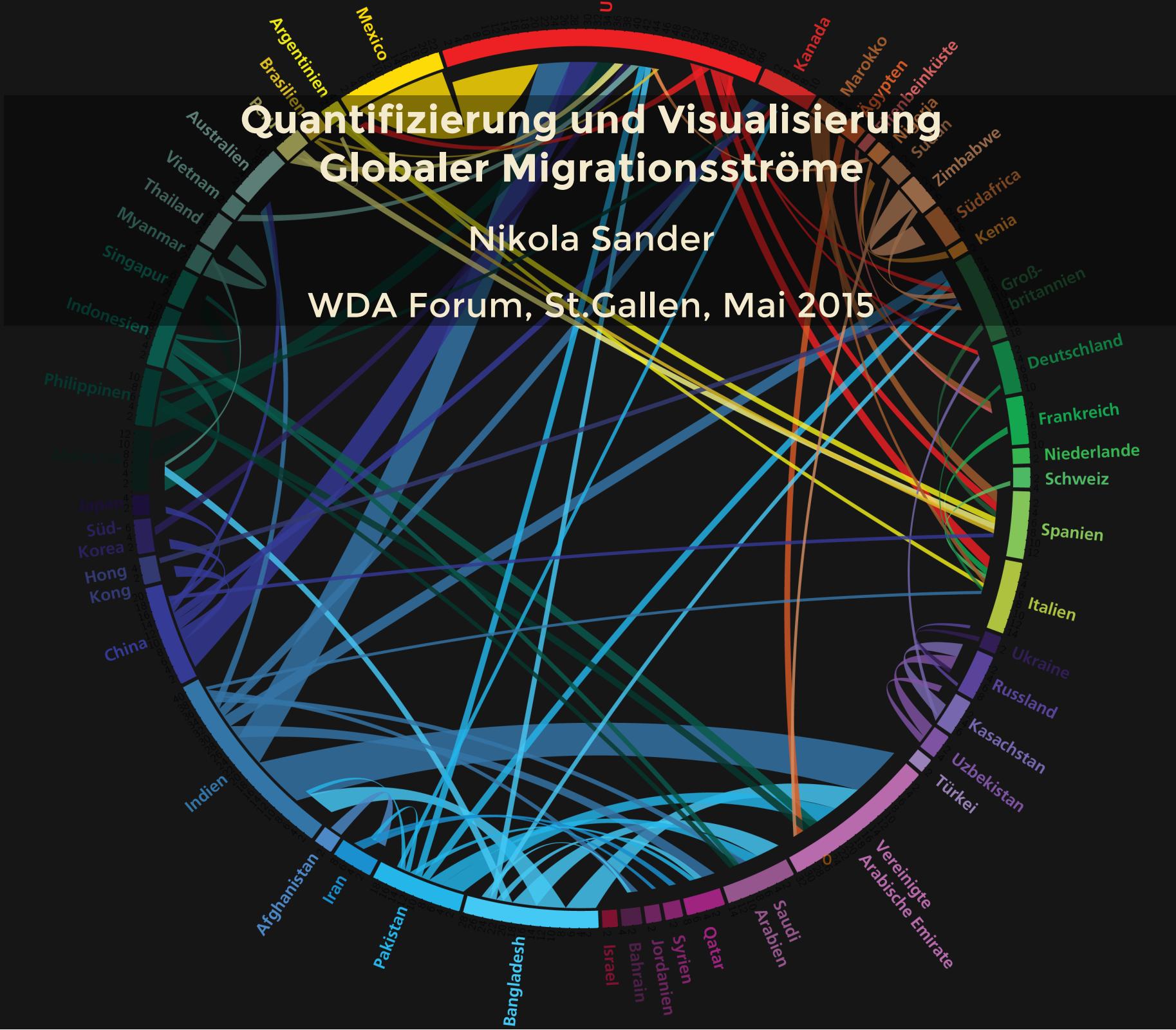


Quantifizierung und Visualisierung Globaler Migrationsströme

Nikola Sander

WDA Forum, St.Gallen, Mai 2015



Motive für Wanderungen

1. wirtschaftlich (z.B. Chancen am Arbeitsmarkt)
2. familiär (z.B. Heirat, Scheidung)
3. Wohnungsmarkt (z.B. größere Wohnung)
4. Bildung (z.B. Studium)
5. politisch (z.B. Demokratie)
6. sozial (z.B. Meinungsfreiheit)

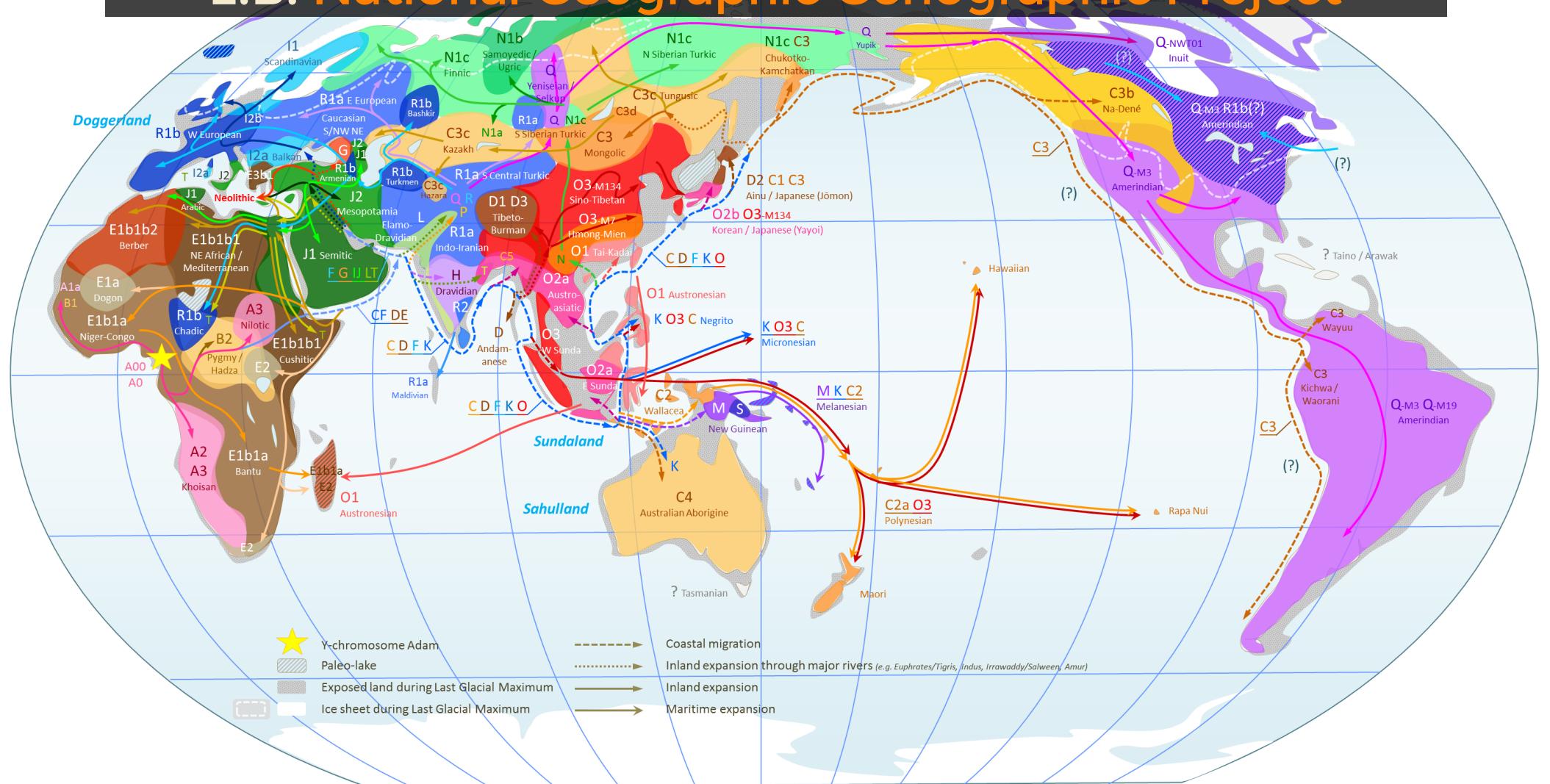
Migration gab es schon vor 60.000 Jahren

World Map of Y-Chromosome Haplogroups

Dominant Haplogroups in Pre-Glacial Populations

with Possible Migrations Routes

z.B. National Geographic Genographic Project



Migration in die Schweiz im Jahr 2013

Einwanderung: 176.000

Auswanderung: 77.000

Wanderungssaldo: 89.000 (1,8% der Bevölkerung)

im Ausland geborene Bevölkerung: 1,35 Millionen (19% der Bevölkerung)

Quelle: [Statistisches Bundesamt](#)

Aber was bedeuten diese Zahlen?

Betrachtung im internationalen Kontext
notwendig!

Kein globaler Datensatz zu Wanderungsströmen

Es gibt keine international einheitliche Definition.

Statistische Erfassung variiert von Land zu Land.

Internationaler Vergleich ähnelt dem zwischen Äpfeln und Birnen.

Harmonisierte Daten bisher nur für Europa, z.B. IMEM.

Wie stark ist die globale Migration?

Je nachdem wie Migration definiert wird....

Stock // Flow

Stock: etwa **3%** der Weltbevölkerung lebten 2010 in einem anderen Land als sie geboren wurden

Flow: **?**% der Weltbevölkerung sind zwischen 2005 und 2010 in ein anderes Land gezogen

Quantifying Global International Migration Flows

Guy Abel & Nikola Sander.

Veröffentlicht in *Science* am 28. März 2014; Vol 343:
1520-1522.



Neues Modell für die Berechnung von Migrationsströmen

UNO Bestandsdaten →

Transitionen zwischen
Geburtsort und
Wohnort

1990, 2000, 2010

~220 Länder

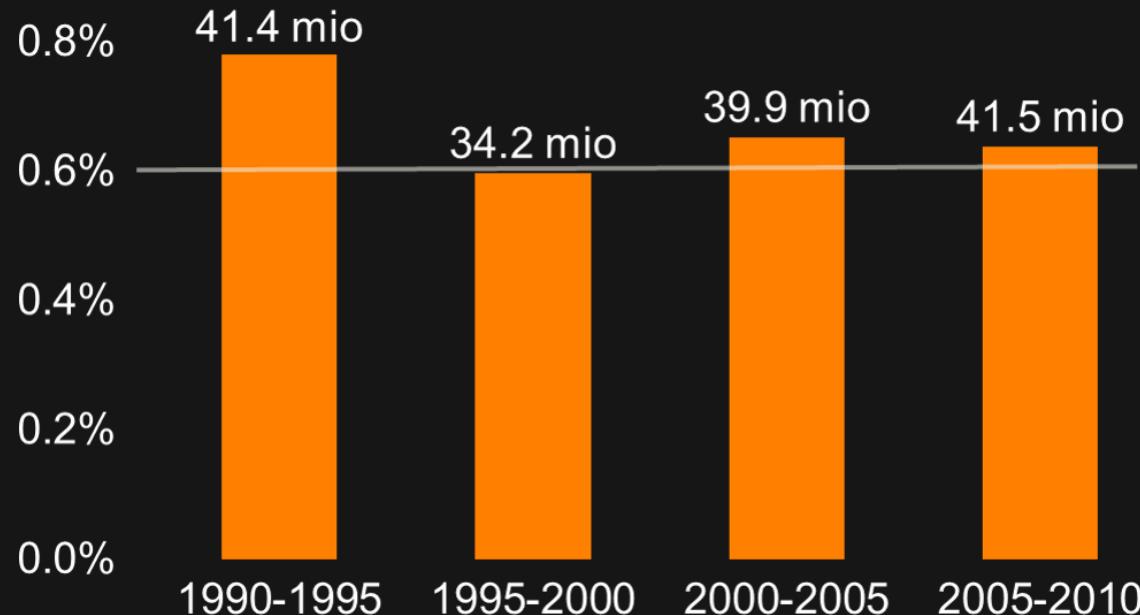
Neue Schätzungen

Transitionen zwischen
Wohnorten über 5
Jahre

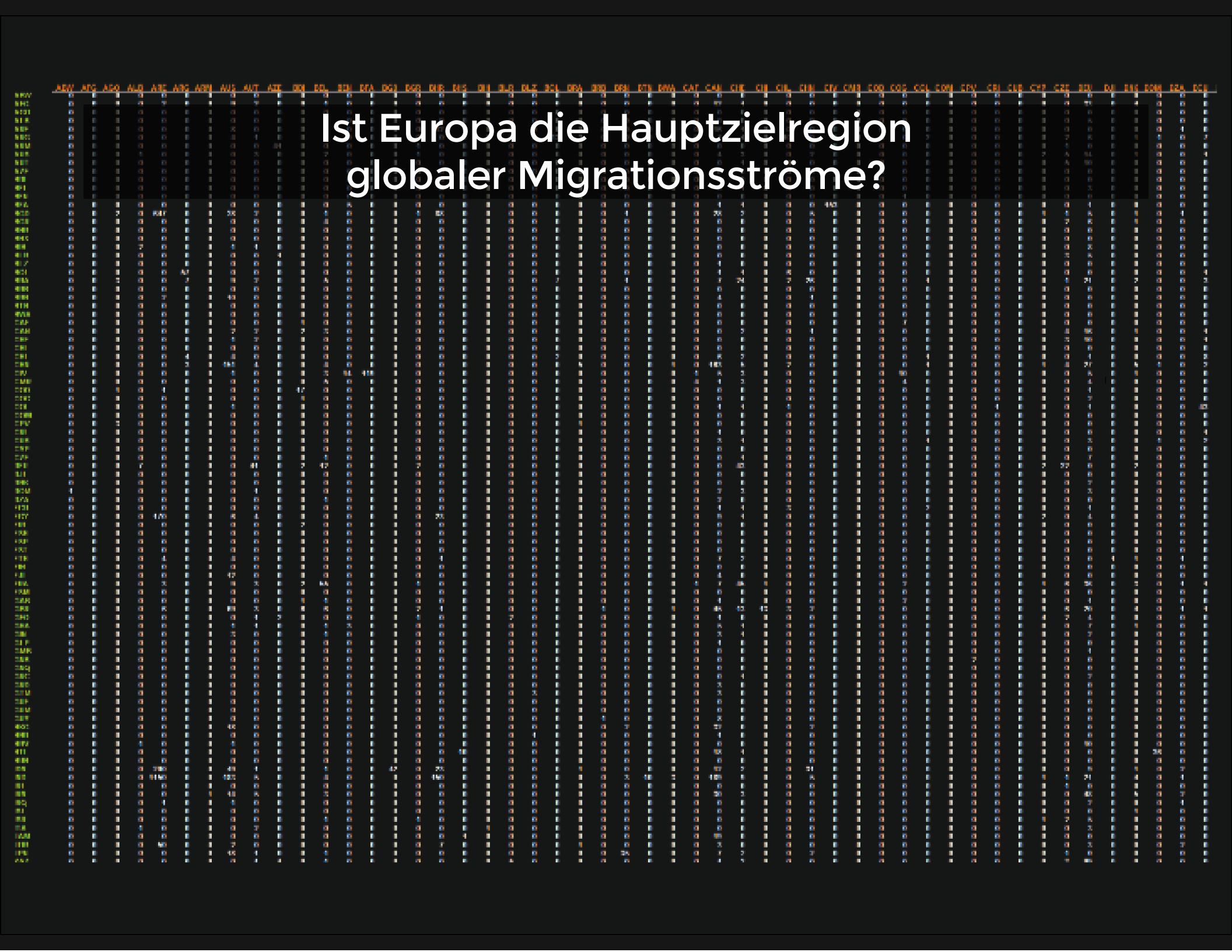
1990-95 bis 2005-10

196 Länder

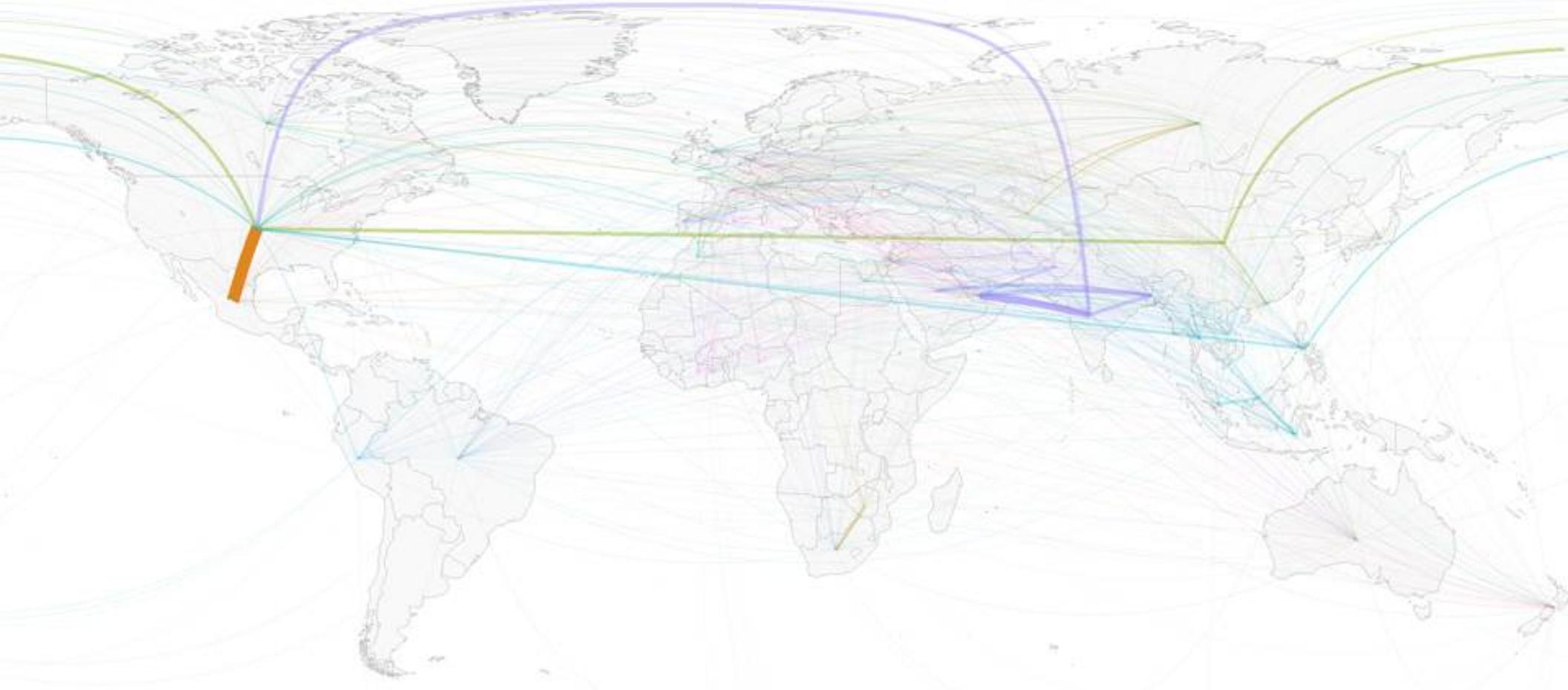
Globale Migration stabil bei 0,6 % der Weltbevölkerung



Ist Europa die Hauptzielregion globaler Migrationsströme?

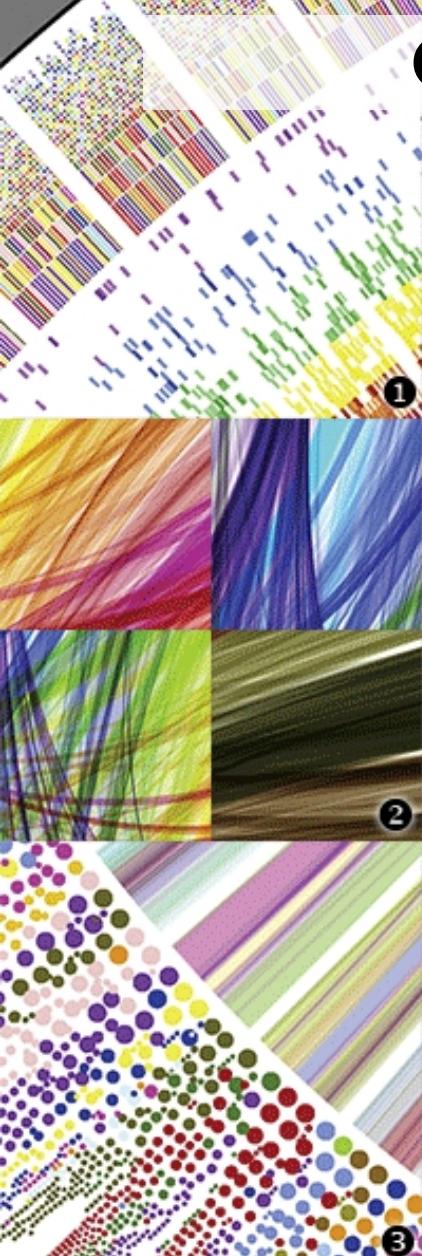


Klassische Visualisierung von Migrationsströmen.



Genetik als Quelle der Inspiration

Canada's Michael Smith Genome Sciences Centre // British Columbia Cancer Research Centre // www.bcgsc.ca



Circos - round is the new square

Circos
We have created a visualization tool, called Circos, to facilitate exploring relationships between genomes and in general any kind of position-instances that exhibit genomic interests. Storing genome data such as these, producing sensible alignments and performing analysis, underpins comparative studies but are opaque to conventional visualization methods designed for 2D data sets. Compared to other tools [2,23], Circos is unique in its combination of circular data domain layout, support for a large number of diverse data tracks, global and local length scale control, extensive customization and automation, maintaining a high data-to-ink ratio [23] without sacrificing clarity or readability. Circos has been used by the international genetics community [14] and its flexibility and aesthetic has garnered interest from mainstream periodicals and newsletters [7]-[9] and, recently, illustrate the dynamics of a US presidential debate [10].

DOWNLOAD CIRCOS AT: <http://www.bcgsc.ca/circos>

At present, laboratories are hard-pressed not only to store and analyze, but to visualize the means of data produced by ultra-high-throughput technologies, such as massively parallel sequencing. Because analytically extracting informative patterns from these large data sets is very difficult, automated visualization tools that generate informative signatures of the data are valuable in data mining and formulating hypotheses.

The design of Circos is based on the fact that a circularly compressed data layout can encode more information between genomic regions more compactly than a linear layout. These relationships are visually encoded by links which can be either straight lines or curves whose control point location can be highly customizable. Other data types that are supported are scatter plots, line plots, histograms, pie charts, heatmaps and labeled ticks. The radial position of data tracks is controlled by the angle of their angular extent in relation of the center of the diagram. Data tracks such as the file and text label have individual elements automatically positioned to avoid overlap.

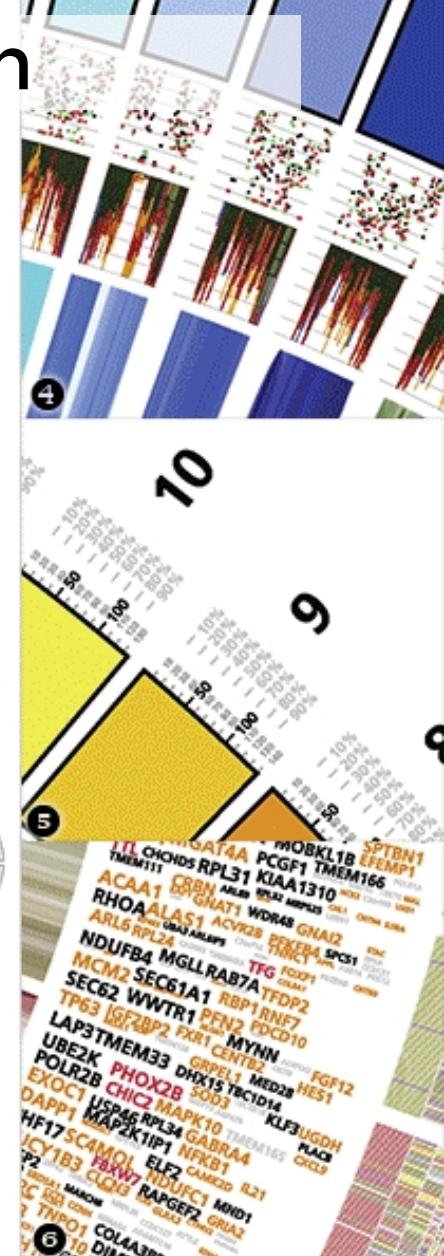
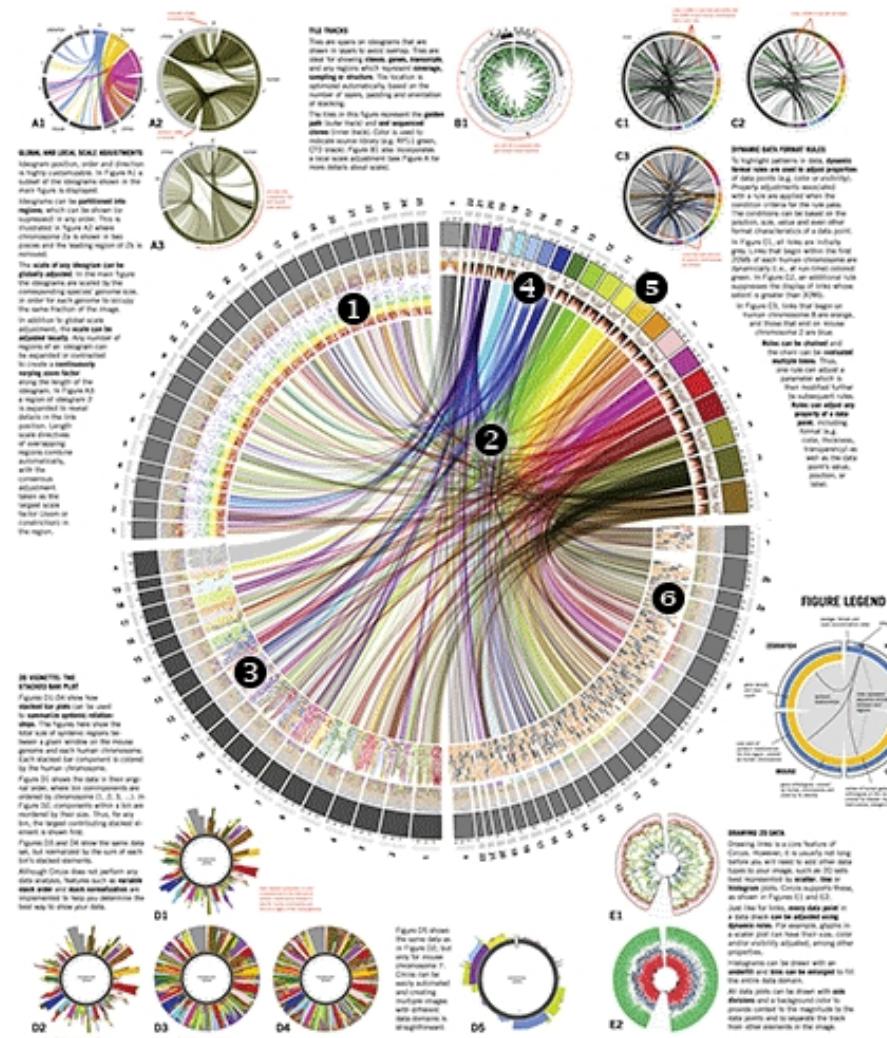
Circos uses plain text files for both input data and configurations. The latter controls the placement and orientation of each data track. The ability to generate both data and configuration files automatically makes Circos highly amenable to incorporation in web-based database mining and visualization.

A feature unique to Circos is not only the ability to adjust the length scale for each chromosome (e.g. display chr 17 at 3x normal size), but to smoothly vary the length scale locally, effectively zooming into regions of interest while still displaying the full data domain (Figure A1-A3). This local and local scale adjustment is useful when illustrating genomic regions in which data density is highly variable. Furthermore, to help draw attention to important data, the ideograms can be divided into any number of disjoint regions, which in turn can be drawn in any order. The resulting axis breaks can be marked up in various styles on the final image to clearly mark the disjunction.

Every aspect of the final image is customizable and output can be generated in either bitmap or SVG format. For example, the color palette used for each chromosome track is customizable, as are the compressing features of the cytogenetic bands. The radial position for each ideogram can be independently set. Each data track, and individual primitives within a track, has an associated z-depth value, which controls how elements stack. Finally, every data type format characteristic, such as color, thickness, data value, label and visibility, can be adjusted by dynamic formatting rules based on data position and value. All this is controlled by the configuration file. These rule sets are stored in the configuration files and separate the definition and storage of formatting rules from the raw data.

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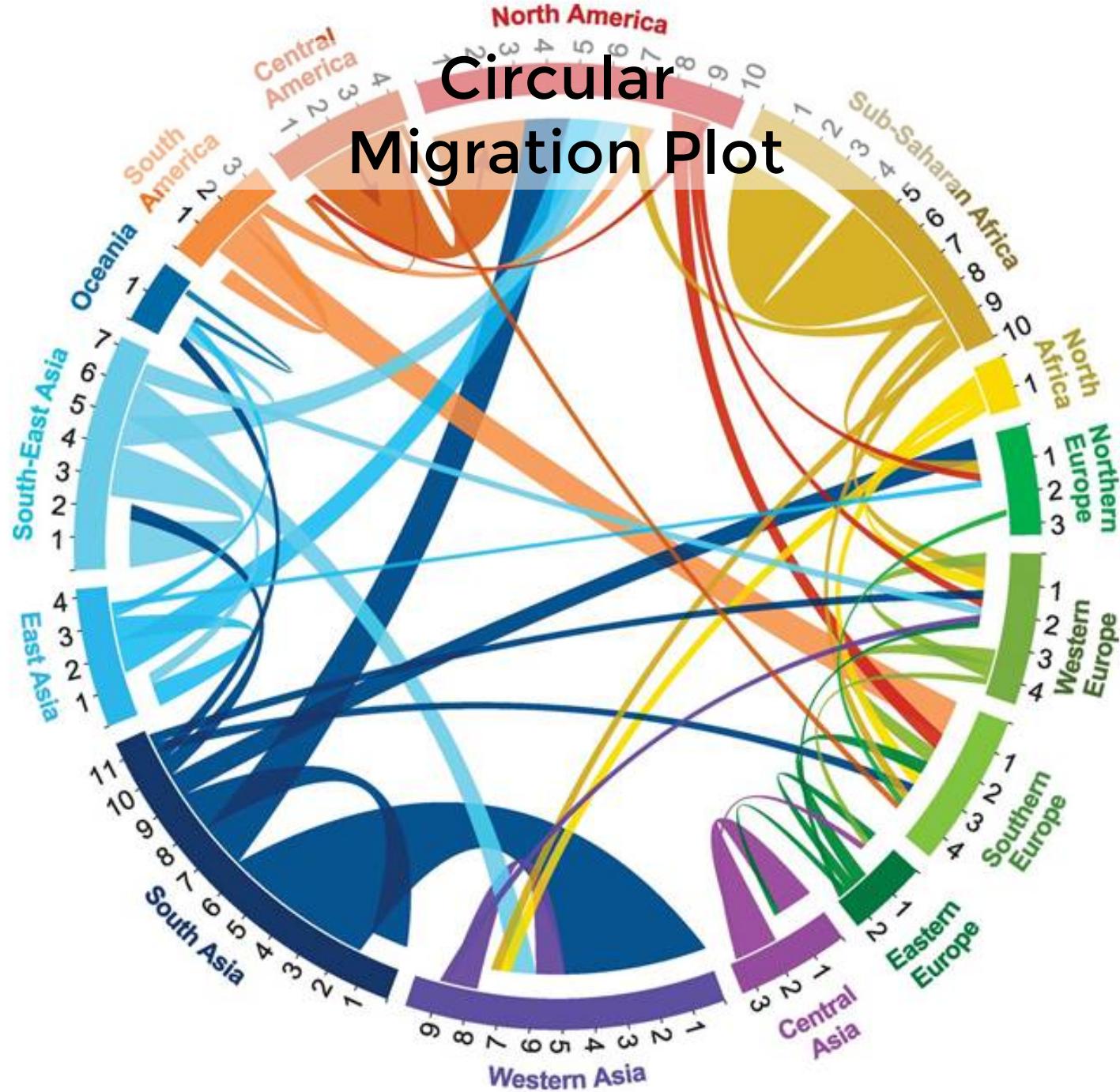
CANADA'S MICHAEL SMITH GENOME SCIENCES CENTRE // BRITISH COLUMBIA CANCER RESEARCH CENTRE // 100-570 W 7TH AVENUE // VANCOUVER BC V5Z 4S6 // CANADA // www.bcgsc.ca

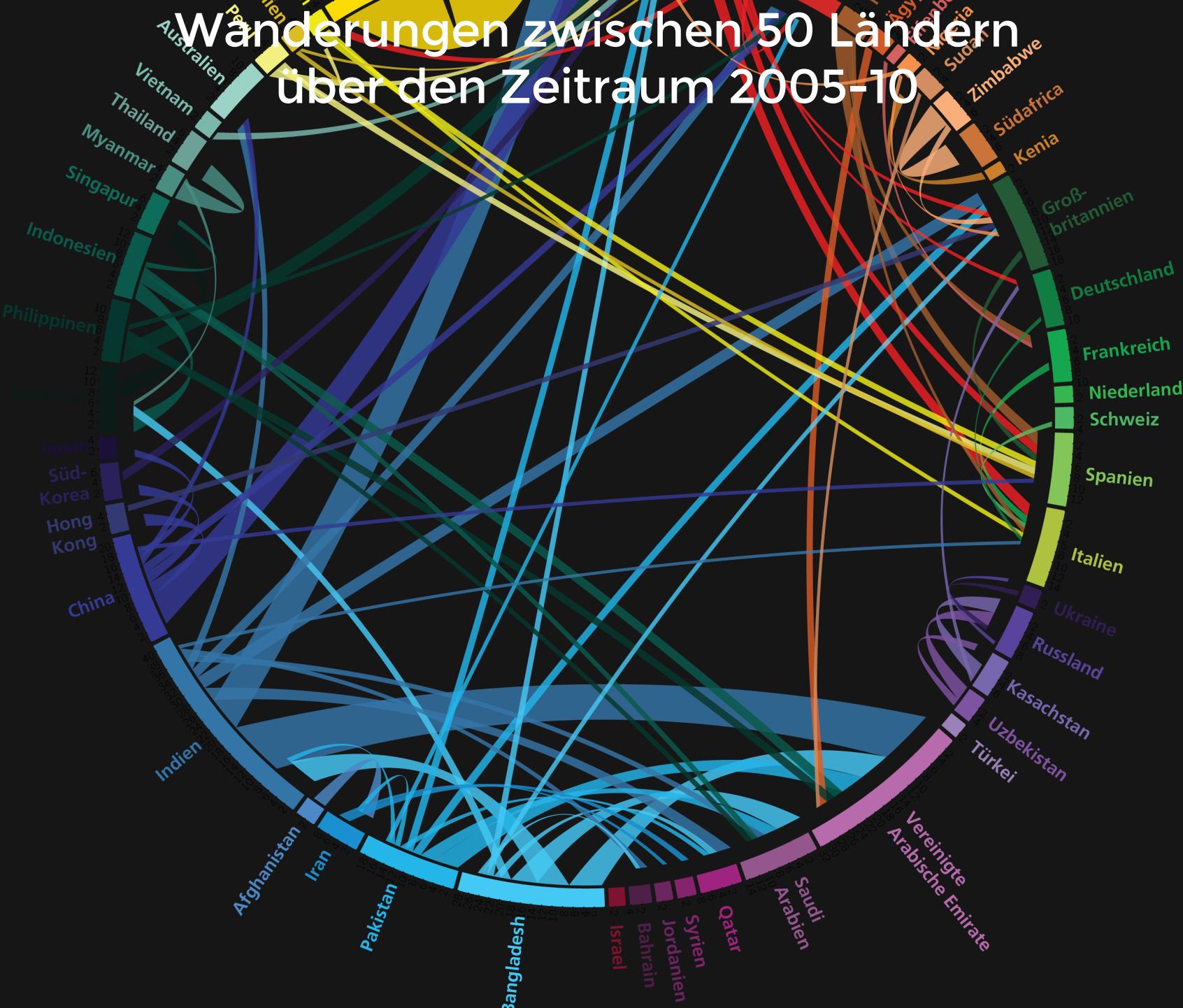


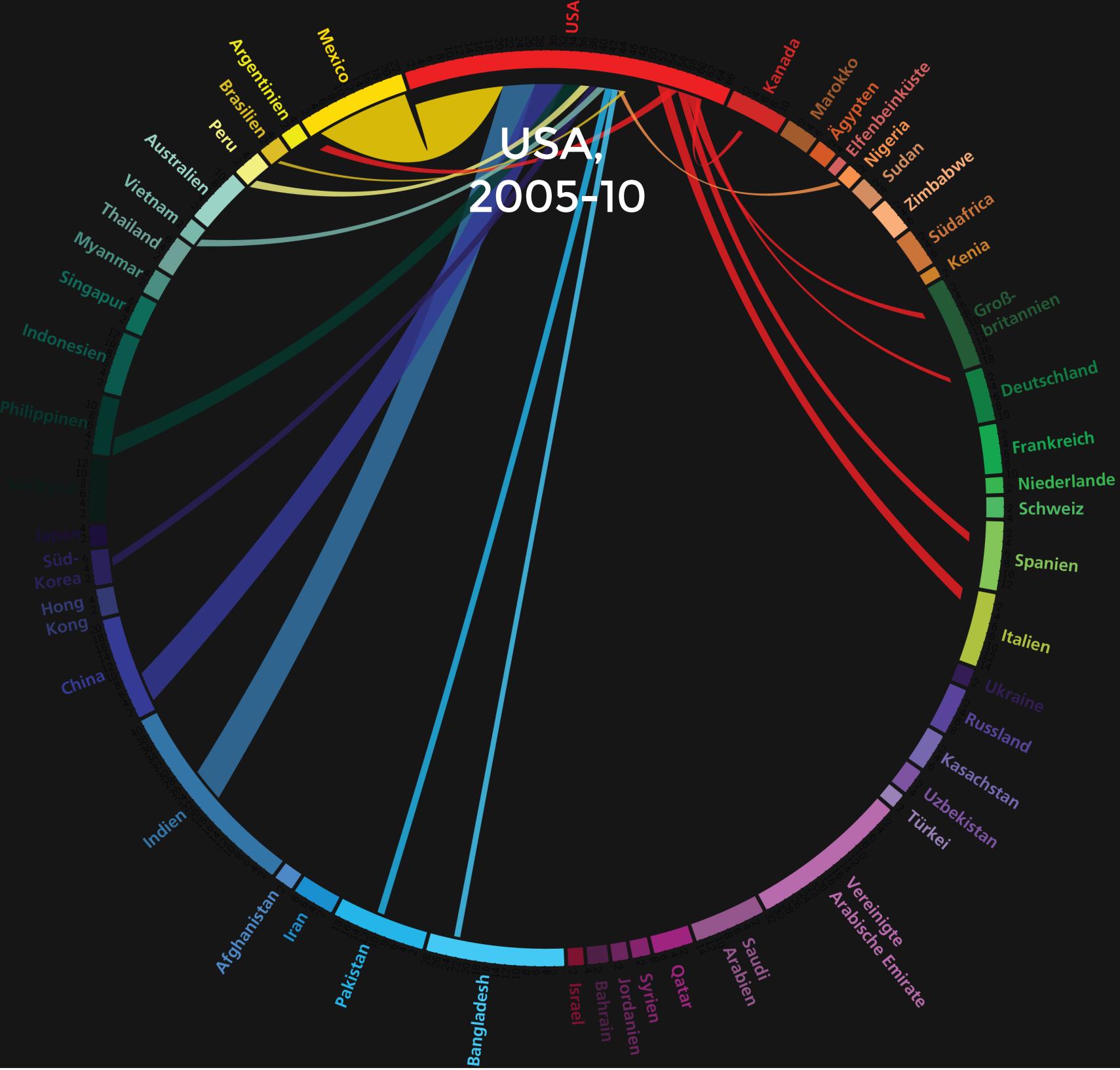
mkweb.bcgsc.ca/circos // martink@bcgsc.ca

Presented at Genome Informatics 2008, Hinxton, UK (September 10-14, 2008)

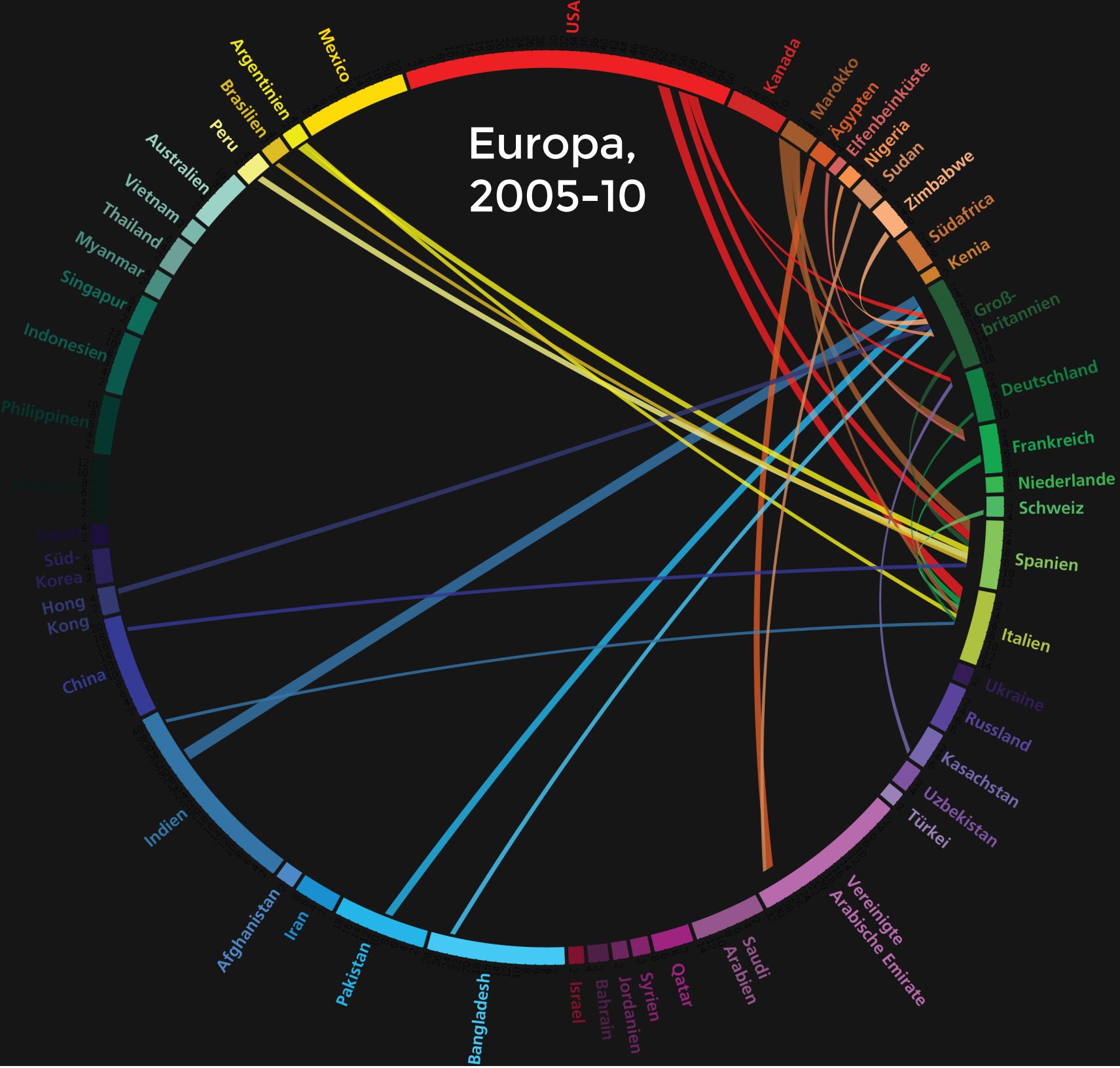
Circular Migration Plot

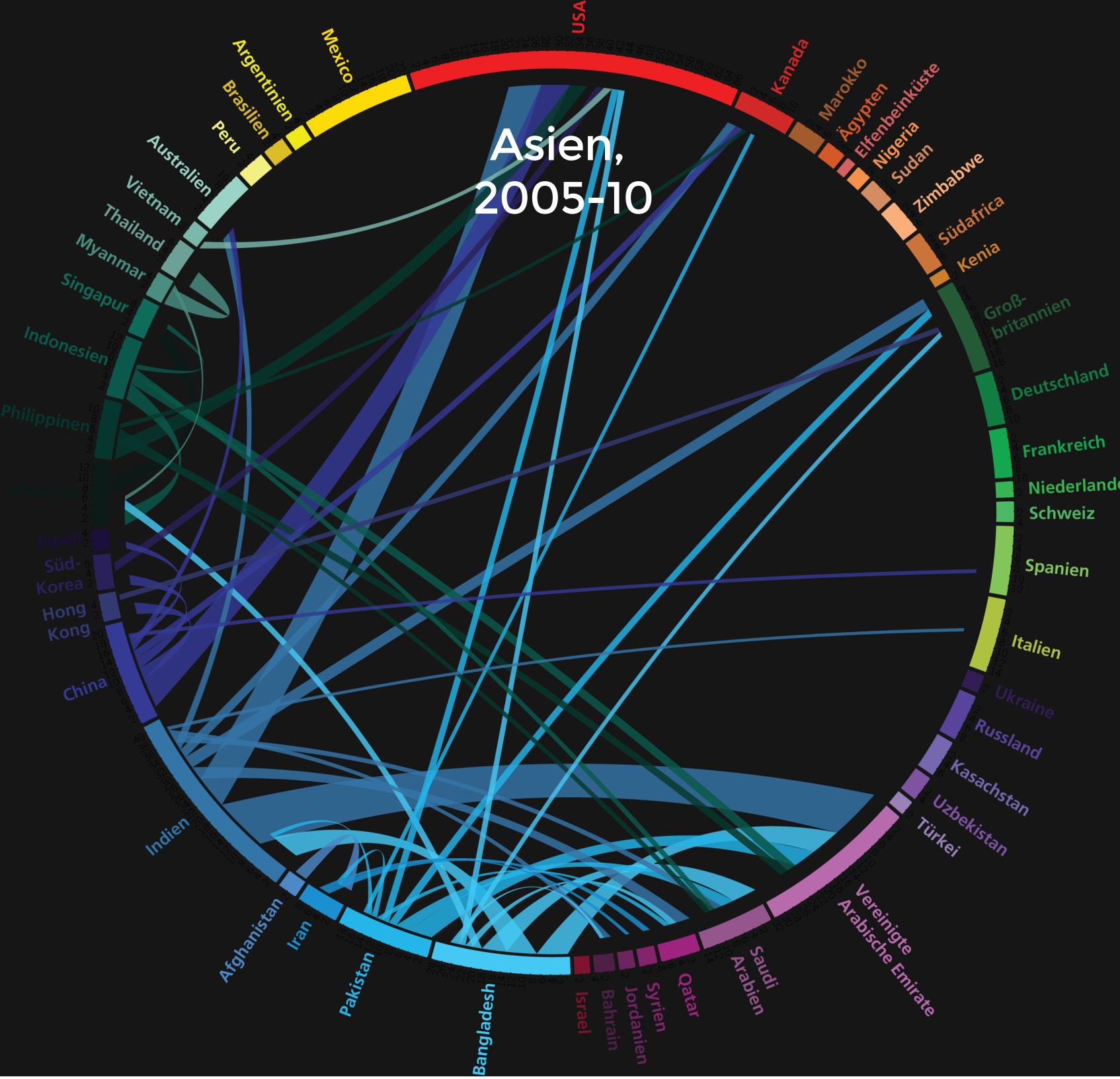




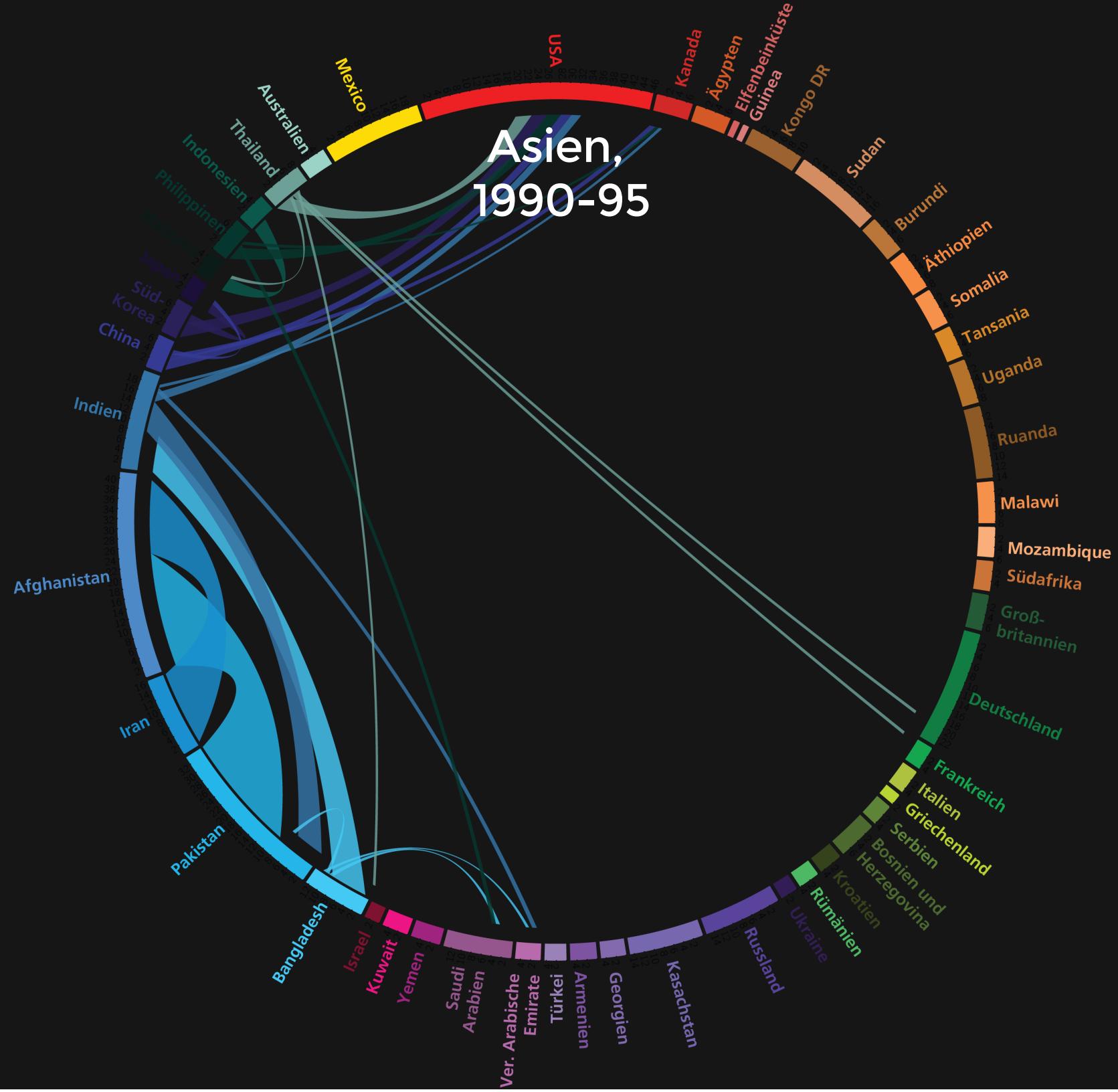


Europa, 2005-10

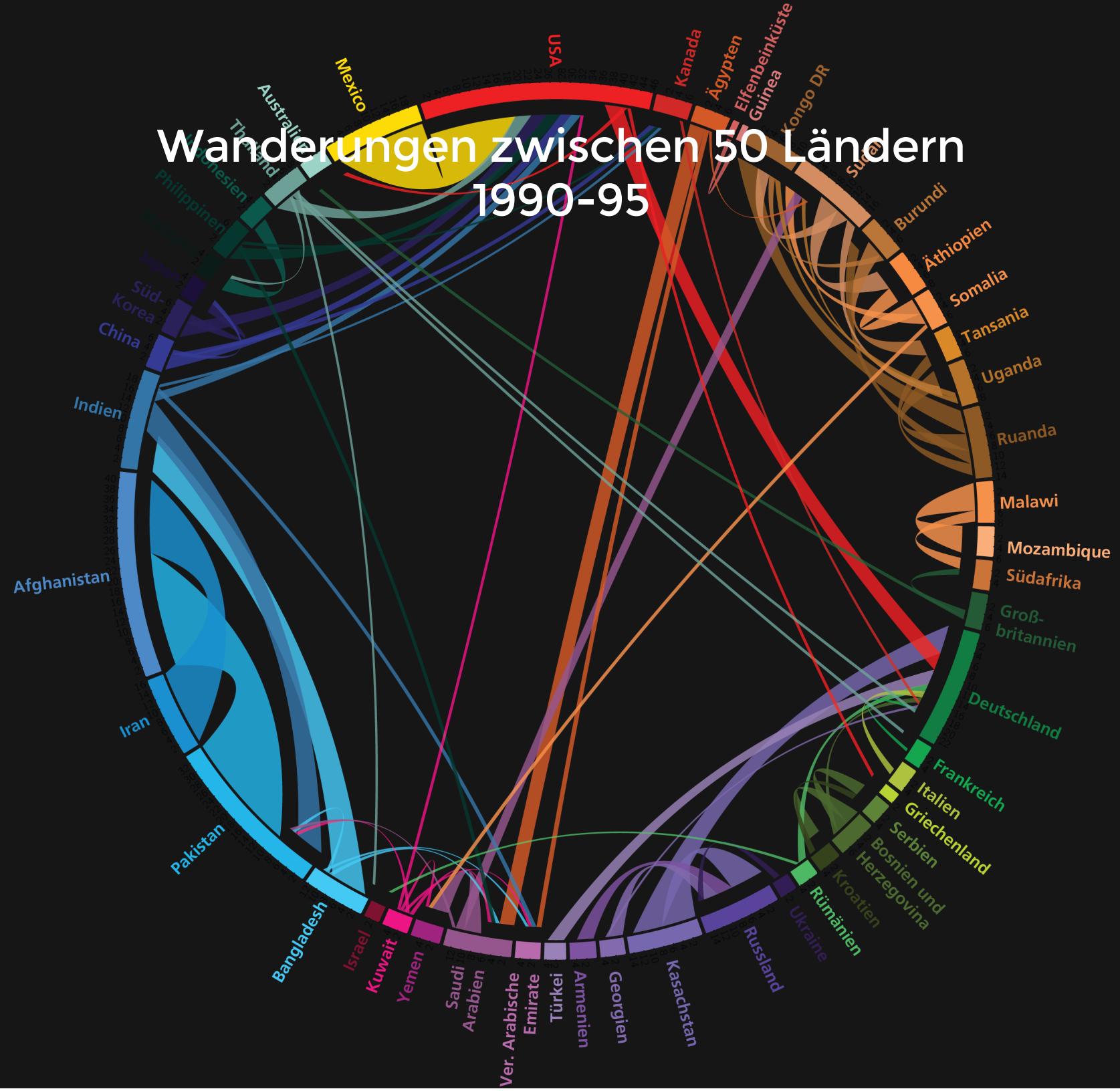




Asien, 1990-95

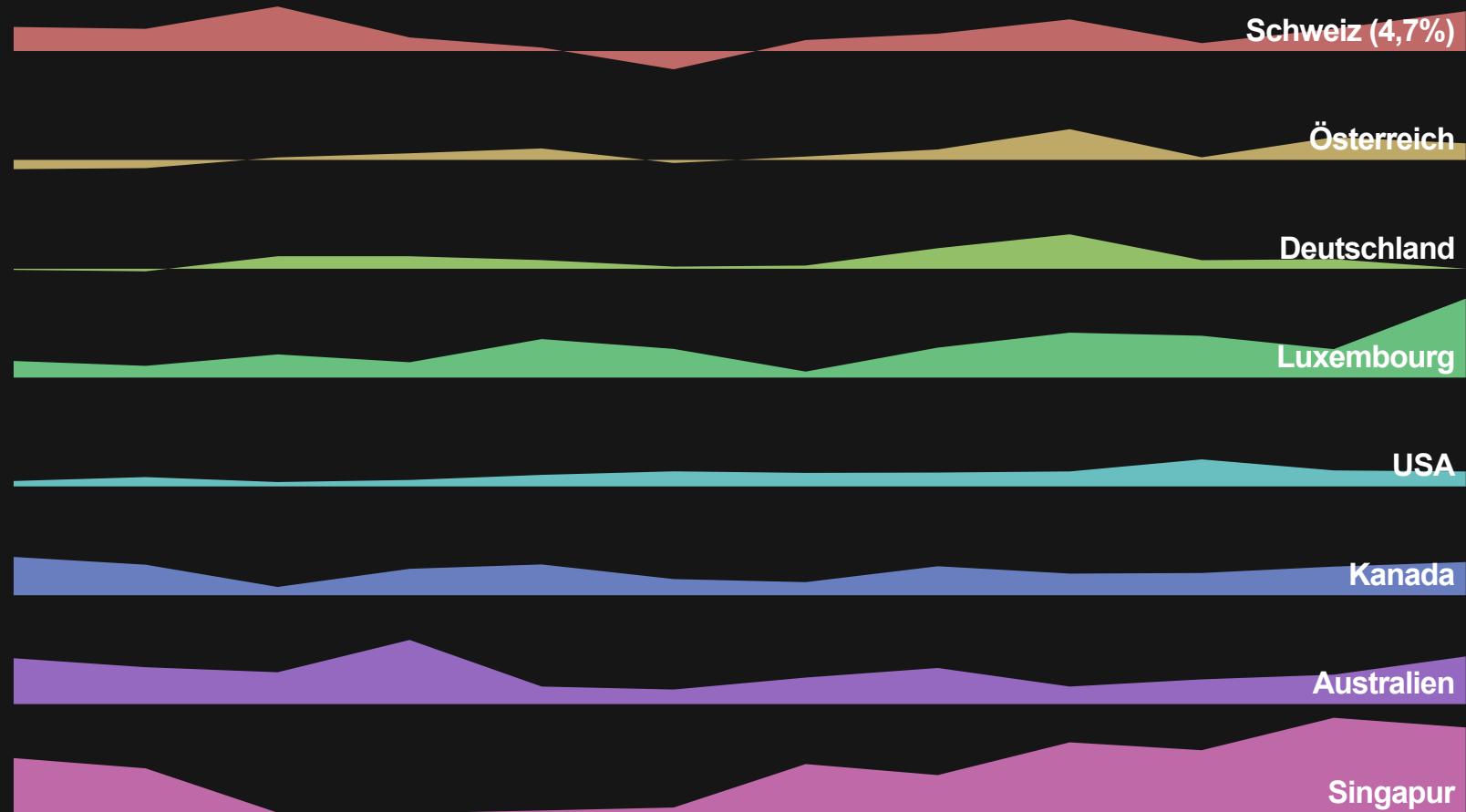


Wanderungen zwischen 50 Ländern 1990-95



Die Schweiz nimmt keine Sonderrolle ein

Wanderungssaldo in % der Bevölkerung, 1950 - 2010



Quelle: Vereinte Nationen

"The Global Flow of People"

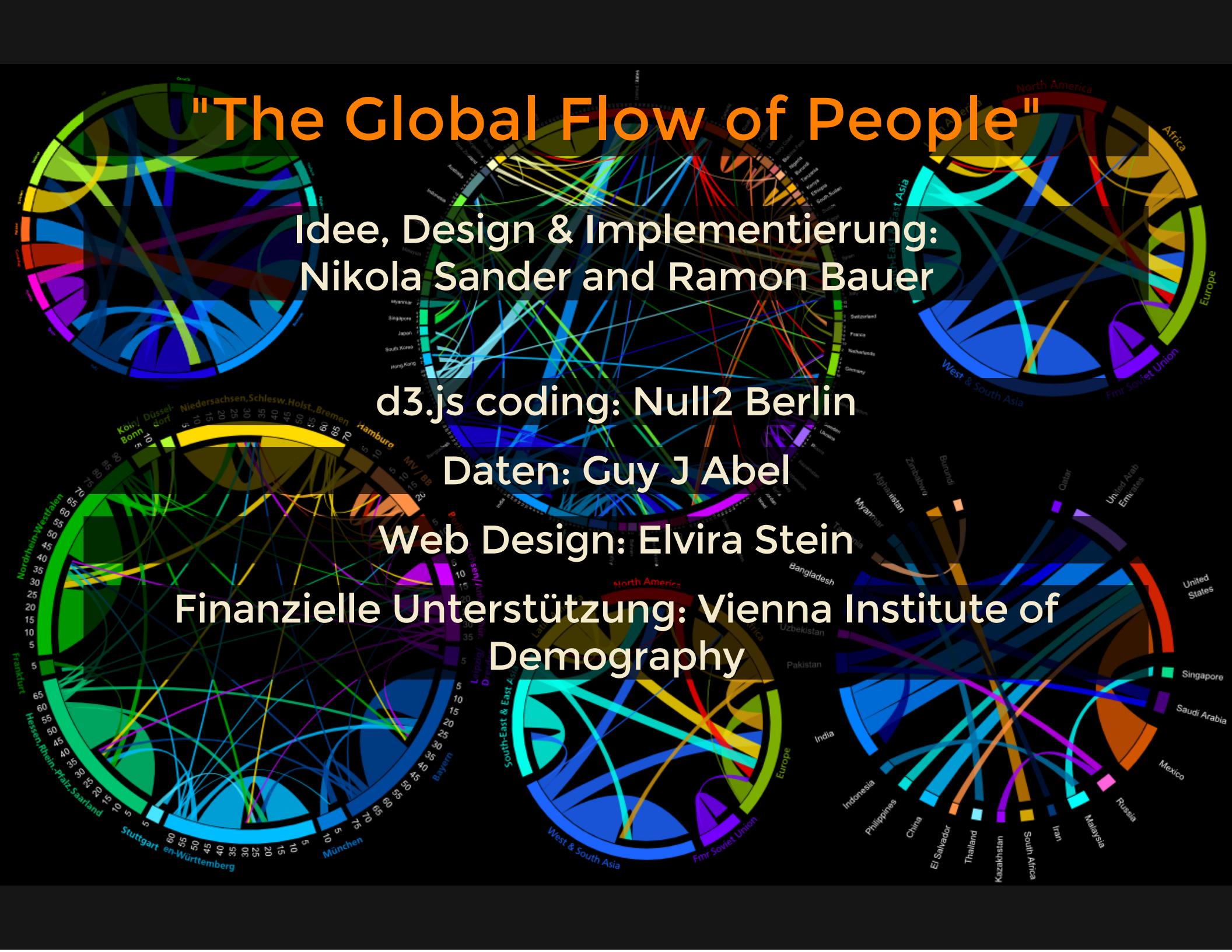
Idee, Design & Implementierung:
Nikola Sander and Ramon Bauer

d3.js coding: Null2 Berlin

Daten: Guy J Abel

Web Design: Elvira Stein

Finanzielle Unterstützung: Vienna Institute of
Demography



Mehr als 0,5 Millionen Besucher seit März 2014



1990–1995

1995–2000

2000–2005

2005–2010



Feedback via Twitter

"Fantastic visualization of global migration data. I'm on there if you zoom in a lot."

"#SomeoneTellMarineLePen African migrants aren't invading us, and here's the data to prove it."

In den Lehrplan für die Sekundarstufe II
in Nordrhein-Westfalen aufgenommen.

Oberstufe



Fazit

Erstmals gelingt die Bezifferung und Visualisierung globaler Migrationsströme.

Globale Migration stabil bei 0,6 Prozent

Migration ist ein komplexes Phänomen das zunehmend an Bedeutung gewinnt und kontrovers diskutiert wird.

Datenvisualisierung als Brücke zwischen Wissenschaft, Politik und Öffentlichkeit

Unser Code ist übertragbar
auf andere Datensätze

z.B. Binnenwanderung in Deutschland
im Jahr 2010

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@nikolasander

Slides: nikolasander.com/wda-forum2015