

# A Population Graph based Style Transmission model

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[https://github.com/nevrome/  
popgen.styletrans.saa2019](https://github.com/nevrome/popgen.styletrans.saa2019)

SAA 2019

Practical Approaches to Identifying  
Evolutionary Processes in the Archaeological  
Record

12/04/2019



## Cultural Evolution – Cultural Transmission – Stylistic Variability

- **Cultural Evolution** theory applies terminology and methods from evolutionary biology to cultural anthropology
  - **Cultural Transmission** investigates processes of idea transmission and diffusion of innovation
  - Ideas spread in space and time. They exist in **social space** and their spread depends on **social relations**
  - The spread of functional and stylistic traits is conceptually different. The fate of stylistic (**selectively neutral**) traits is determined by stochastic processes: **Stylistic Variability**
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- There are many different ways to simulate the spread of **neutral traits**

**Yet another simulation approach:  
Population Graph based Style  
Transmission**

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# Simulation concept: Idea agents in a diachronic population network

## Idea agents

- Ideas are the **agents**, not humans (*the meme's eye view*)
  - Ideas have simple behaviour: **greedy expansion**
  - Ideas live in a diachronic **population network**
- 

## Network world

- Each **node** represents a **social entity** (**humans**, households, . . .)
- Each **edge** represents a **social relationship**
- Social entities **only** have relations to partners in **temporal vicinity**
- Social entities have **stronger** relations to partners in **social vicinity**

## Population generation

- **Populations** are divided into **units** (villages, clans, regions, . . . )
- Each **unit** has a name and a size development function and is made up of **humans**
- Each human has a year of birth and a year of death

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R package **popgenerator**: <https://github.com/nevrome/popgenerator>

```
popgenerator::init_population_settings() %>%  
  popgenerator::generate_population()
```

## Population generation: Code sample I

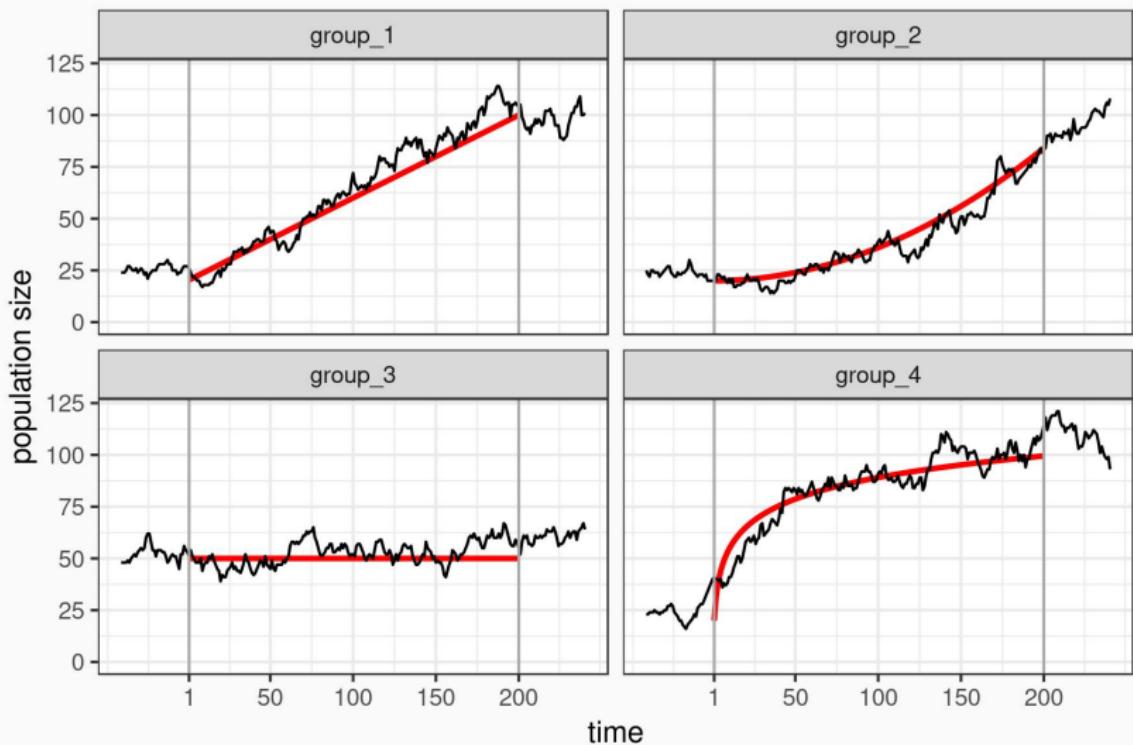
```
time <- 1:200

unit_names <- factor(c("group_1", "group_2", "group_3", "group_4"))

unit_size_functions <- list(
  "group_1" = function(t) {20 + 0.4 * t},
  "group_2" = function(t) {20 + (0.04 * t)^2},
  "group_3" = function(t) {50},
  "group_4" = function(t) {20 + 15 * log(t)}
)

popgenerator::init_population_settings(
  time, unit_names, unit_size_functions,
  age_distribution_function, age_range
) %>% popgenerator::generate_population() -> population
```

## Population generation: Result



## Relations generation

- Each **human** can have multiple **vertical** (Parent-Child) and **horizontal** (Friendship, Teacher-Student, ...) relations
- Relations have a **weight**, which will be relevant for the idea transmission
- The amount of **cross-unit relations** depends on a unit interaction matrix and type based interaction probabilities

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R package **popgenerator**: <https://github.com/nevrome/popgenerator>

```
popgenerator::init_relations_settings() %>%  
  popgenerator::generate_relations()
```

## Relations generation: Code sample II

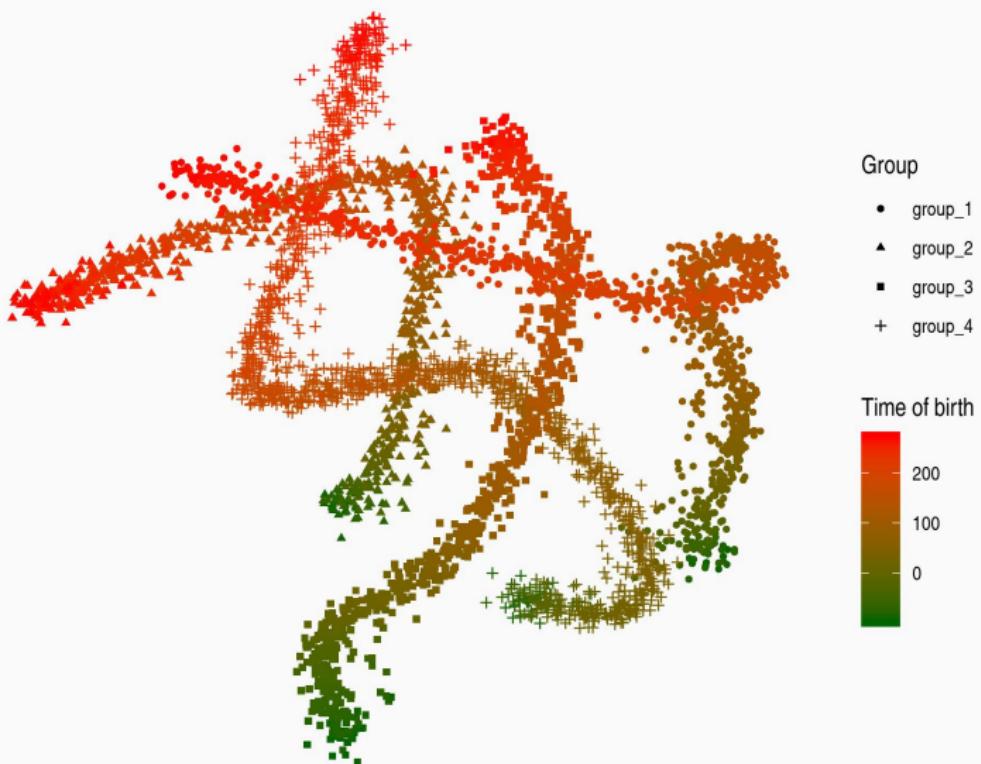
```
amount_friends <- 10

weight_child_of <- 50
weight_friend <- 10

distance_matrix_equal <- matrix(1, 4, 4) %>% `diag<-`(0)
cross_unit_proportion_child_of <- 0.002
cross_unit_proportion_friend <- 0.01

popgenerator::init_relations_settings(
  population, amount_friends, distance_matrix_equal,
  cross_unit_proportion_child_of, cross_unit_proportion_friend,
  weight_child_of, weight_friend
) %>% popgenerator::generate_relations() -> relations
```

## Relations generation: Result



## Idea expansion

- **Ideas** start at some nodes at  $t = 0$  and expand **greedily** in **cycles**
- Expansion can only happen **along edges**
- Success of conversion depends on **edge weight** and **chance**
- The simulation **ends**, when the ideas stop expanding

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C++ CLI program **gluesless**: <https://github.com/nevrome/gluesless>  
(missing: gluesless-R interface)

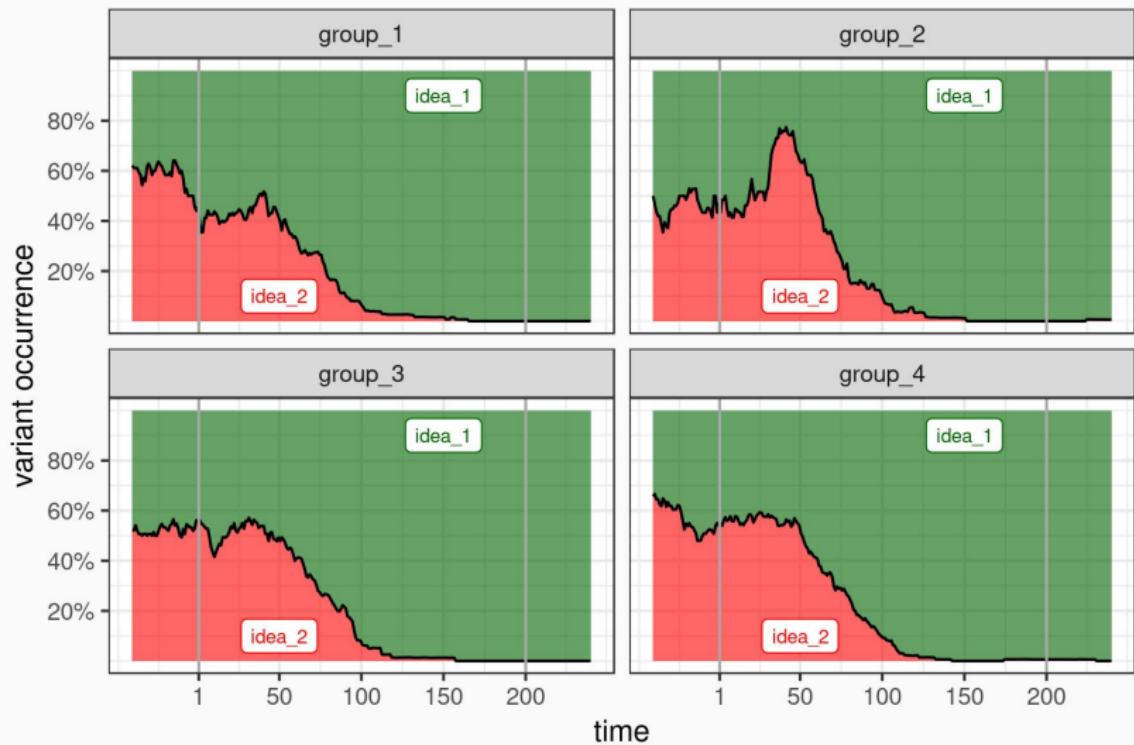
```
gluesless -pi network.paj -ii idea_config.txt -o output.txt
```

## Idea expansion: Code sample III

```
system2(
  "../gluesless/build/gluesless",
  args = c(
    "-pi", graph_file,
    "-ii", ideas_file,
    "-o", output_file, "-q"
  )
)
result <- readLines("tmp_data/gluesless_result.txt")

idea_development <- population %>%
  dplyr::mutate(
    idea = ifelse(id %in% result_idea_1, "idea_1", "idea_2"),
    from = birth_time - abs(birth_time - death_time)/2,
    to = death_time
  ) %>%
  aoristAAR::aorist(
    split_vars = c("unit", "idea")
  )
```

## Idea expansion: Result



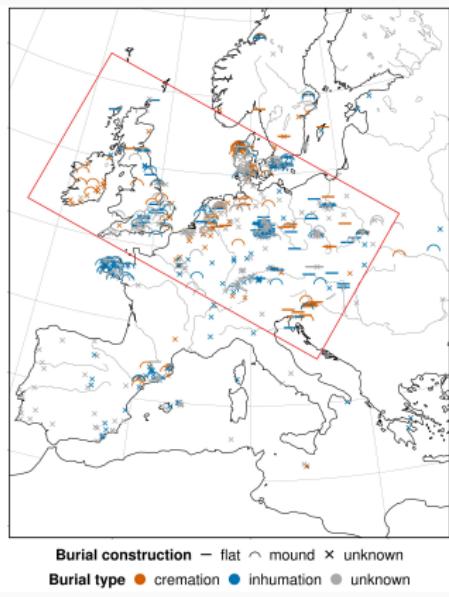
## **What YOU could do now**

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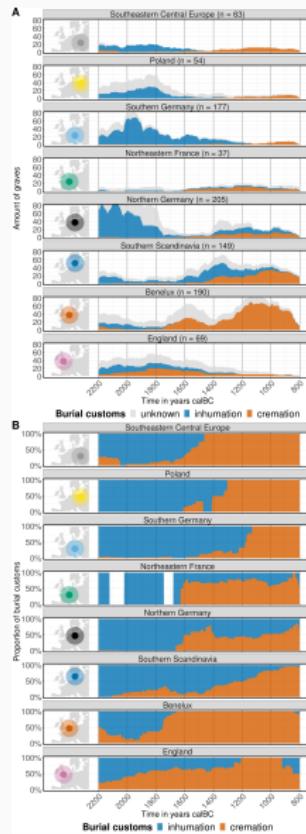
## Comparing real world time series with simulation results

- Identify processes of fashion change and idea transmission and try to describe them with quantitative (!) **time series**
  - Compare these time series and calculate measures of **cultural distance**
  - Compare multiple measures of cultural and **spatial distance** to identify **correlation**
- 
- Explore **models of idea transmission** to understand the **relation of trait distribution and the structure and behaviour of populations**

# Processes of Cultural Transmission: Bronze Age burial rites



Schmid, Evaluating Cultural  
Transmission in Bronze Age burial rites  
of Central, Northern and North-western  
Europe using radiocarbon data,  
Adaptive Behavior, forthcoming



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