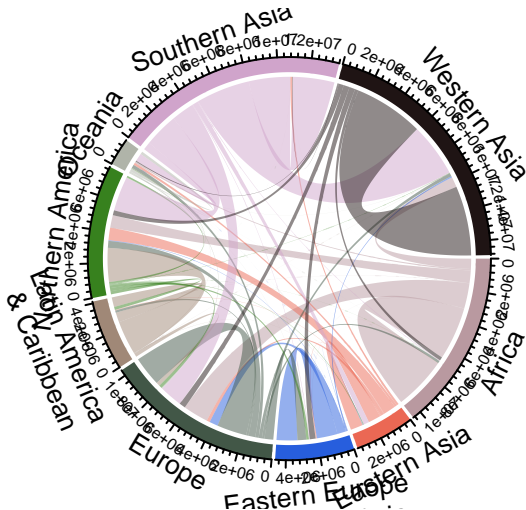
```
## # A tibble: 6 x 3
```

##	origRegion	destRegion	flowTotal
##	<chr>	<chr>	<dbl>
## 1	Africa	"Africa"	3412806
## 2	Africa	"Eastern Asia"	1083
## 3	Africa	"Eastern Europe \n& Central Asia"	14504
## 4	Africa	"Europe"	1634143
## 5	Africa	"Latin America \n& Caribbean"	10694
## 6	Africa	"Northern America"	813775

Example 2: Global migration flow data :: Chord diagram

► Basic chord diagram

```
chordDiagram(migrat2010)
```



Example 2: Global migration flow data :: Chord diagram

► Advanced chord diagram settings (based on Abel's [GitHub](#))

```
# Setting parameters
circos.clear()
circos.par(
  start.degree = 90,           # Start at 12 o'clock
  gap.degree = 4,             # Increase gaps between sectors
  track.margin = c(-0.1, 0.1), # Narrow the track margin
  points.overflow.warning = FALSE # Subdue warning messages
)
par(mar = rep(0, 4))          # no margins in the plot
```

Example 2: Global migration flow data :: Chord diagram

► Advanced chord diagram settings (based on Abel's [GitHub](#))

```
# Get nice colors
colors <- RColorBrewer::brewer.pal(9, "Paired")

# More advanced settings in `chordDiagram()`
chordDiagram(migrat2010,
  # Set colors
  grid.col = colors,
  # Indicate chords are directional
  directional = 1,
  # Directionality is illustrated by arrows and height differences
  direction.type = c("arrows", "diffHeight"),
  # Set height difference
  diffHeight = -0.04,
  # Use big arrows
  link.arr.type = "big.arrow",
  # Sort the chords and plot the smallest chords first
  link.sort = TRUE, link.largest.ontop = TRUE,
)

# Save the output
dev.copy2pdf(file = "output/migratChord.pdf", height = 8, width = 8)
```

Example 2: Global migration flow data :: Chord diagram

► Final output

