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Spatial and temporal variation in a sexual population of *Phytophthora infestans*

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Sexual reproduction → genetic variation

- This talk is not about the evidence for sexual reproduction of *P. infestans* in Sweden
- Builds on previous work done to examine questions about
    - Inoculum sources (tubers or external)
    - Possible selection processes from reduced fungicide doses
    - Relationships between geographically separated samples of *P. infestans* from within Sweden
- Important tools needed for this work—microsatellite markers and relevant computer programs

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Reducerade fungiciddoser vid bekämpning av potatisbladmögel

– Vilka blir följderna?

Reduced doses of fungicide for the control of potato late blight

– What are the consequences?

Magnus Jönsson och Gabriella Olsson

Institutionen för skoglig mykologi och växtpatologi
Magisterarbete • 30 hp
Agronom mark/växt
Uppsala 2015

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Genotypic and phenotypic variation of *Phytophthora infestans* on potato in the two Swedish regions Bjäre and Östergötland in 2015

Ida Petersson

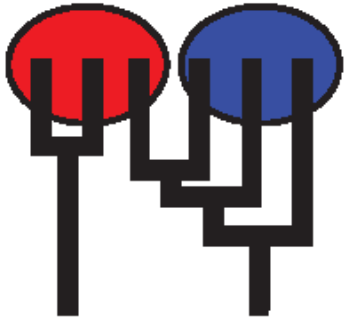
Department of Forest Mycology and Plant Pathology
Independent Project in Biology • Master's thesis • 30 HEC • Uppsala • 2015

Analyses done with

POPPR

Population Genetics in R

1

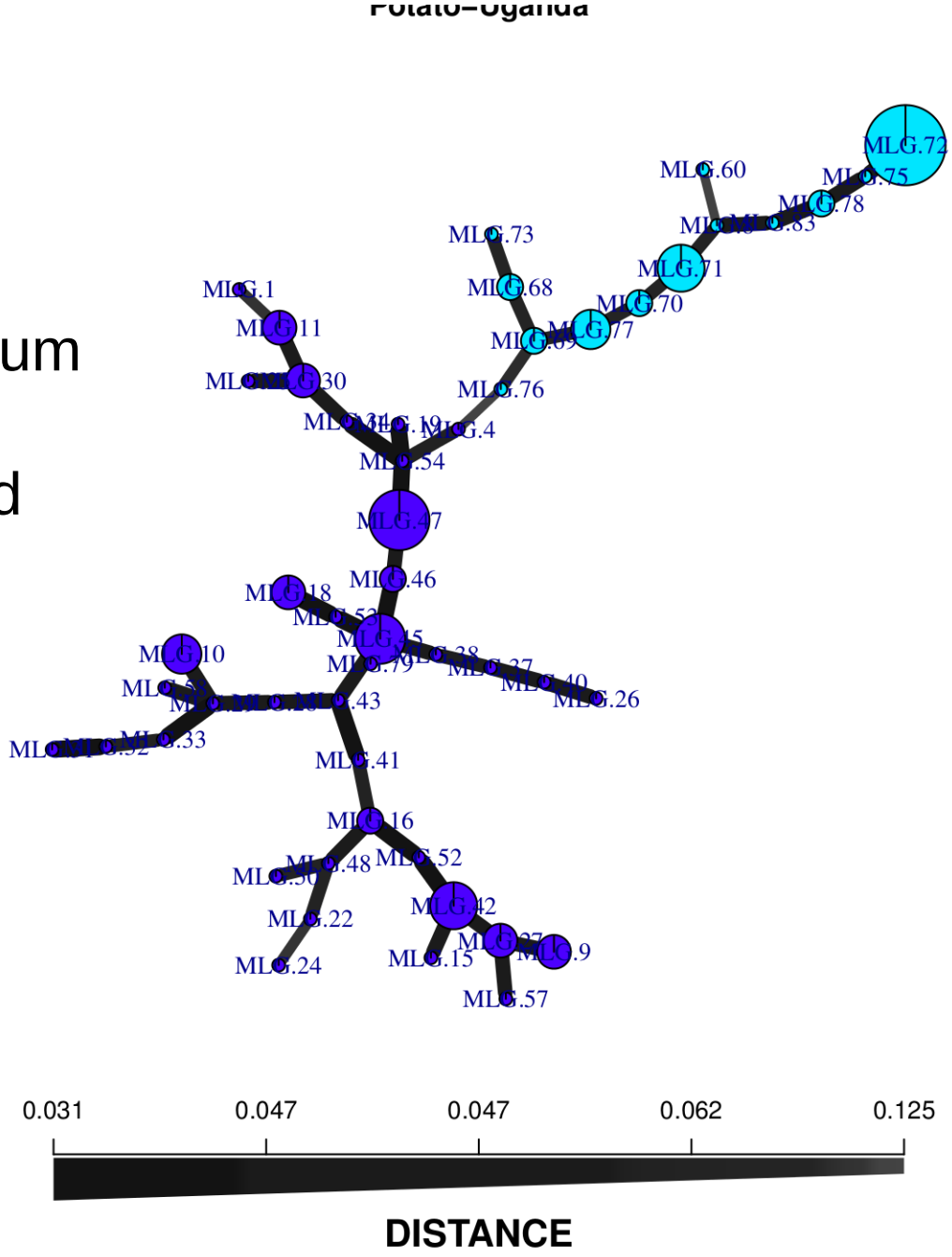


Migrate-n

Poppr functions used:

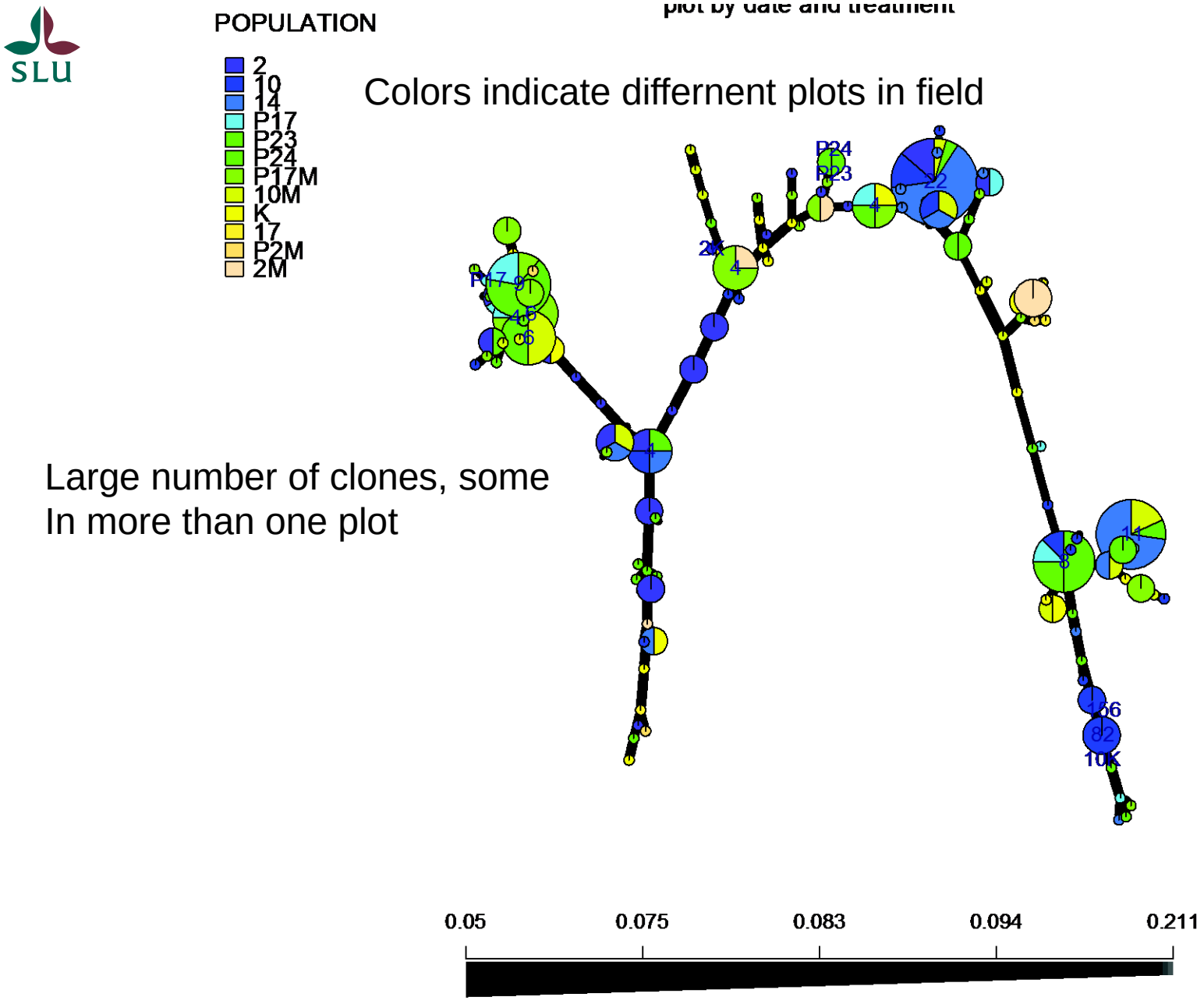
- Bruvo distance: includes information about the difference in the number of repeats. Larger difference in number of repeats – bigger difference.
- Minimum spanning networks. Size of circle indicates number of indviduals with that genotype, thickness of line represents how closely related they are.

Example of a minimum spanning network comparing US-1 and KE-1 from Uganda



Inoculum sources?

- The tuber infection experiment and the selection processes/reduced dosages experiment had multiple samplings during the course of the late blight epidemic.
- Genotypes that were in the infected seed tubers did not contribute significantly to the resulting epidemic
- Reduced fungicide dosages did not cause any selection in the population present in that experiment.
- Multiple time points enable a comparison of genotypes during the epidemics
- 221 samples used in the following analyses



2011 study, infection sources

POPULATION

Inoc
Jul1
Jul8
Jul15
Jul22

Look at time of sampling

Most clones appear at only one sampling time, though some appeared more than once.

2011 study, infection sources

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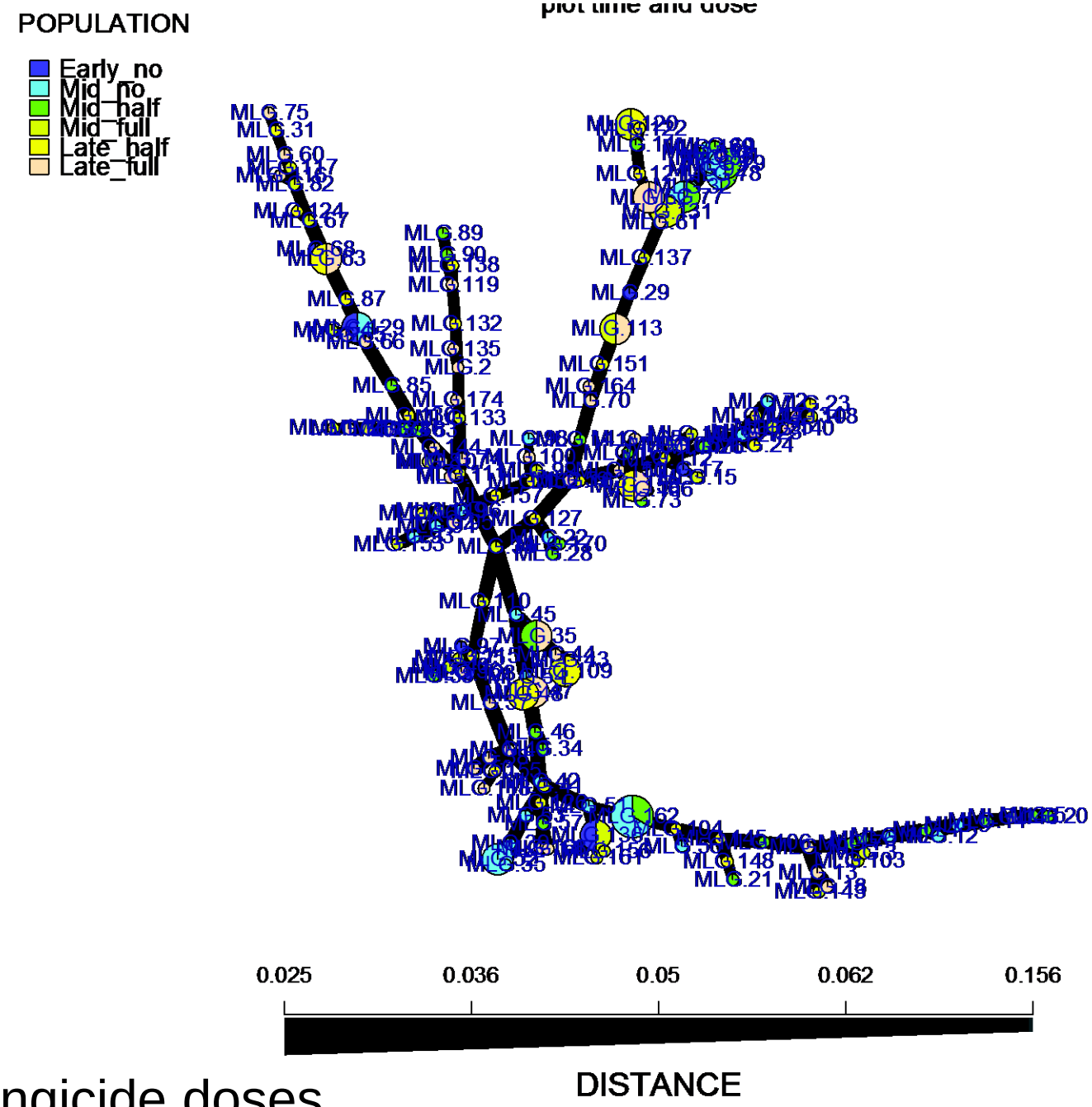
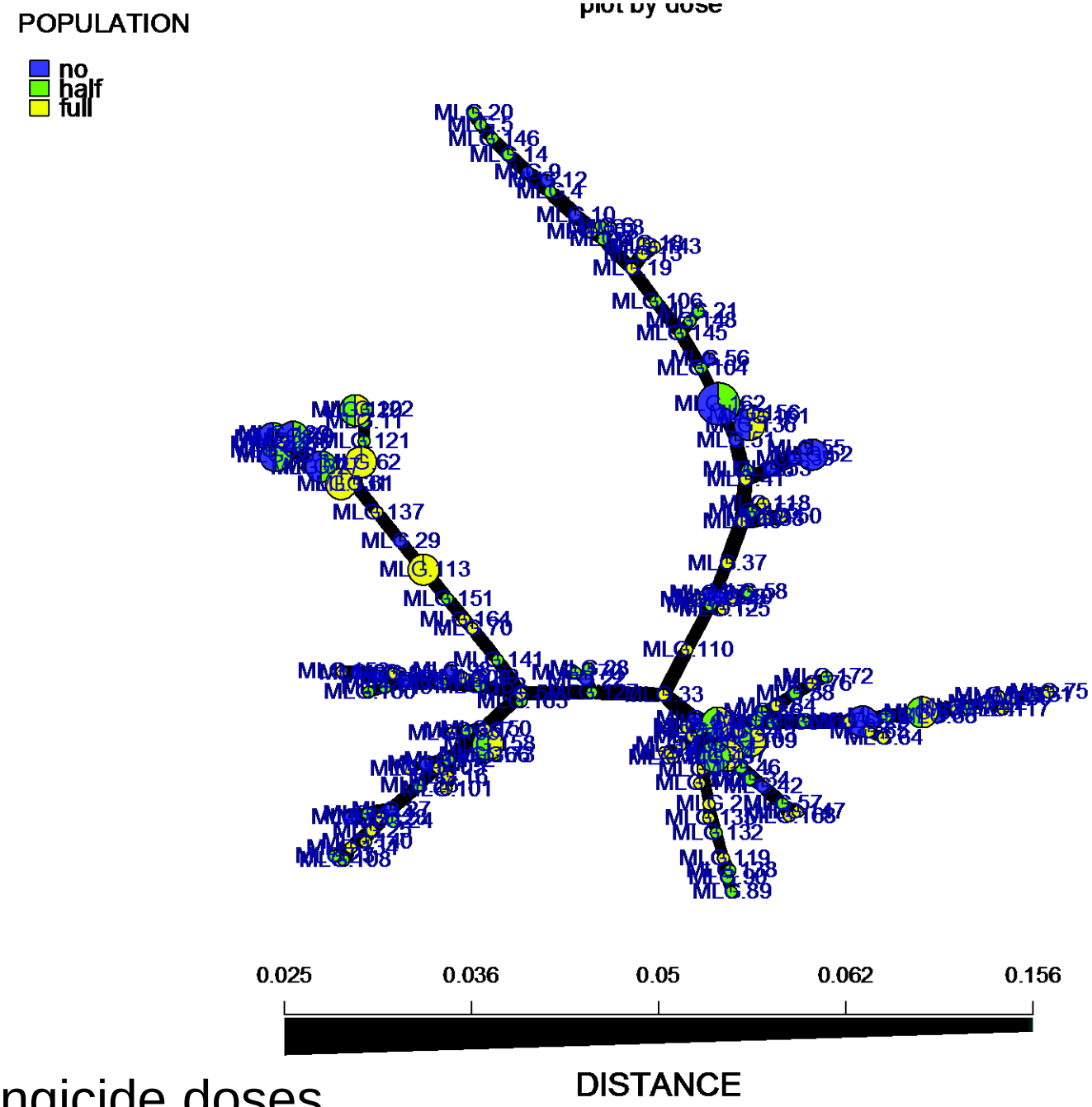
Uppsala 2015

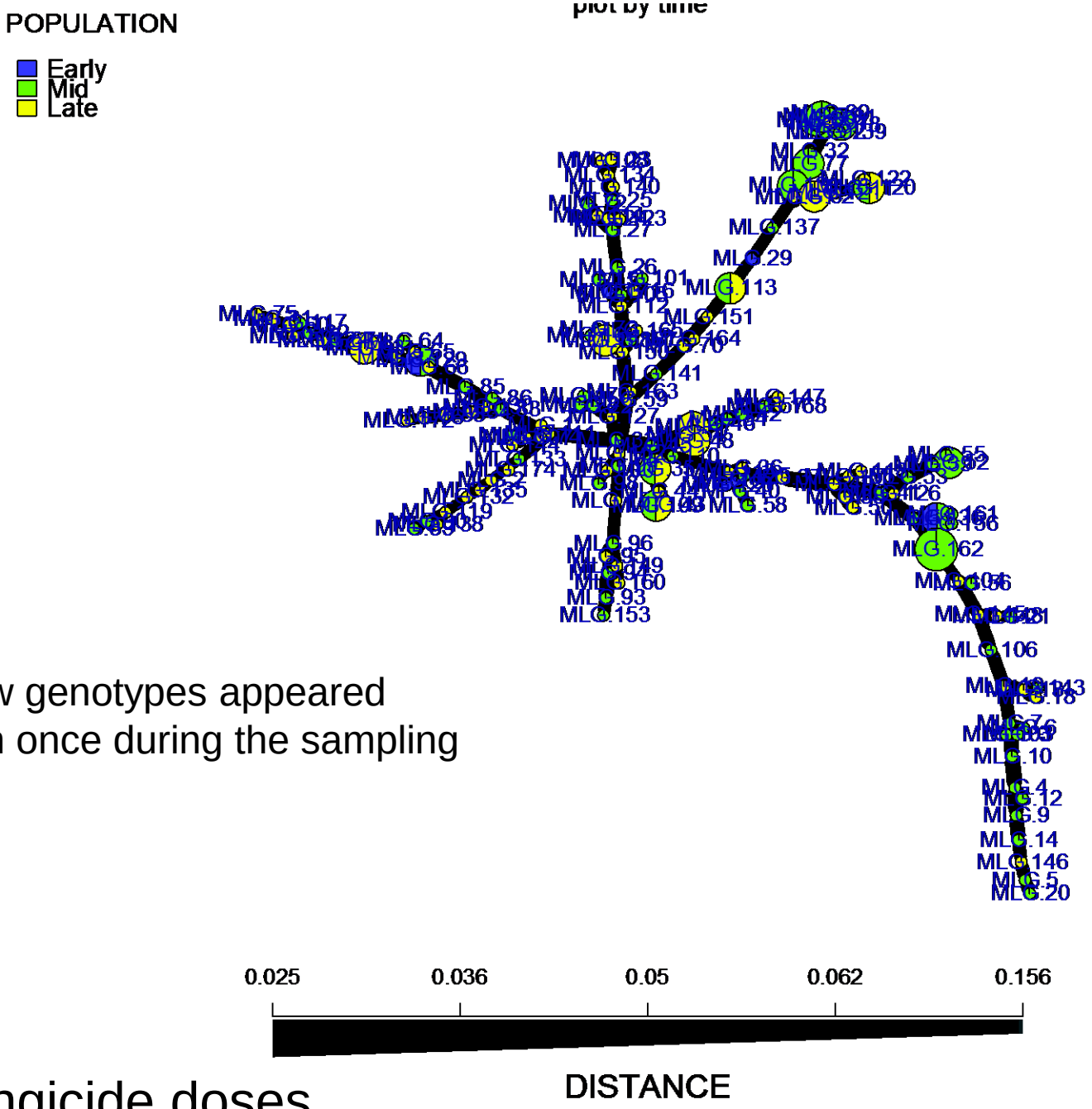
- Study had different fungicides and doses
- 3 sampling time points
- 170 samples after editing and removing individuals with too many missing values



2015, fungicide doses



2015, fungicide doses

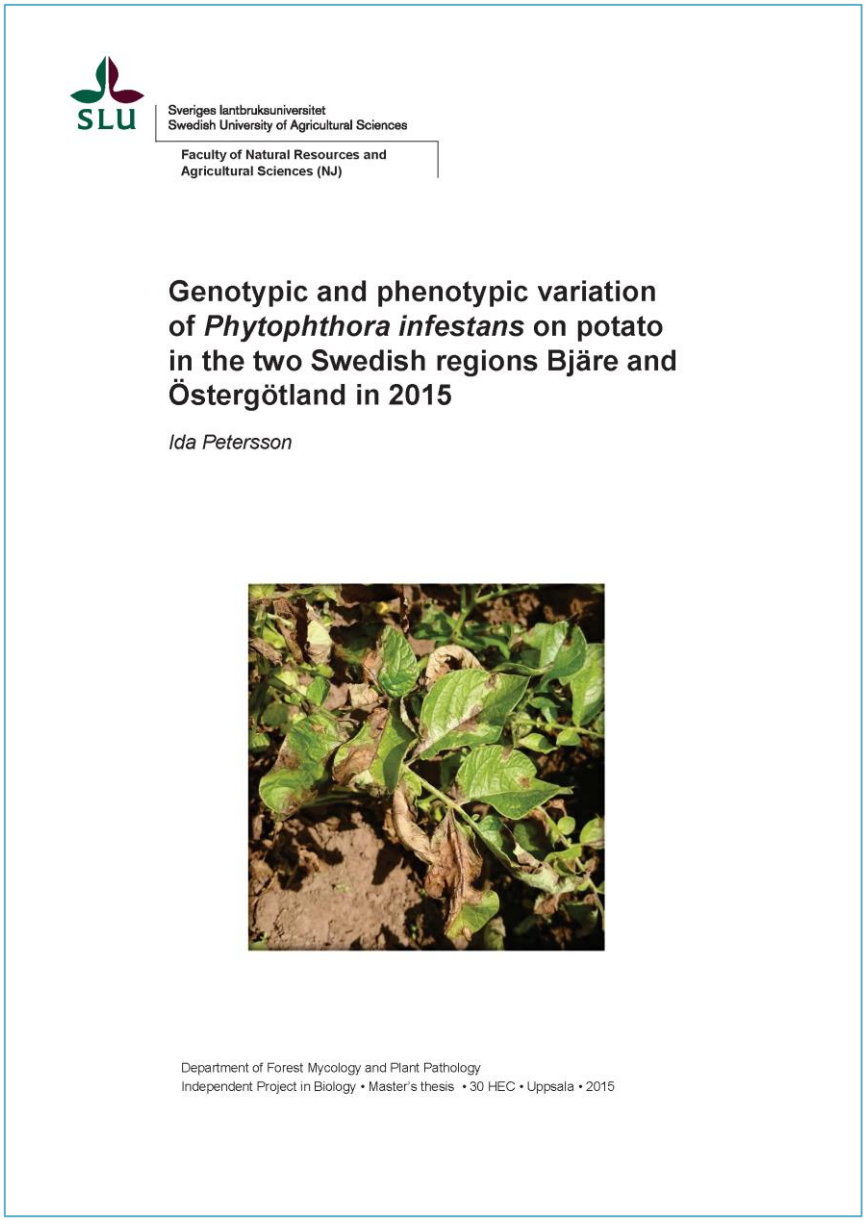


Only a few genotypes appeared more than once during the sampling period.

2015, fungicide doses

Where does inoculum come from?

- External sources (from outside the field) are the primary source of inoculum.
- Those clones that invade a field at the beginning are not necessarily those that dominate at the end.
- Control of inoculum sources from outside any particular field can be extemely important for that field (regional control strategies?)
- Population seems to the stratified in time but we have no biological data that indicates why some clones appear earlier than others.



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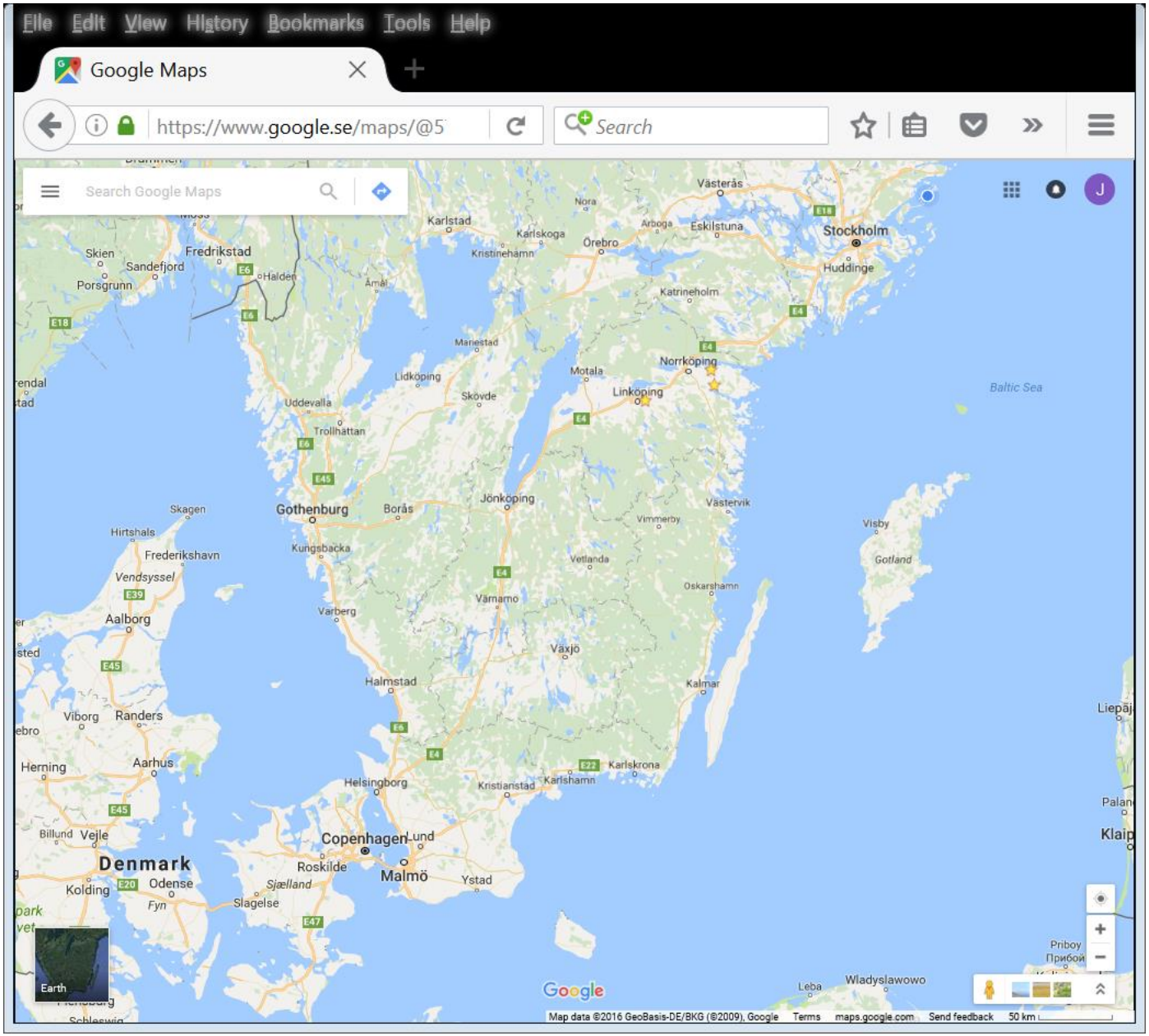
A comparison between samples from two different regions in Sweden

- Samples taken from Bjäre and Östergötland
- Two fields in each region
- Two foci in each field
- 200 samples total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Google Maps
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Search
Search Google Maps
Stockholm
Huddinge
Västerås
Eskilstuna
Örebro
Karlskoga
Karlstad
Nora
Arboga
Kristinehamn
Fredrikstad
Sandefjord
Skien
Porsgrunn
Halden
Åmål
Katrineholm
Norrköping
Motala
Linköping
Lidköping
Skövde
Mariestad
Uddevalla
Trollhättan
Baltic Sea
Gothenburg
Borås
Jönköping
Västervik
Vimmerby
Visby
Gotland
Kungsbacka
Vetlanda
Oskarshamn
Värnamo
Varberg
Växjö
Kalmar
Halmstad
Helsingborg
Kristianstad
Karlshamn
Karlskrona
Hirtshals
Skagen
Frederikshavn
Vendsyssel
Aalborg
Viborg
Randers
Aarhus
Herning
Billund
Vejle
Denmark
Kolding
Odense
Fyn
Slagelse
Sjælland
Roskilde
Copenhagen
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Malmö
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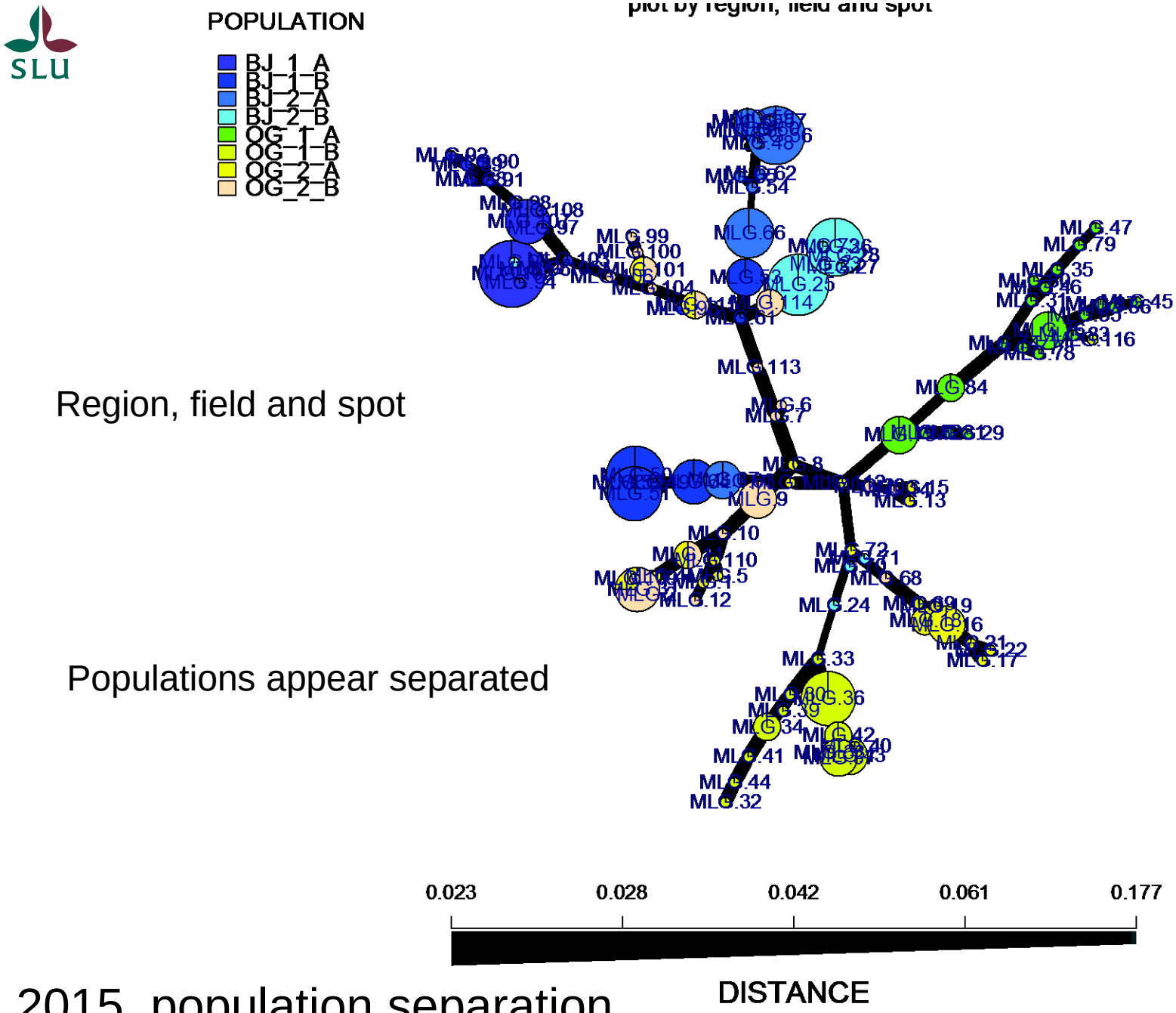
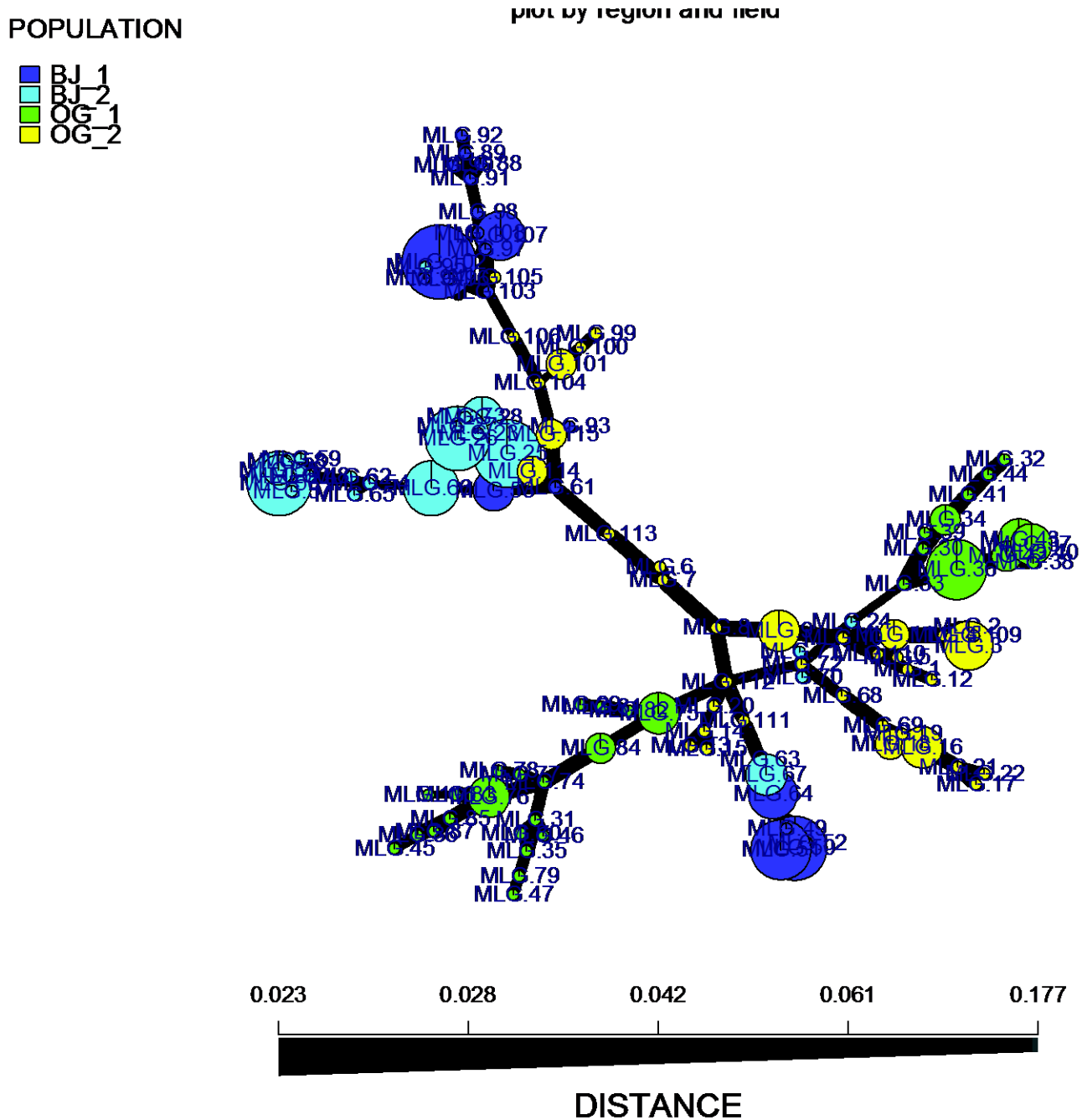


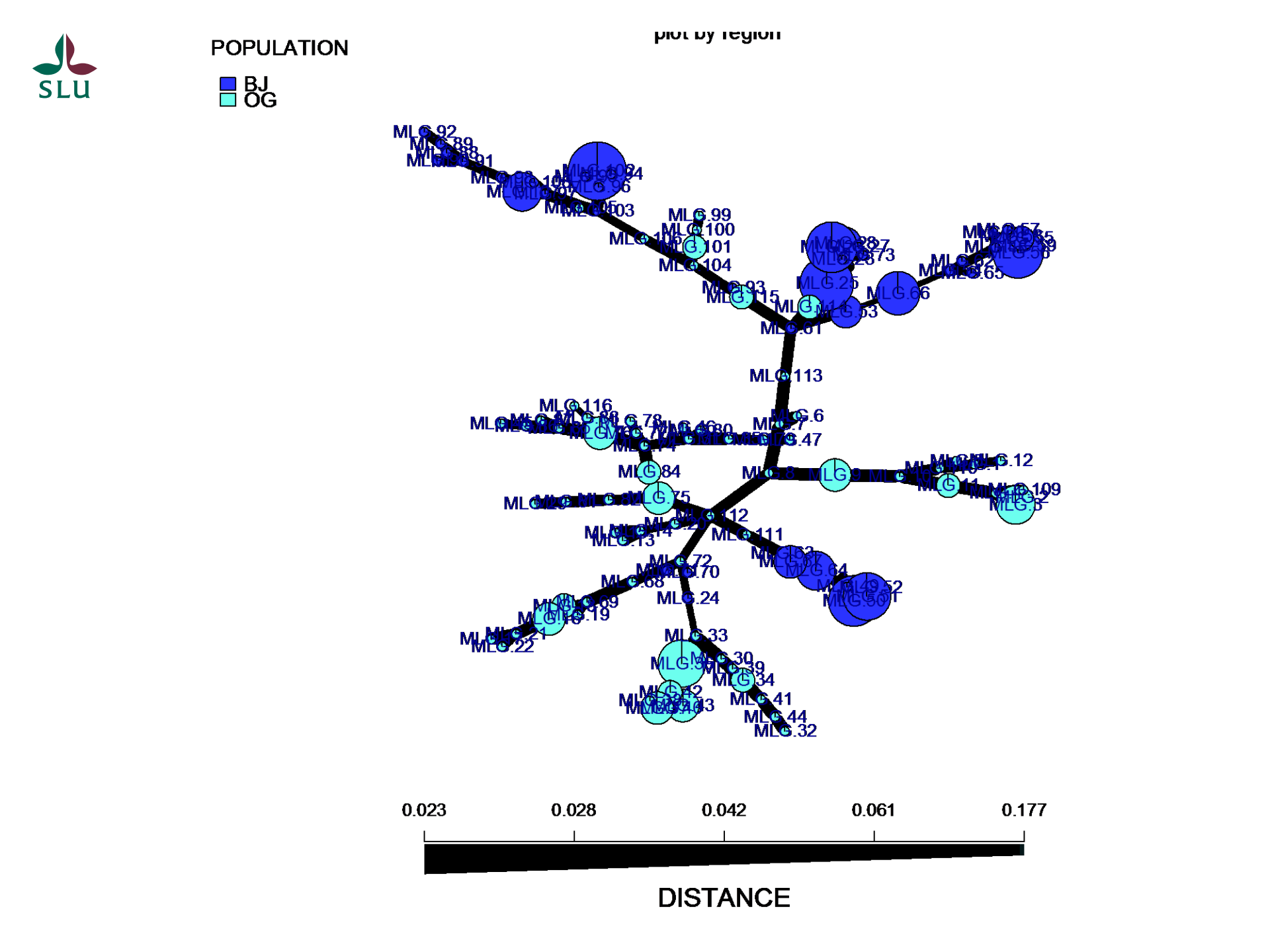
Region, field and spot

Populations appear separated

2015, population separation

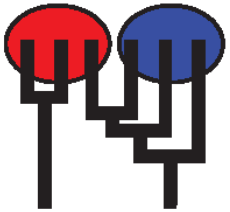


plot by region and field
POPULATION
BJ_1
BJ_2
OG_1
OG_2
0.023
0.028
0.042
0.061
0.177
DISTANCE


POPULATION
BJ
OG
plot by region
MLG.92
MLG.99
MLG.100
MLG.101
MLG.104
MLG.25
MLG.66
MLG.61
MLG.113
MLG.116
MLG.6
MLG.47
MLG.84
MLG.8
MLG.9
MLG.12
MLG.109
MLG.75
MLG.111
MLG.72
MLG.70
MLG.68
MLG.24
MLG.64
MLG.52
MLG.33
MLG.30
MLG.34
MLG.41
MLG.44
MLG.32
0.023
0.028
0.042
0.061
0.177
DISTANCE

Can we estimate migration?

POPPR
Population Genetics in R



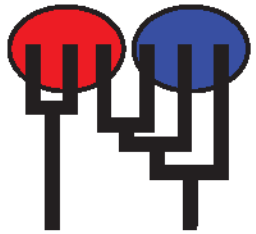
D:\shared\r\poppr\lb_sweden\genclone2migrate.R - R Editor

```
genind2migrate <- function(gid, filename="migrate.txt", repMotif=repeats)
{
# convert to a data frame
df <- genind2df(gid,sep=".",usepop=TRUE)

# if both alleles are missing
df[is.na(df)] <- "?.?"

# if one is missing it is missed so we fix
df2 <- as.data.frame(sapply(df,gsub,pattern="NA",replacement="?"))

pop_names <- levels(gid@pop)
pop_n <- length(pop_names)
```

- Use Bayesian inference within migrate-n to estimate population size and migration rates with different models
- Use Bayes's Factor to compare different models.

Somewhat computation intensive...

MIGRATION RATE AND POPULATION SIZE ESTIMATION
using the coalescent and maximum likelihood or Bayesian inference
Migrate-n version 3.5.1 []
  Compiled for a PARALLEL COMPUTER ARCHITECTURE
  One master and 6 compute nodes are available.
Program started at Sat Jul 9 08:59:36 2016
Program finished at Sat Jul 9 18:22:36 2016



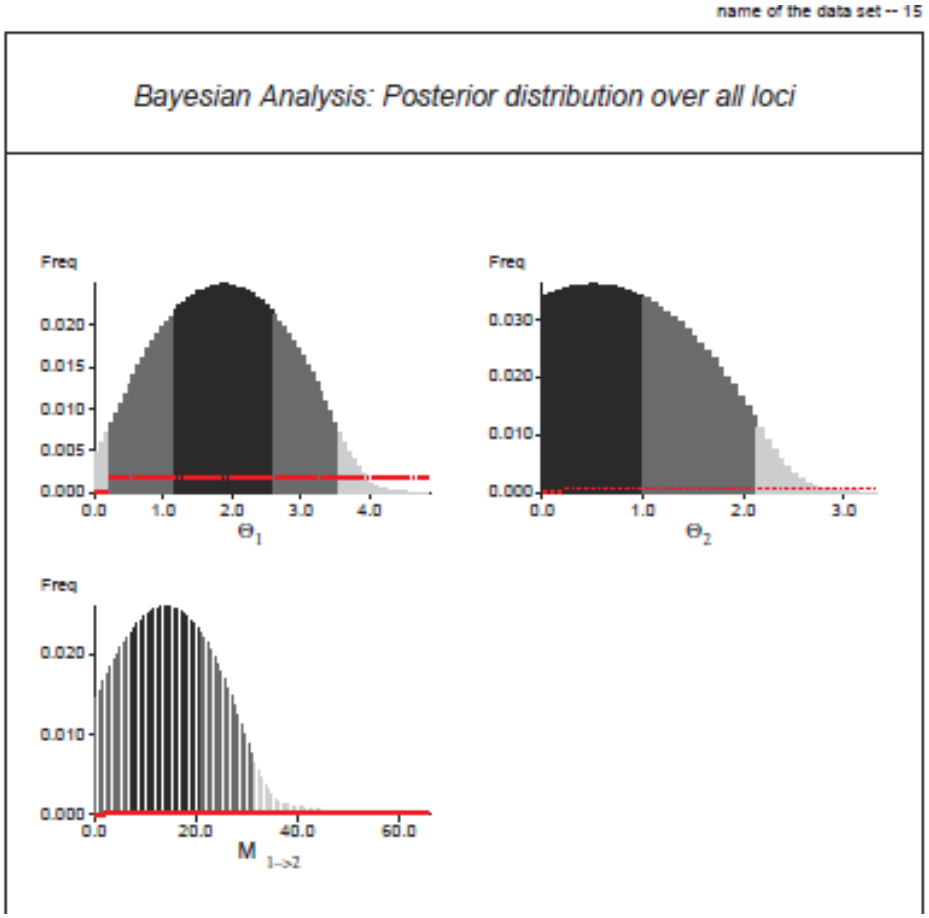
Run for a 4 parameter model (2 population sizes and 2 migration rates)

Comparison with Bayes's Factor

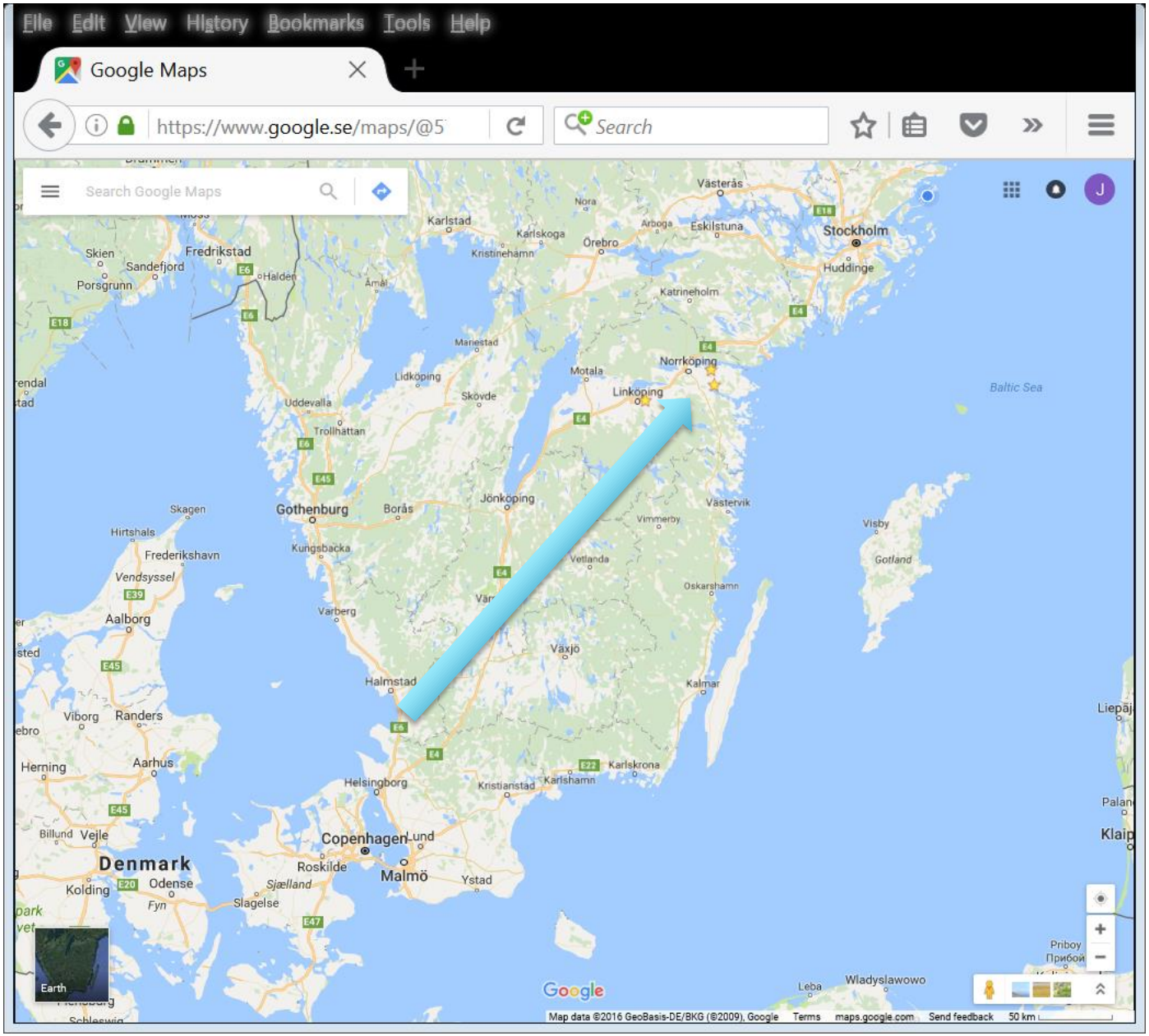
	Marginal Likelihoods				
Model	Run 1	Run 2	Run 3	Run 4	Average
1 single population	-1341.36	-1291.8	-1333.39	-1312.27	-1319.705
2 populations, 2-way migration	-1316.6	-1407.32	-1352.26	-1321.58	-1349.44
2 populations, Bjäre to Östergötland only	-1178.38	-1188.34	-1179.57	-1179.64	-1181.4825
2 populations, Östergötland to Bjäre only	-1169.57	-1209.05	-1201.77	-1199.04	-1194.8575

Larger value Marginal Likelihood → better model. Best model here is 2 populations with migration only from Bjäre to Östergötland

Estimates of population sizes and migration



Bjäre population is larger than the one in Östergötland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Google Maps
https://www.google.se/maps/@5
Search
Search Google Maps
Stockholm
Huddinge
Västerås
Eskilstuna
Örebro
Karlskoga
Karlstad
Nora
Arboga
Kristinehamn
Katrineholm
Norrköping
Linköping
Motala
Mariestad
Lidköping
Skövde
Uddevalla
Trollhättan
Baltic Sea
Gothenburg
Borås
Jönköping
Kungsbacka
Varberg
Halmstad
Växjö
Kalmar
Oskarshamn
Vetlanda
Vimmerby
Västervik
Visby
Gotland
Skagen
Hirtshals
Frederikshavn
Vendsyssel
Aalborg
Fredrikstad
Sandefjord
Skien
Porsgrunn
Halden
Åmål
Viborg
Randers
Aarhus
Herning
Billund
Vejle
Denmark
Kolding
Odense
Fyn
Slagelse
Sjælland
Roskilde
Copenhagen
Lund
Malmö
Ystad
Helsingborg
Kristianstad
Karlshamn
Karlskrona
Liepāj
Klaip
Priboy
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Send feedback
50 km

Exploit genetic variation to understand late blight epidemiology

- We can use the variation to study temporal stratification in *P. infestans*.
- Different clones appear at different times but many do not seem to persist
- Most new infections come from sources external to the field
- Spatial variation also exists in *P. infestans* in Sweden. Local populations exist and migration (genetic exchange) between these populations can be estimated.
- *P. infestans* likes to move around but apparently not too far all at once…….