

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
- Behaviour/Ideas/Cultural traits 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. Stochastic processes determine the fate of **selectively neutral** traits:
Stylistic Variability

One modelling aproach: Population Graph based Style Transmission

Simulation concept: Idea agents in a diachronic population network

Idea agents

- Ideas are the **entities/agents**, not humans (*the meme's eye view*)
 - Ideas have simple behaviour: **greedy expansion**
 - Ideas live in a configurable, 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
- Individual humans are generated by unit according to an age distribution function and the size development function

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

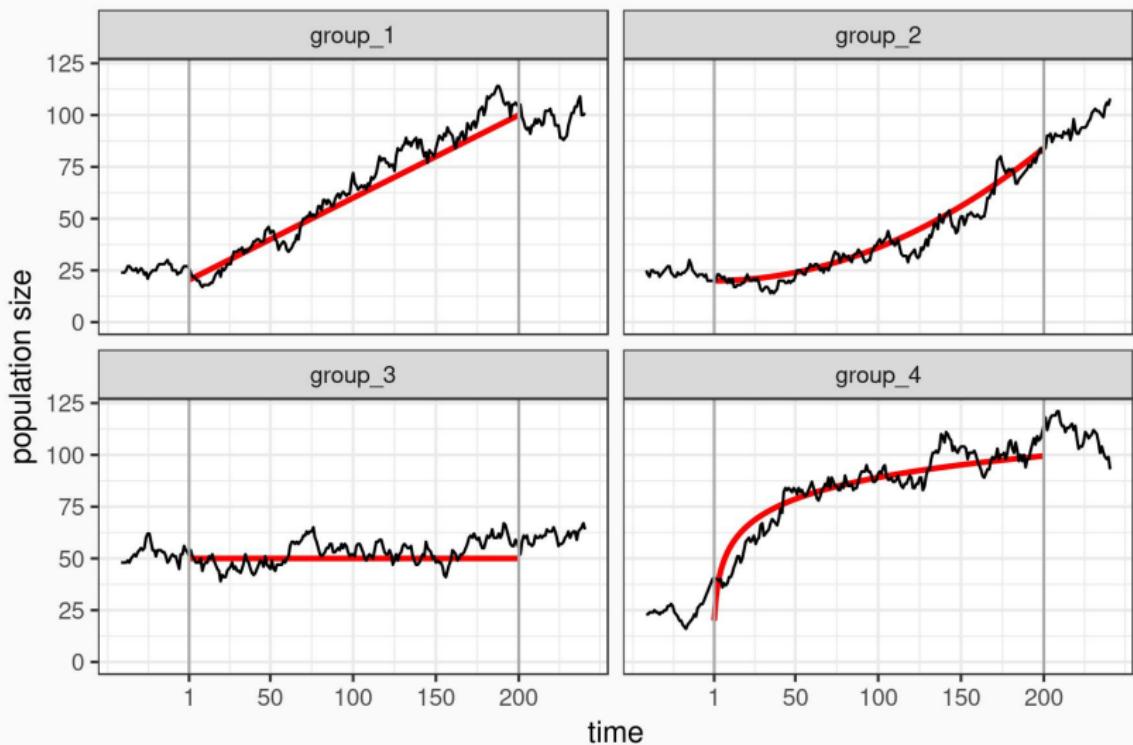
```
popgenerator::init_population_settings() %>%  
  popgenerator::generate_population()
```

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)}
)
age_distribution_function <- function(x) {
  1 / (1 + 0.0004 * 0.7^(-7 * log(x)))
}
age_range <- 1:90

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 are generated imprecisely with a vector based approach for performance reasons
- Relations have a **weight**, which is relevant for the idea transmission
- Cross-unit relations depend on a **unit interaction matrix** and **type based interaction probabilities**

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

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

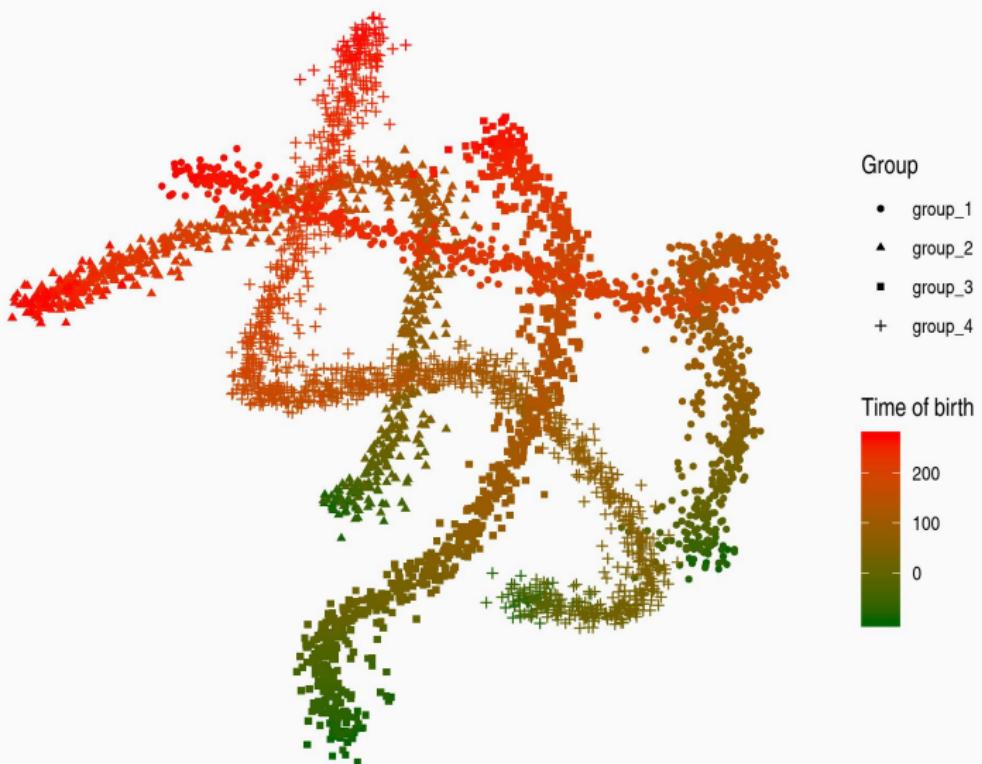
Relations generation: Code sample II

```
amount_friends <- 10
distance_matrix_equal <- matrix(1, 4, 4) %>% `diag<-`(0)
cross_unit_proportion_child_of <- 0.002
cross_unit_proportion_friend <- 0.01
weight_child_of <- 50
weight_friend <- 10

settings <- popgenerator::init_relations_settings(
  population, amount_friends, distance_matrix_equal,
  cross_unit_proportion_child_of, cross_unit_proportion_friend,
  weight_child_of, weight_friend
)

relations <- popgenerator::generate_relations(settings)
```

Relations generation: Result



Idea expansion

- Ideas start at some nodes at $t = 0$ and expand blindly and greedily
- Expansion can only happen along edges. Success of conversion depends on edge weight and chance
- Nodes occupied by ideas are documented and then removed for the next cycle: The network shrinks
- The simulation ends, when the ideas stop expanding.

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

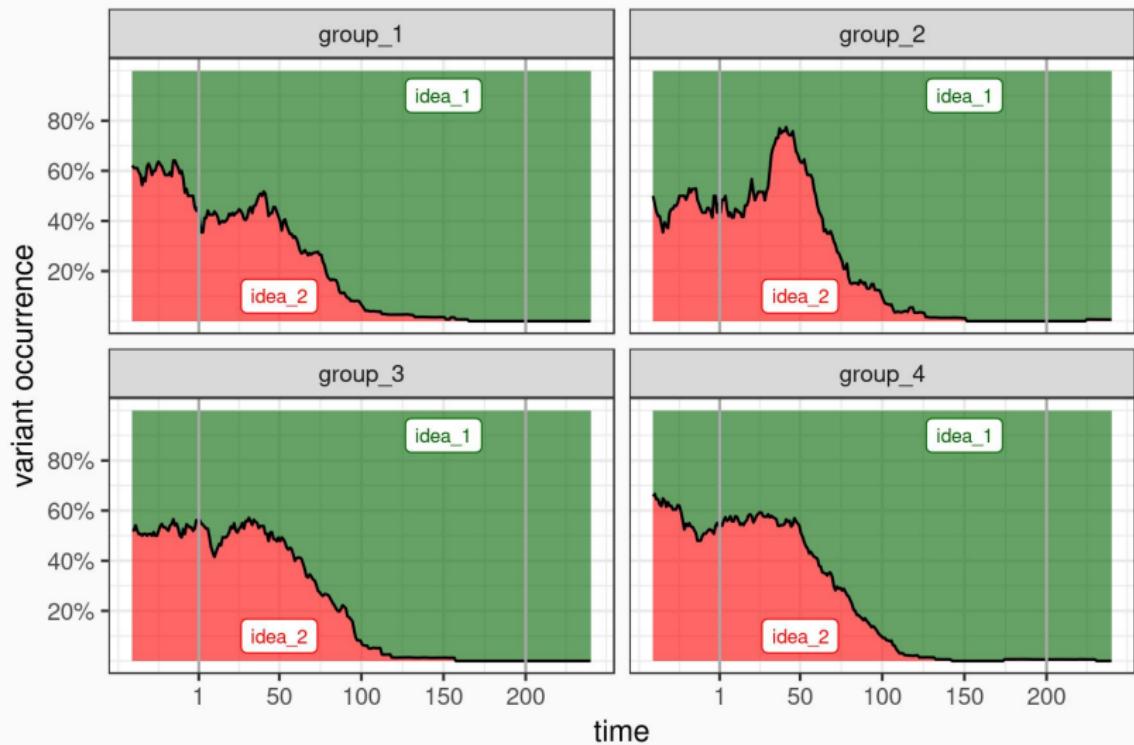
```
gluesless -pi network.paj -ii idea_config.txt -o output.txt
```

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

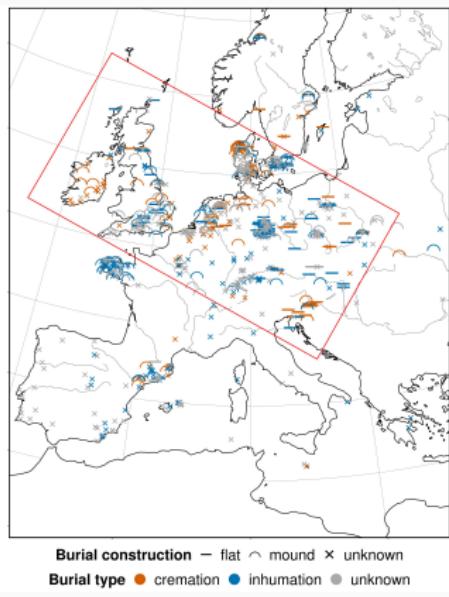


What YOU could do NOW

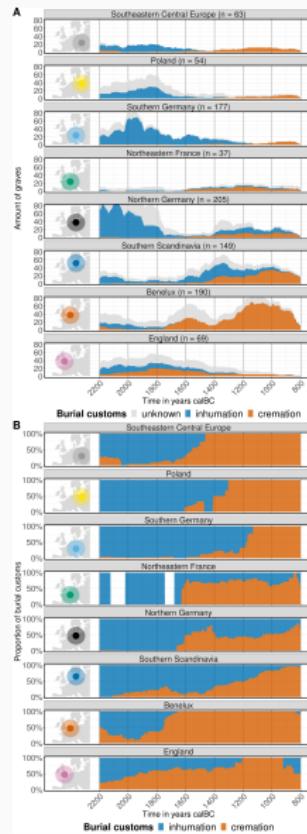
Comparing real world proxies with simulation results

- Identify processes of fashion change and idea propagation 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 propagation** 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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