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Replication of Similarities and differences in concepts of mental life among adults and children in five cultures

Reporter: Ao Lu, Yang Mengyao

Group Member: Zhu Shanshan, Zou Huiling, Yu Yueyang

Nature Human Behaviour **volume**

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About the author

She, an expert in folk theories and their impact on human behaviors, relationships, and phenomenal experiences, has a keen interest in examining how conceptual representations vary, or remain constant, across different developmental stages, cultural backgrounds, and individuals.

- Possessing a certain level of challenge.
- Broadening one's horizon in various domains.
- Imparting knowledge on how to process, learn from, and emulate large-scale datasets.

NATURE HUMAN BEHAVIOUR

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JCR Category	Category Rank	Category Quartile
MULTIDISCIPLINARY SCIENCES *in SCIE edition*	3/73	Q1
NEUROSCIENCES *in SCIE edition*	2/272	Q1
PSYCHOLOGY, EXPERIMENTAL *in SSCI edition*	1/89	Q1

Experience

2011-2013

Elizabeth Spelke Lab, Harvard University

• Research Assistant

2011-2013

Curry School of Education, University of Virginia

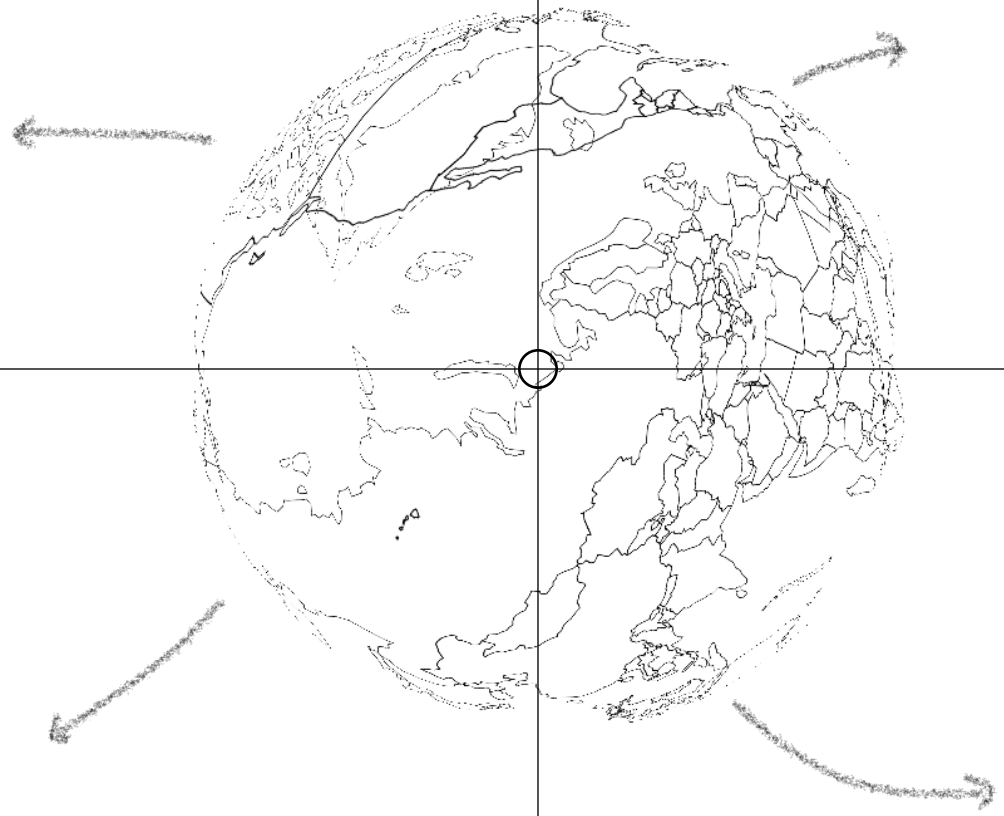
• Research Coordinator for Preschool Relationships Enhancement Project & Effective Classroom Interactions MOOC

X°N, Y°E

OUTLINE

X°N, Y°E

X°N, Y°E



X°N, Y°E

01
Introduction

02
Methods

03
Replication
Results and
Conclusion

04
Summary and
Insights

Mental Life

Body

Heart

Mind

Background

there are differences in how mental life is understood across **cultures**

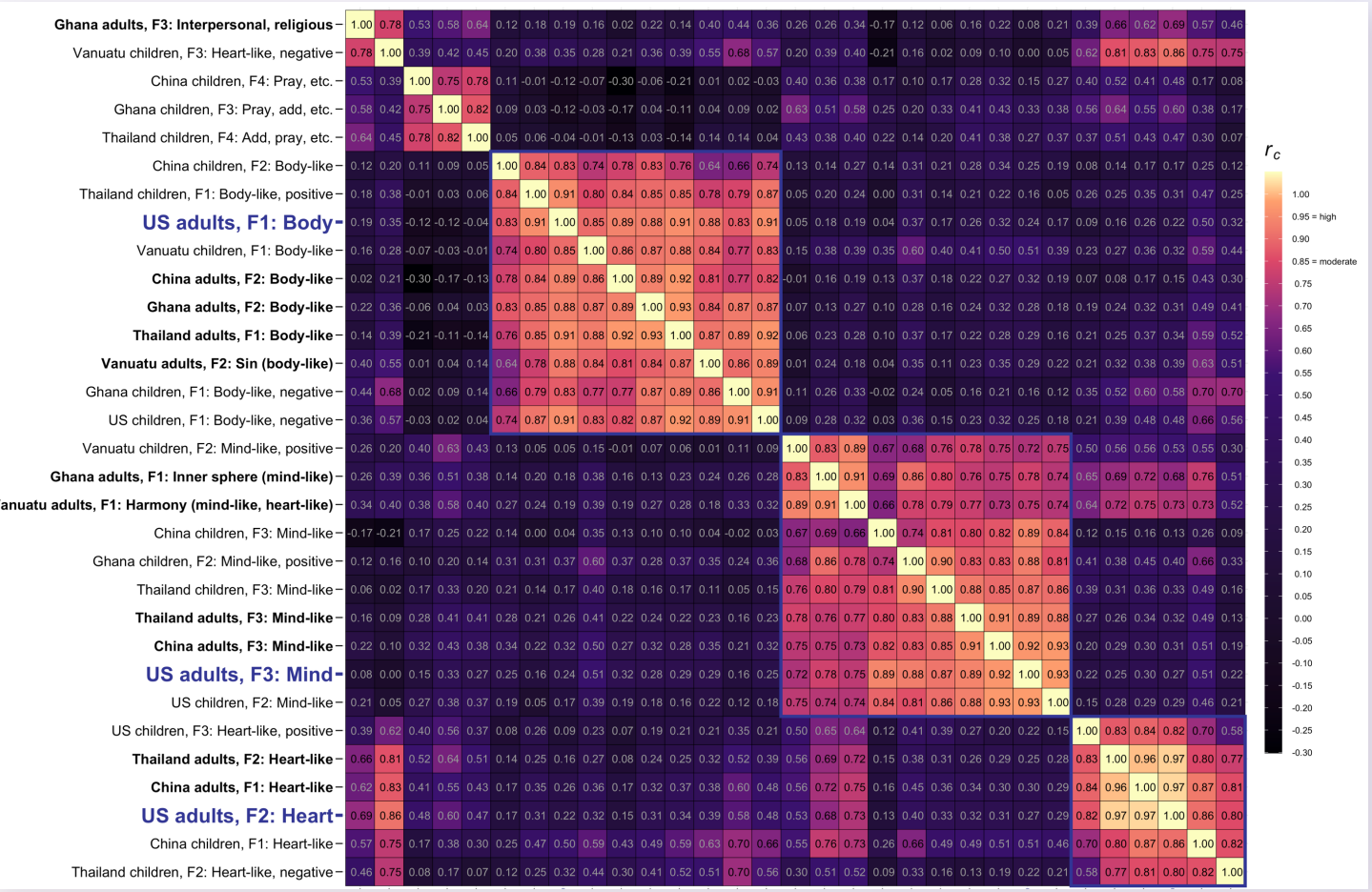
Research Questions

how **adults and children** from different cultural backgrounds understand concepts of mental life?

Hypotheses

these understandings have certain **universal aspects**,
but may show significant differences in **social-emotional abilities**

Research Results and Conclusions



Cultural comparisons

- physiological sensations
- cognitive abilities
- social–emotional abilities

all sites

Developmental comparisons

- physiological sensations
- cognitive abilities
- social–emotional abilities

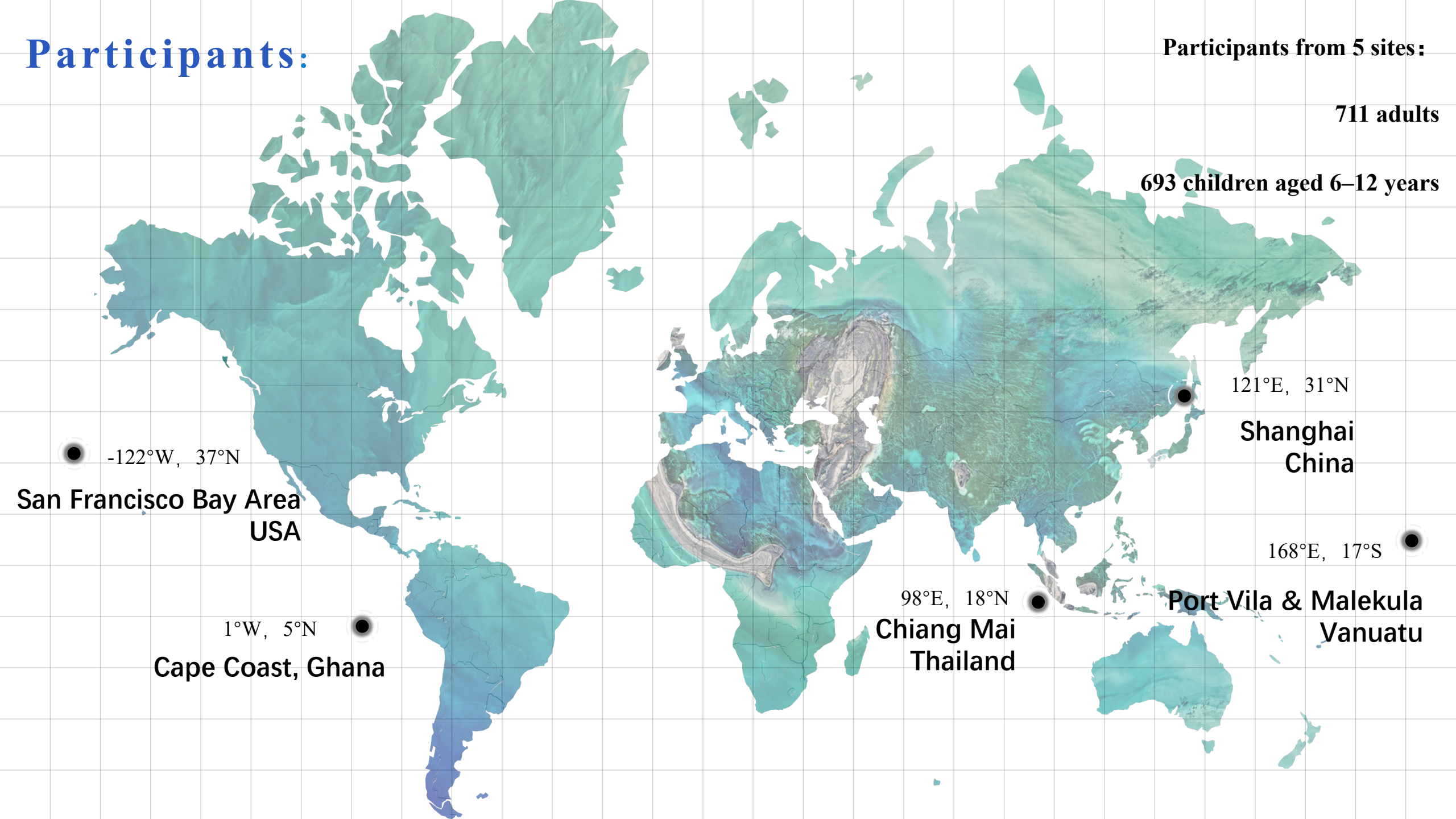
6-12 age

About data

- **Possible reason:** Large and precious

- **The code for data preprocessing uses '*raw*' statements to hide the raw data (see .gitignore file)**

Participants:



Participants from 5 sites:

711 adults

693 children aged 6–12 years

Data Analysis

Exploratory factor analysis (EFA) :

identify latent constructs or core components of the concept of mental life within each cultural sample

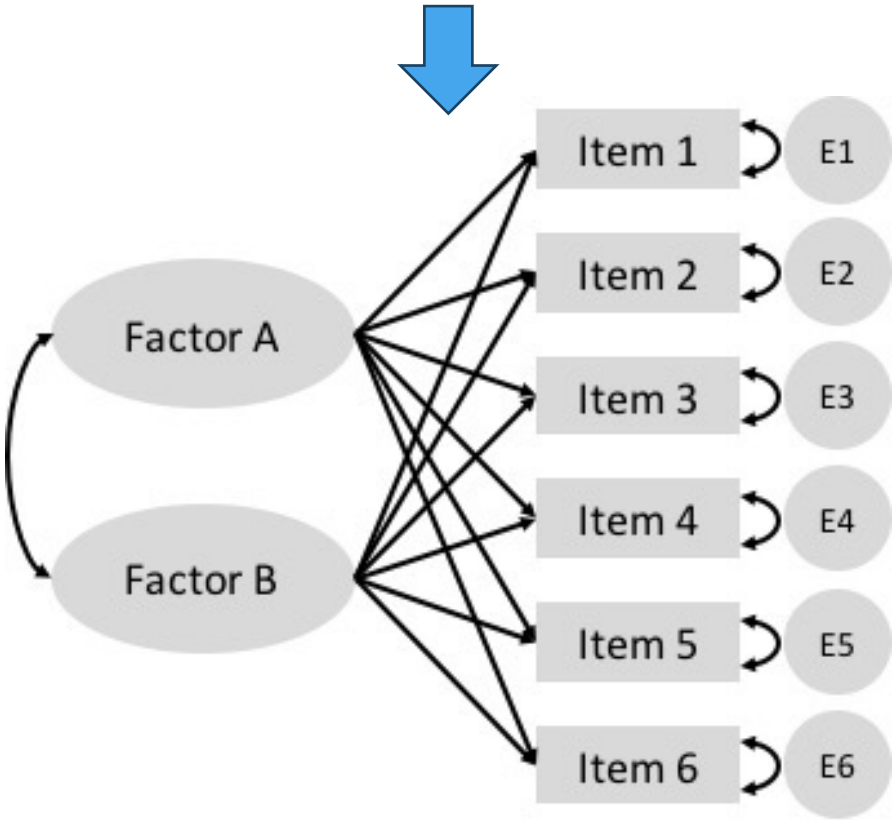
Parallel analysis :

determine the number of factors to retain, and oblique transformation was used to interpret factor loadings

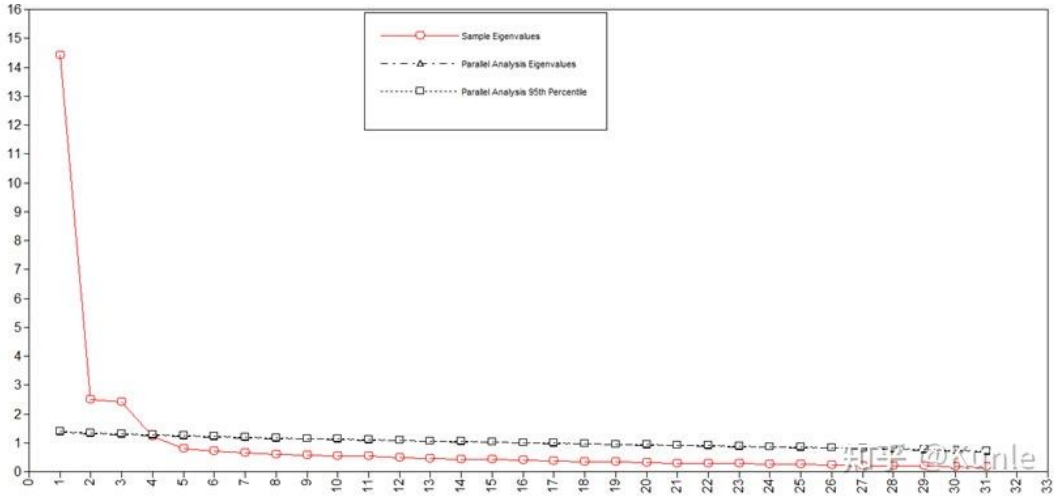
Vector cosine (rc) :

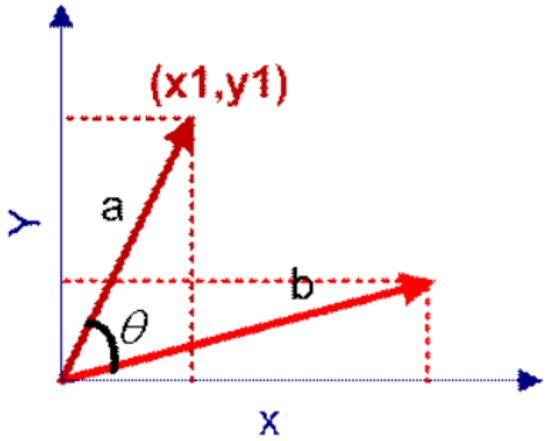
compares cultural sites and age groups by gauging the similarity of factors

EFA



Parallel analysis





Vector cosine

Programming environment

Software and code

Policy information about availability of computer code

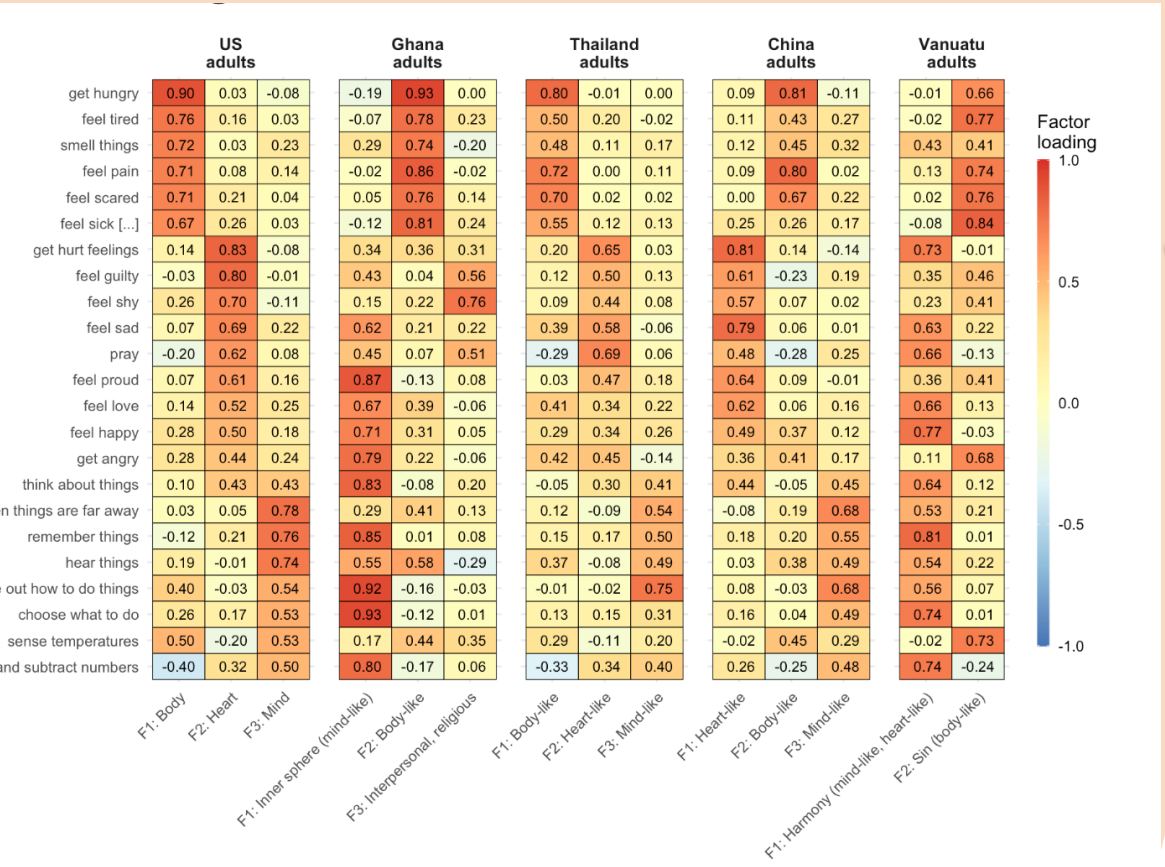
Data collection	No software was used to collect data
Data analysis	All analyses were conducted in R (version 4.0.0); platform: x86_64-apple-darwin17.0 (64-bit); running under: macOS Catalina 10.15.7. Analysis code is available on Github (https://github.com/kgweisman/mental-life-culture-development), and makes use of the following packages: tidyverse (version 1.3.0), lubridate (version 1.7.8), readxl (version 1.3.1), psych (version 1.9.12.31), cowplot (version 1.0.0), reshape2 (version 1.4.4), sjstats (version 0.18.0), lsa (version 0.73.2), langcog (version 0.1.9001; available at https://github.com/langcog/langcog-package), betareg (version 3.1.3), lme4 (verison 1.1.23), lmerTest (version 3.1.2).

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research guidelines for submitting code & software for further information.

All our analyses were conducted in the R version 4.3.1 environment, on thearm64-apple-darwin platform, with macOS Sonoma 14.5 as the operating system (R CoreTeam,2023).

```
> print(package_versions)
                dplyr                 tidyr               ggplot2
      "dplyr: 1.1.4"       "tidyr: 1.3.0"     "ggplot2: 3.5.1"
               papaja           tidyverse             lubridate
     "papaja: 0.1.2"  "tidyverse: 2.0.0"  "lubridate: 1.9.3"
               readxl                 psych               cowplot
     "readxl: 1.4.3"       "psych: 2.3.9"     "cowplot: 1.1.1"
                here             reshape2               sjstats
      "here: 1.0.1"    "reshape2: 1.4.4"    "sjstats: 0.19.0"
                 lsa              langcog          GPArotation
      "lsa: 0.73.3" "langcog: 0.1.9001" "GPArotation: 2024.3.1"
                 irr          kableExtra              janitor
      "irr: 0.84.1" "kableExtra: 1.4.0"    "janitor: 2.2.0"
               knitr
     "knitr: 1.45"
>
```

➢ **Exploratory factor analysis**: Factor loadings



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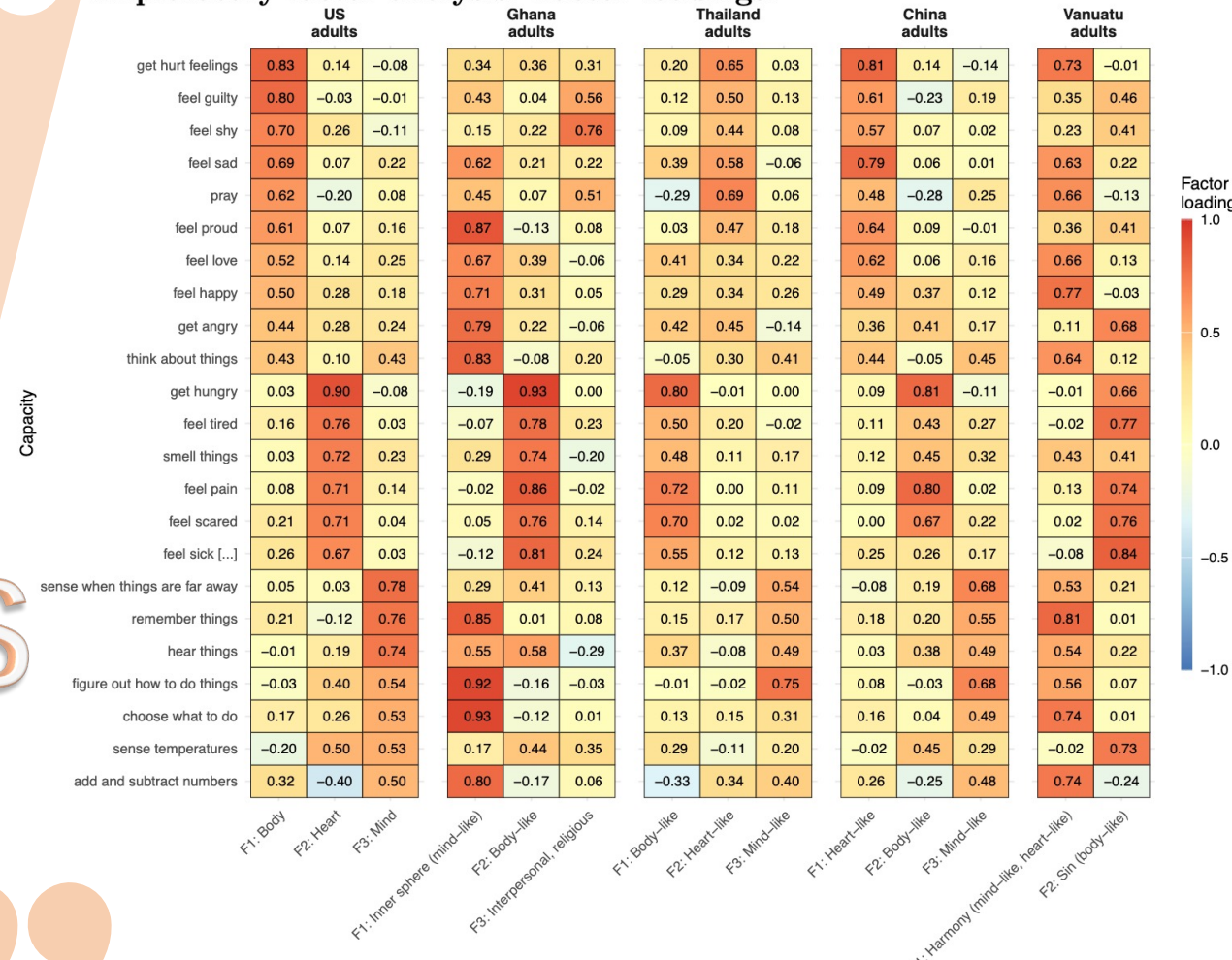
Exploratory factor analysis: Factor loadings.



- **Original**
- **Replication**

````
### Exploratory factor analysis: Factor loadings
```{r efa adults, echo=FALSE}
# Exploratory factor analysis

set.seed(54321)

# do exploratory factor analysis: adults
efa_us_adults <- fa_fun(d_us_adults_w,
                        n = median(pa_outcomes_dist_adults$us),
                        chosen_n.iter = 1000,
                        chosen_rot = "oblimin")
colnames(efa_us_adults$loadings) <- paste0("usADULTS_",

colnames(efa_us_adults$loadings))

efa_gh_adults <- fa_fun(d_gh_adults_w,
                        n = median(pa_outcomes_dist_adults$gh),
                        chosen_n.iter = 1000,
                        chosen_rot = "oblimin")
colnames(efa_gh_adults$loadings) <- paste0("ghADULTS_",

colnames(efa_gh_adults$loadings))
````

````
```{r efa adults}
set.seed(54321)

# do exploratory factor analysis: adults
efa_us_adults <- fa_fun(d_us_adults_w,
                        n = median(pa_outcomes_dist_adults$us),
                        chosen_n.iter = 1000,
                        chosen_rot = "oblimin")
colnames(efa_us_adults$loadings) <- paste0("usADULTS_",
                                           colnames(efa_us_adults$loadings))

efa_gh_adults <- fa_fun(d_gh_adults_w,
                        n = median(pa_outcomes_dist_adults$gh),
                        chosen_n.iter = 1000,
                        chosen_rot = "oblimin")
colnames(efa_gh_adults$loadings) <- paste0("ghADULTS_",
                                           colnames(efa_gh_adults$loadings))
````

````
```{r heatmap adults, fig.width = 9, fig.asp = 0.6, echo=FALSE,
warning=FALSE}
# make heatmap figure: adults
loadings_adults %>%
  mutate(factor_num = as.numeric(gsub(".*F", "", factor))) %>%
  mutate(sample = paste(country, "adults", sep = "\n")) %>%
  left_join(factor_names_adults) %>%
  mutate(country = factor(country, levels = levels_country)) %>%
  ggplot(aes(x = reorder(factor_labdescript, factor_num),
             y = reorder(capacity, desc(capacity_ord_us)),
             fill = loading)) +
  facet_grid(~ reorder(sample, as.numeric(country)), scales = "free",
space = "free") +
  geom_tile(color = "black", size = 0.2) +
  geom_text(aes(label = format(round(loading, 2), nsmall = 2)), size = 3)
+
  scale_fill_distiller(palette = "RdYlBu", limits = c(-1, 1),
                       guide = guide_colorbar(barheight = 20, barwidth =
0.5)) +
  theme_minimal() +
  theme(axis.text.x = element_text(angle = 45, hjust = 1, vjust = 1),
        panel.spacing.x = unit(0.8, "lines"),
        strip.text.x = element_text(size = 10, face = "bold")) +
  labs(x = NULL, y = "Capacity", fill = "Factor\nloading")
# ggsave("/Users/ss/Desktop/Re_Weisman_2021_Group1_2024/figures/plot02.pn
g", width = 12, height = 8, dpi = 300)

```
````

````
```{r heatmap adults, fig.width = 5, fig.asp = 0.7}
# make heatmap figure: adults
loadings_adults %>%
  mutate(factor_num = as.numeric(gsub(".*F", "", factor))) %>%
  mutate(sample = paste(country, "adults", sep = "\n")) %>%
  left_join(factor_names_adults) %>%
  mutate(country = factor(country, levels = levels_country)) %>%
  ggplot(aes(x = reorder(factor_labdescript, factor_num),
             y = reorder(capacity, desc(capacity_ord_us)),
             # y = reorder(capacity, desc(capacity_ord_ec)),
             # y = reorder(capacity, desc(capacity_ord_gh)),
             # y = reorder(capacity, desc(capacity_ord_th)),
             # y = reorder(capacity, desc(capacity_ord_ch)),
             # y = reorder(capacity, desc(capacity_ord_vt)),
             fill = loading)) +
  facet_grid(~ reorder(sample, as.numeric(country)), scales = "free", space = "free") +
  geom_tile(color = "black", size = 0.2) +
  geom_text(aes(label = format(round(loading, 2), nsmall = 2)), size = 3) +
  scale_fill_distiller(palette = "RdYlBu", limits = c(-1, 1),
                       guide = guide_colorbar(barheight = 20, barwidth = 0.5)) +
  theme_minimal() +
  theme(axis.text.x = element_text(angle = 45, hjust = 1, vjust = 1),
        panel.spacing.x = unit(0.8, "lines"),
        strip.text.x = element_text(size = 10, face = "bold")) +
  labs(x = NULL, y = "Capacity", fill = "Factor\nloading")
```
````

- **Vector cosines (rc)** between all pairs of factors in the EFA solutions

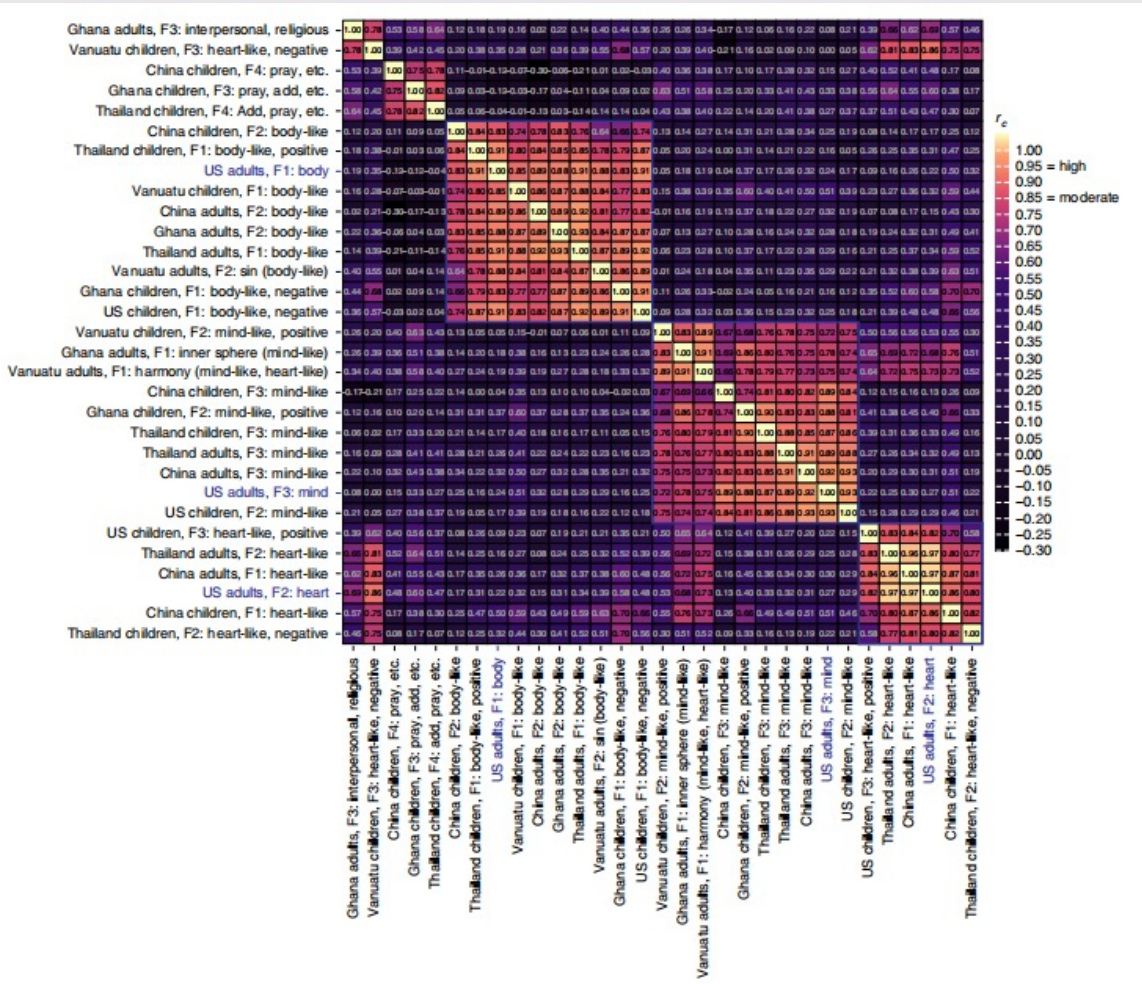


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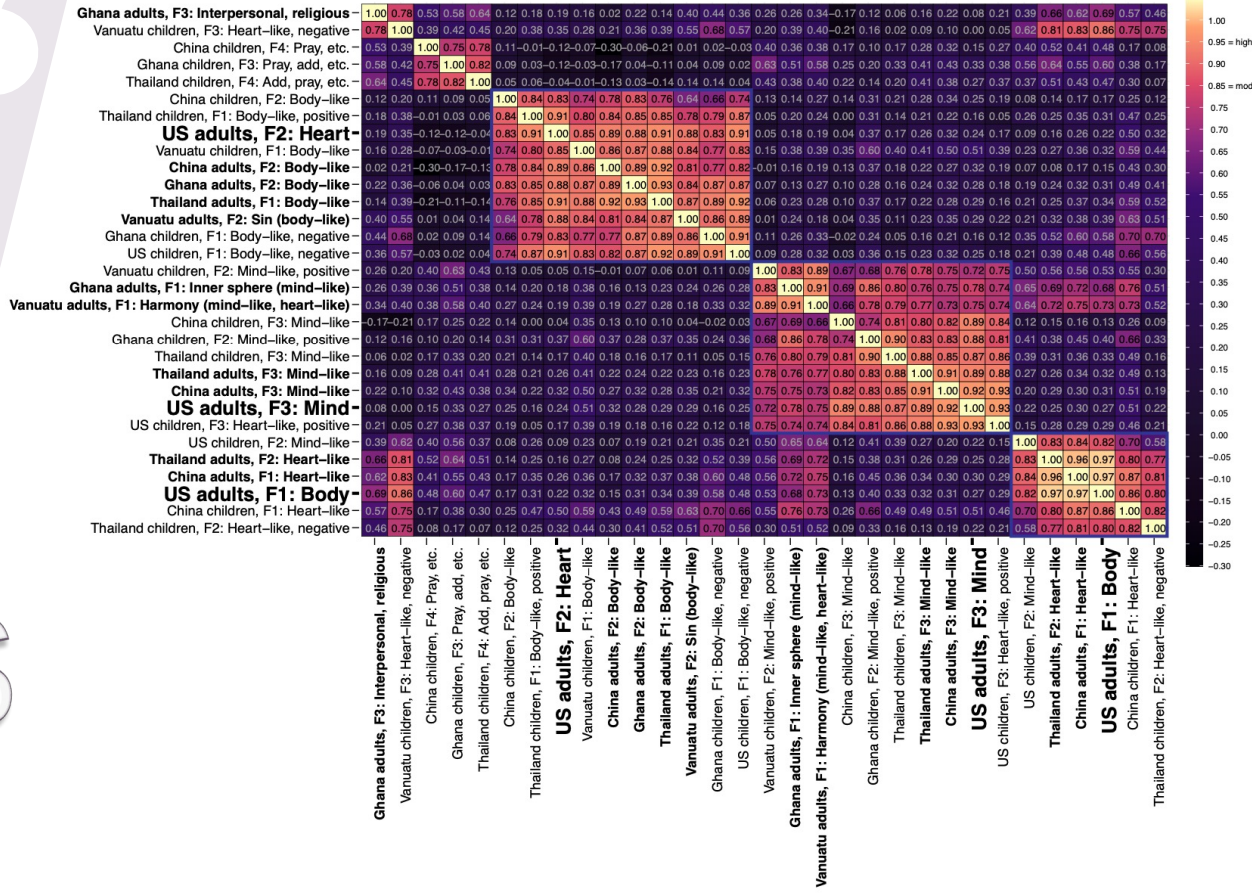
Figure 2.



- **Original**
- **Replication**

Code

```
```{r cong all pairs plot a, fig.width = 9.5, fig.asp = 0.9}
# FIGURE 2
cong_lower_lim <- ifelse(min(cong_all_ordered$cong) > -0.05, -0.05,
                         min(cong_all_ordered$cong))
# cong_plot_colors <- c("red4", "blue4", "darkorchid4", "black")
# cong_plot_colors <- c("black", "black", "black", "black")
# cong_plot_colors <- c("red4", "red4", "red4", "black")
cong_plot_colors <- c("#313695", "#313695", "#313695", "black")

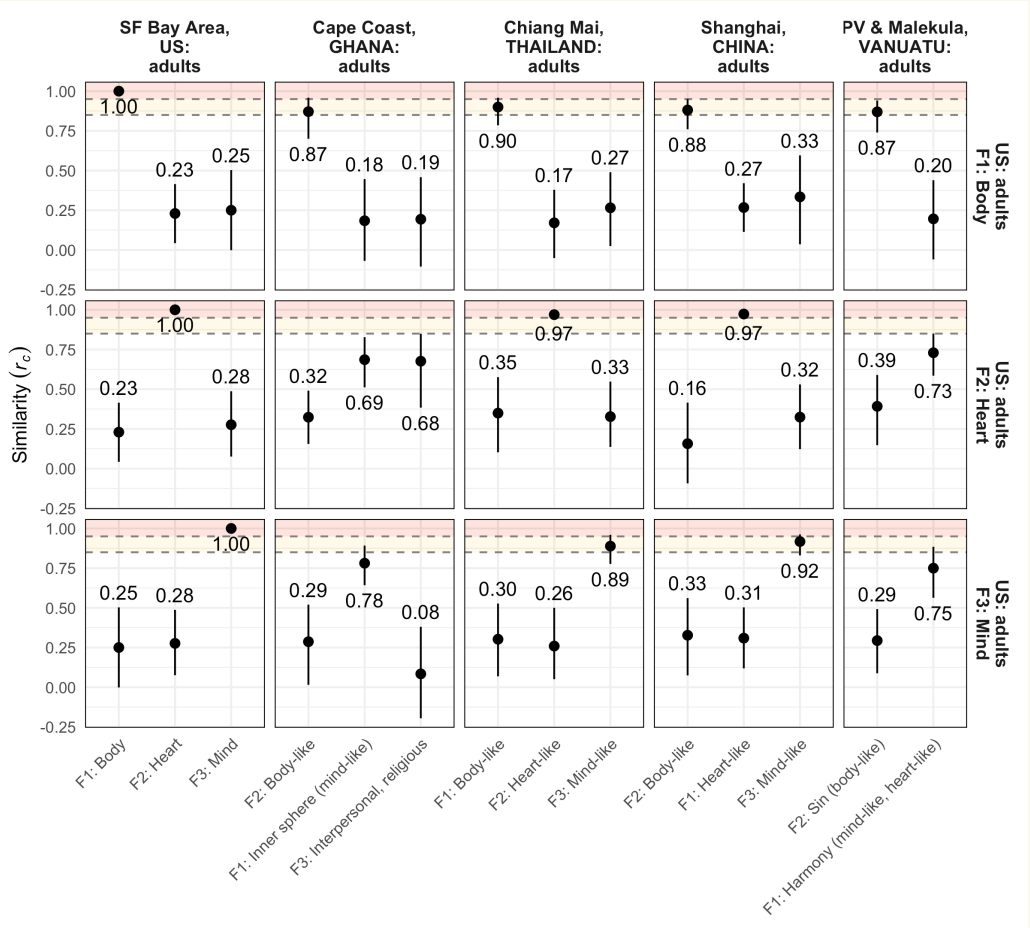
cong_all_ordered %>%
  ggplot(aes(x = reorder(lab_A, as.numeric(factor_A_ordered)),
             y = reorder(lab_B, as.numeric(desc(factor_B_ordered))),
             fill = cong)) +
  geom_tile(color = "black", size = 0.2) +
  geom_text(aes(label = format(round(cong, 2), nsmall = 2),
                color = case_when(cong > 0.85 ~ "a",
                                  cong > 0.75 ~ "b",
                                  cong > 0.65 ~ "c",
                                  TRUE ~ "d")),
            show.legend = F) +
  # body-like factors
  annotate("rect", xmin = 5.5, xmax = 15.5, ymin = 16.5, ymax = 26.5,
           color = cong_plot_colors[1], size = 1.5, alpha = 0) +
  # mind-like factors
  annotate("rect", xmin = 15.5, xmax = 25.5, ymin = 6.5, ymax = 16.5,
           color = cong_plot_colors[2], size = 1.5, alpha = 0) +
  # heart-like factors
  annotate("rect", xmin = 25.5, xmax = 31.5, ymin = 0.5, ymax = 6.5,
           color = cong_plot_colors[3], size = 1.5, alpha = 0) +
  # scale_fill_viridis_c(#trans = scales::exp_trans(base = exp(1)),
  #                      limits = c(cong_lower_lim, 1),
  #                      breaks = seq(cong_lower_lim, 1, 0.05),
  #                      labels = c(format(seq(cong_lower_lim, 0.8, 0.05), nsmall
= 2),
  #                                 "0.85 = moderate", "0.90",
  #                                 "0.95 = high", "1.00"),
  #                      option = "magma",
  #                      guide = guide_colorbar(barheight = 40)) +
  scale_fill_gradientn(#trans = scales::exp_trans(base = exp(1)),
    limits = c(cong_lower_lim, 1),
    breaks = seq(cong_lower_lim, 1, 0.05),
    labels = c(format(round(seq(cong_lower_lim, 0.8, 0.05), 2), nsmall = 2),
               "0.85 = moderate", "0.90"
```

```
```{r cong all pairs plot a, fig.width = 18, fig.asp = 1, echo=FALSE,
warning=FALSE}

# FIGURE 2
cong_lower_lim <- ifelse(min(cong_all_ordered$cong) > -0.05, -0.05,
                         min(cong_all_ordered$cong))
cong_plot_colors <- c("#313695", "#313695", "#313695", "black")

cong_all_ordered %>%
  ggplot(aes(x = reorder(lab_A, as.numeric(factor_A_ordered)),
             y = reorder(lab_B, as.numeric(desc(factor_B_ordered))),
             fill = cong)) +
  geom_tile(color = "black", size = 0.2) +
  geom_text(aes(label = format(round(cong, 2), nsmall = 2),
                color = case_when(cong > 0.85 ~ "a",
                                  cong > 0.75 ~ "b",
                                  cong > 0.65 ~ "c",
                                  TRUE ~ "d")),
            show.legend = FALSE) +
  annotate("rect", xmin = 5.5, xmax = 15.5, ymin = 16.5, ymax = 26.5,
           color = cong_plot_colors[1], size = 1.5, alpha = 0) +
  annotate("rect", xmin = 15.5, xmax = 25.5, ymin = 6.5, ymax = 16.5,
           color = cong_plot_colors[2], size = 1.5, alpha = 0) +
  annotate("rect", xmin = 25.5, xmax = 31.5, ymin = 0.5, ymax = 6.5,
           color = cong_plot_colors[3], size = 1.5, alpha = 0) +
  scale_fill_gradientn(
    limits = c(cong_lower_lim, 1),
    breaks = seq(cong_lower_lim, 1, 0.05),
    labels = c(format(round(seq(cong_lower_lim, 0.8, 0.05), 2), nsmall = 2),
               "0.85 = moderate", "0.90",
               "0.95 = high", "1.00"),
    colors = viridisLite::magma(6),
    values = c(0, 0.65, 0.75, 0.85, 0.95, 1),
    guide = guide_colorbar(barheight = 40)) +
  scale_color_manual(values = c("black", "black", "black", "gray60")) +
  theme_minimal() +
  theme(
    axis.text.x = element_text(
      angle = 90, hjust = 1, vjust = 1,
```

➢ **similarity** across cultures groups



• Original

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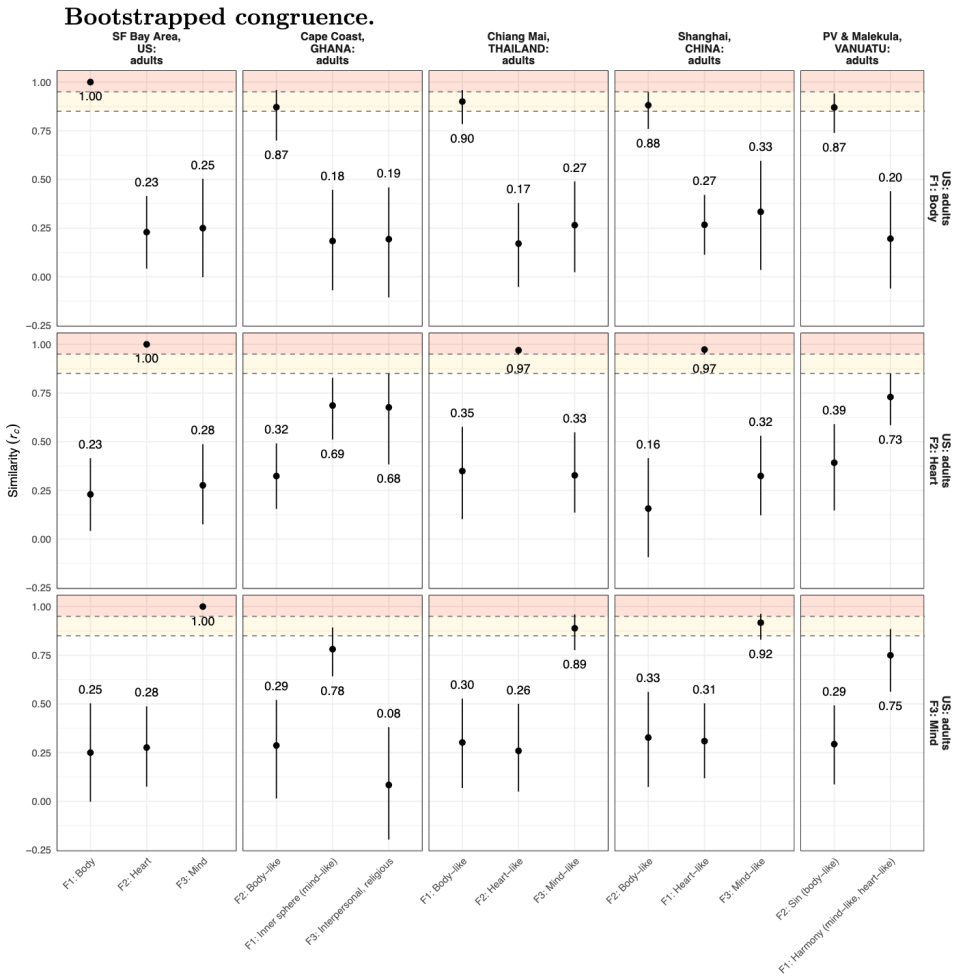


• Replication

Code

```
```{r cong min adults}
# find minimum value to set constant lower bound of plots
min_cong_adults <- cong_df_adults %>%
  summarise(min_cong = min(ci_lower, na.rm = T))
```

Figure 3

```{r cong cis us base adults, fig.width = 4, fig.asp = 0.9}
# FIGURE 3
cong_plot_fun(cong_df = cong_df_adults, which_country = "US") +
  labs(x = NULL)
ggsave("../figures/fig03_oblique.png")
ggsave("../figures/fig03_oblique.pdf")
```
```

```
```{r cong min adults}
# find minimum value to set constant lower bound of plots
min_cong_adults <- cong_df_adults %>%
  summarise(min_cong = min(ci_lower, na.rm = T))
```

```{r cong cis us base adults, fig.width = 12, fig.asp = 1, echo=FALSE,
warning=FALSE}
# FIGURE 3
cong_plot_fun(cong_df = cong_df_adults, which_country = "US") +
  labs(x = NULL)

# ggsave("/Users/ss/Desktop/Re_Weisman_2021_Group1_2024/figures/fig03_oblique.png"
, width = 10, height = 7, dpi = 300)

```
```

Adults ✔ Like "Body" factor

	factor_A	factor_B	mean	ci_lower	ci_upper	age_group_A	country_A	factor_name_A	δ	评级
原文	chADULTS_F2	usADULTS_F1	0.881	0.760	0.950	adults	China	Ch. adults Factor 2	0%	完全一致
复现	chADULTS_F2	usADULTS_F1	0.871	0.700	0.959	adults	China	Ch. adults Factor 2		
原文	ghADULTS_F2	usADULTS_F1	0.871	0.700	0.959	adults	Ghana	Gh. adults Factor 2	0%	完全一致
复现	ghADULTS_F2	usADULTS_F1	0.871	0.700	0.959	adults	Ghana	Gh. adults Factor 2		
原文	thADULTS_F1	usADULTS_F1	0.900	0.785	0.959	adults	Thailand	Th. adults Factor 1	0%	完全一致
复现	thADULTS_F1	usADULTS_F1	0.900	0.785	0.959	adults	Thailand	Th. adults Factor 1		
原文	vtADULTS_F2	usADULTS_F1	0.870	0.739	0.941	adults	Vanuatu	Va. adults Factor 2	0%	完全一致
复现	vtADULTS_F2	usADULTS_F1	0.870	0.739	0.941	adults	Vanuatu	Va. adults Factor 2		

- the result of the comparison between adults and children like those above

表 3 计算可重复性的评估表

可重复性情况	数量及占比	
	N	%
完全一致($\delta = 0\%$)	248	97.63%
偏差较小($0\% < \delta < 10\%$)	2	0.78%
偏差较大($\delta > 10\%$)	4	1.57%
因舍入导致的偏差	0	0%

Cultural comparisons

- **Body**
- **Heart**
- **Mind**

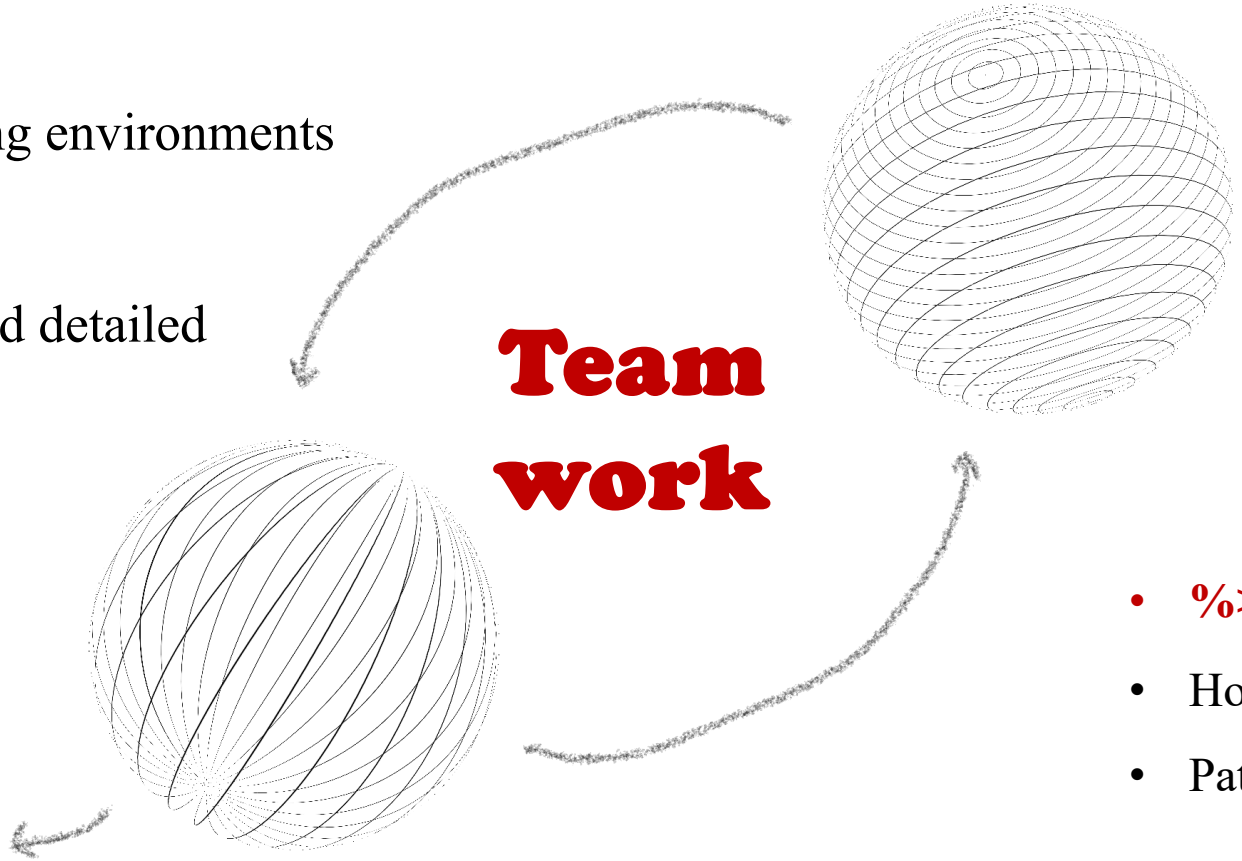
Developmental comparisons

- **Child**
  social–emotional abilities
- **Adult**

➢ **Possible causes of deviations: different version of R package**

➢ Reasons for consistent replication and no errors:

- Similar programming environments
- Pre-processed data
- The code is clear and detailed



➢ From R:

- %>%
- How to debug
- Patient and just do it

➢ Improvement :

- Use of the R package papaja


```
.
├── Doc_Re_Weisman_2021_Group1_2024.Rmd.pdf
├── Report_Re_Weisman_2021_Group1_2024.pptx
├── Script_Re_Weisman_2021_Group1_2024.Rmd
├── References
│   └── R_papaja_example.pdf
│
├── Supplementary_information
│   ├── Re_Supplementary_data
│   │   ├── fig_d_phi.png
│   │   ├── ...
│   │   └── plot02.png
│   ├── Script_Re_Weisman_2021_Group1_2024.ttt
│   ├── Group_1-r-references.bib
│   └── Script_Re_Weisman_2021_Group1_2024.tex
│
├── Script_Re_Weisman_2021_Group1_2024_files
│   ├── Figure_latex
│   │   ├── alt fig 3-1.pdf
│   │   ├── ...
│   │   └── unnamed-chunk-20-1.png
│   ├── Repeatability_figures
│   │   ├── table1.png
│   │   ├── ...
│   │   └── table18.png
│
└── README.md
```

https://github.com/shanshan717/Re_Weisman_2021_Group1_2024

Thanks for your attention and time!

Do you have any questions?