

# Statistical and mathematical modelling for sero-epidemiological data of tropical infectious diseases

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**Centro de Estatística e Aplicações  
Universidade de Lisboa**



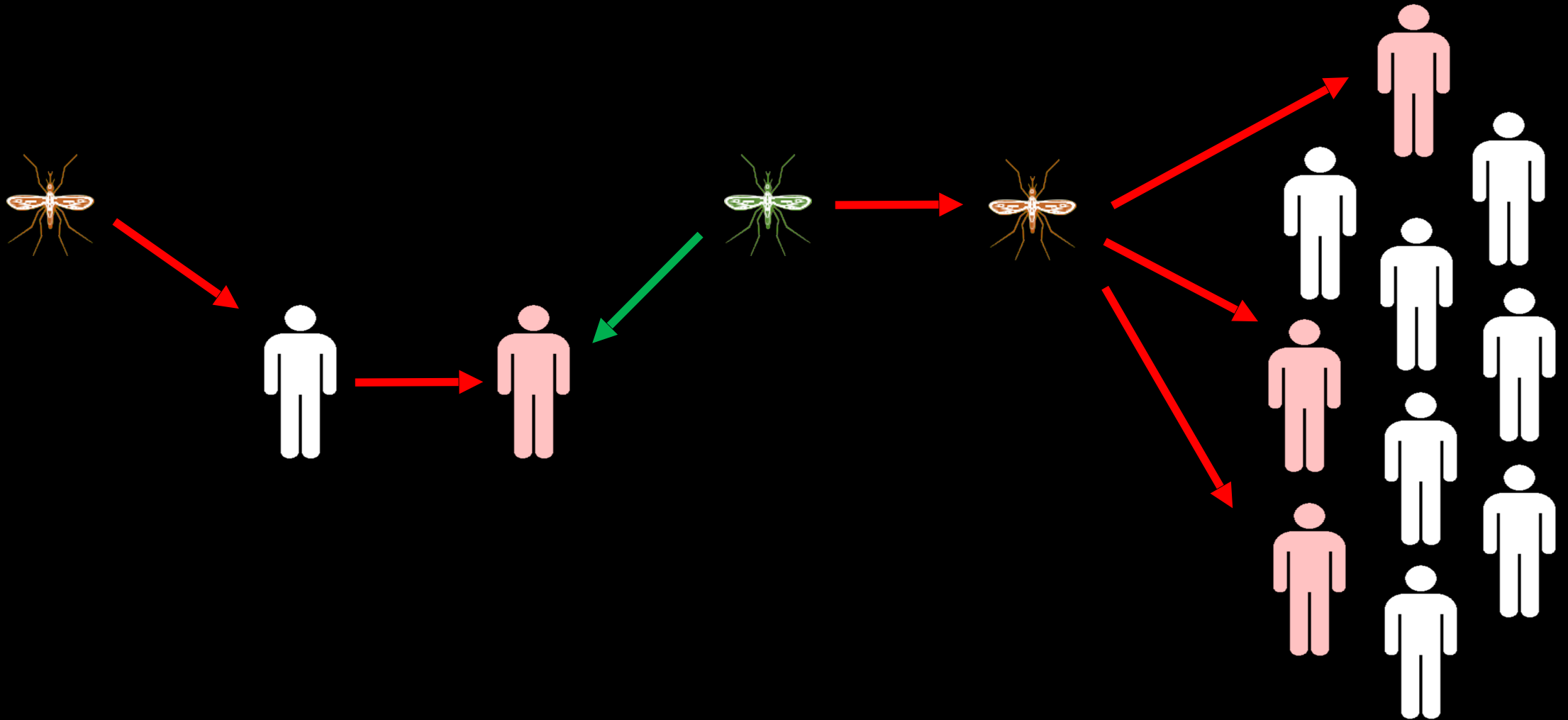
# Workshop content

1. Defining seropositivity (using two-Gaussian mixture models) and estimating seroprevalence
2. Estimating seroconversion rate (using reversible catalytic models)
3. Calculating sample size for controlling precision of seroconversion rate

GitHub:

[https://github.com/immune-stats/Workshop\\_Malaria\\_PALOP\\_2025](https://github.com/immune-stats/Workshop_Malaria_PALOP_2025)

# How to measure malaria transmission?



# How to measure malaria transmission?

1. Prevalence of infection or parasite rate (non-informative when disease transmission intensity is low)
2. Entomological inoculation rate (trick to estimate)
3. Seroprevalence (prevalence of exposure)
4. Seroconversion rate (proxy of transmission intensity)

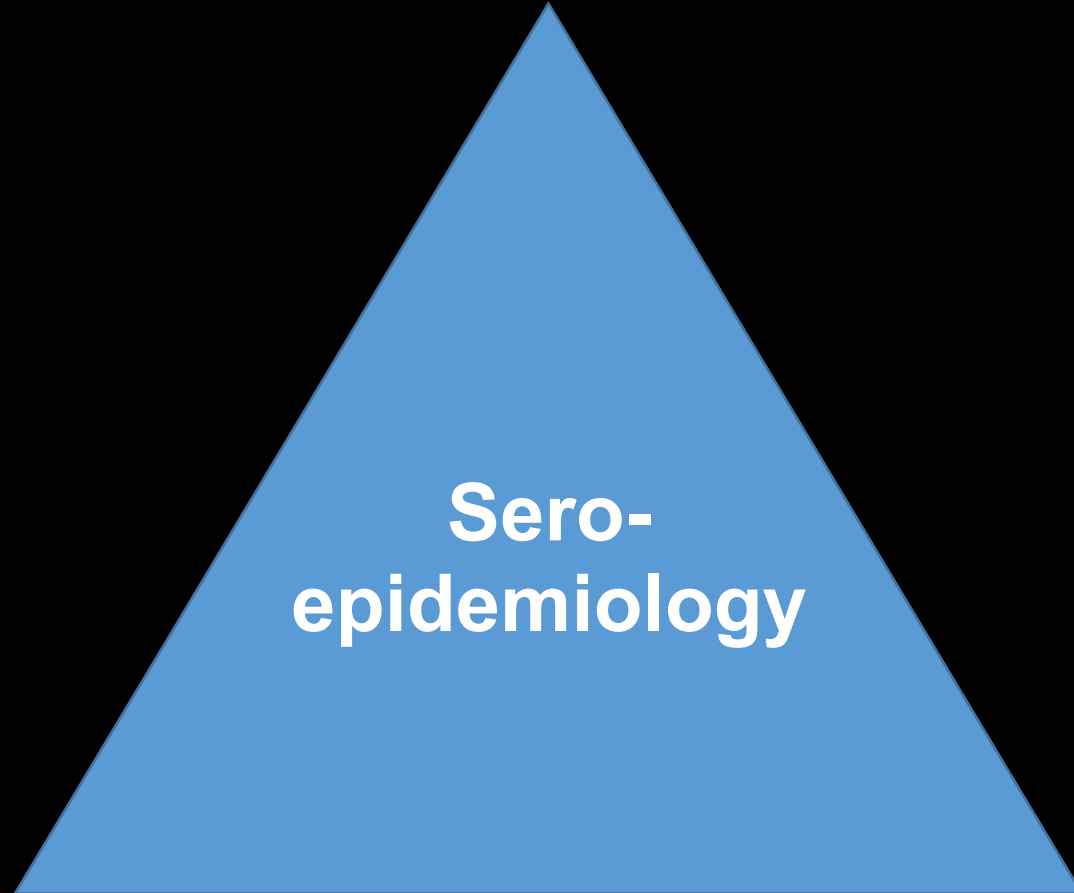
Seroepidemiology

**Epidemiology**

**Sero-  
epidemiology**

**Immunology**

**Statistics**

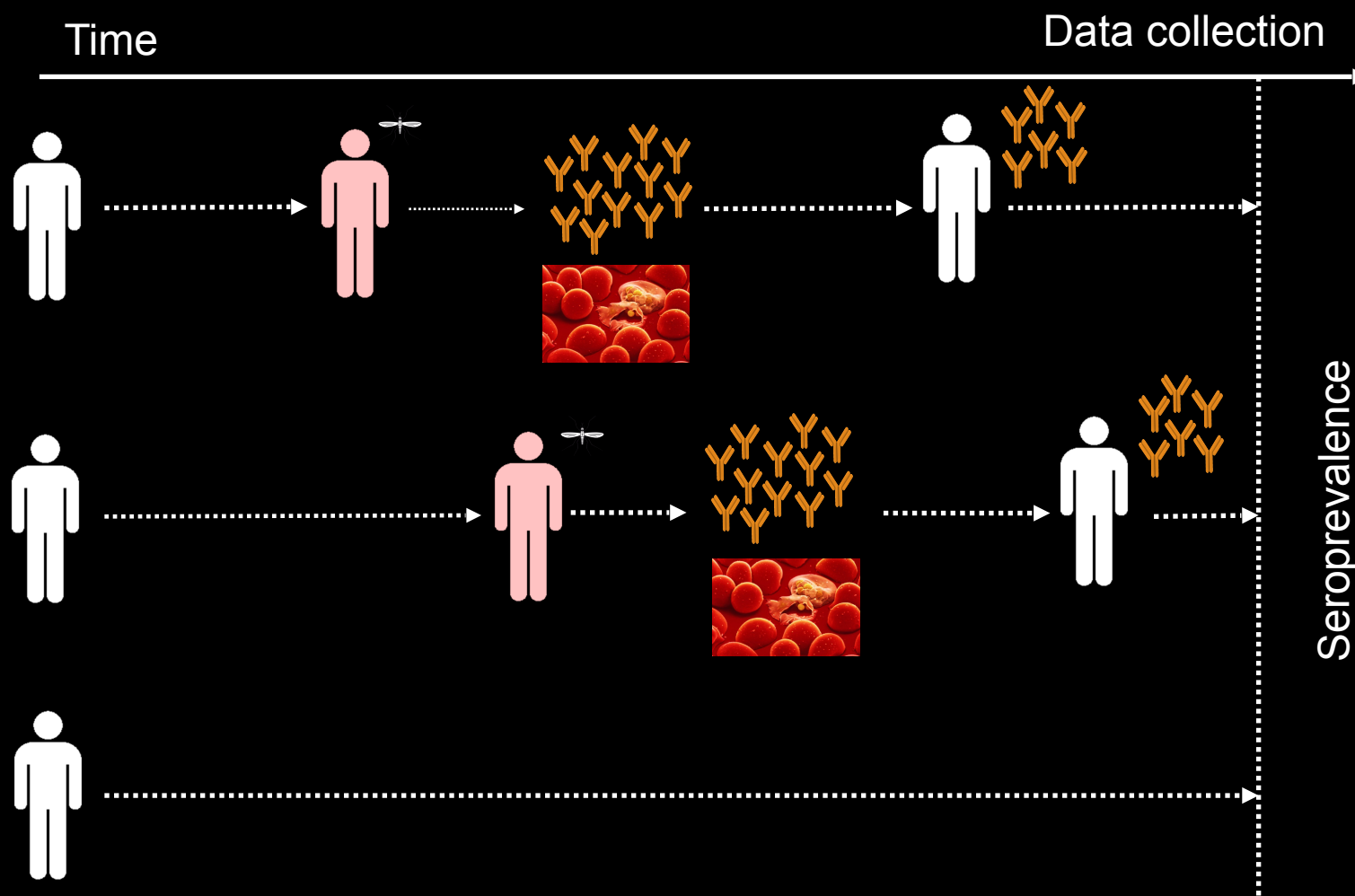


1.

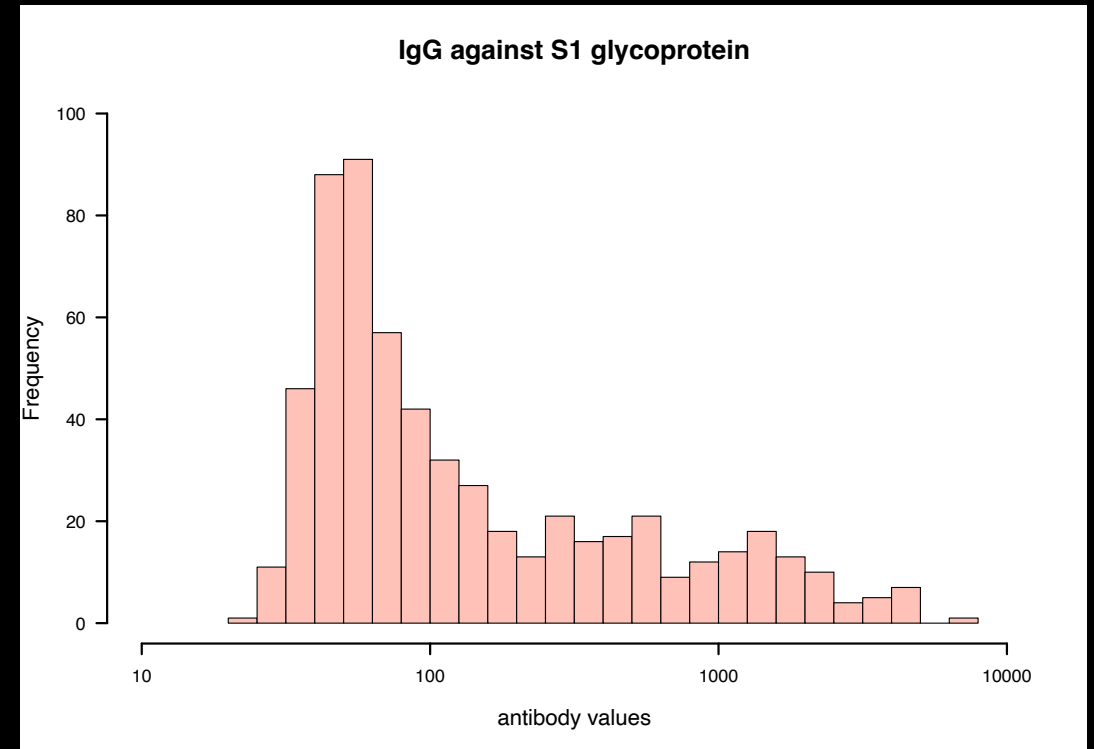
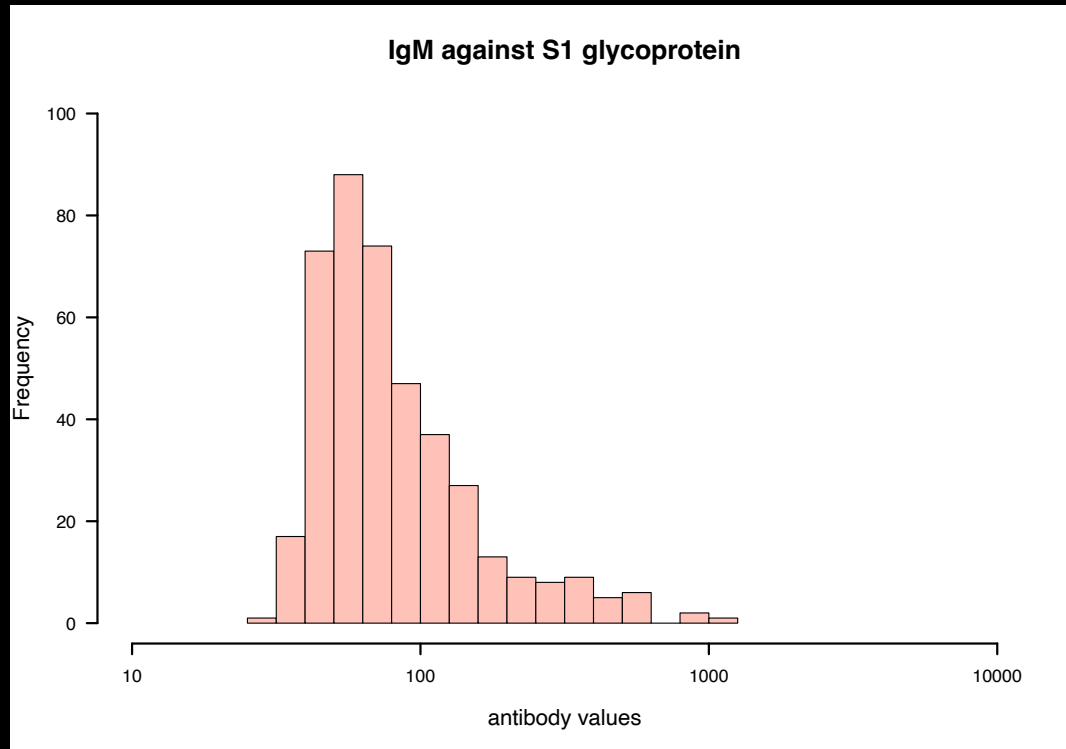
Defining seropositivity (using two-Gaussian mixture models) and estimating seroprevalence



# Basic principle

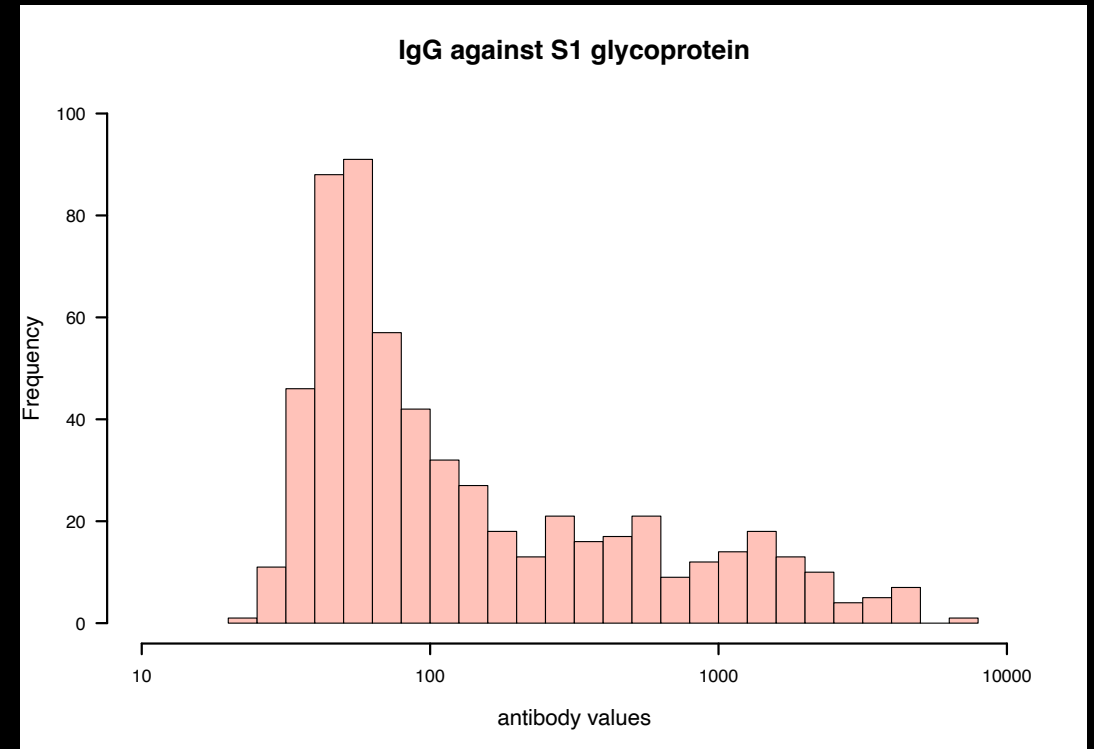
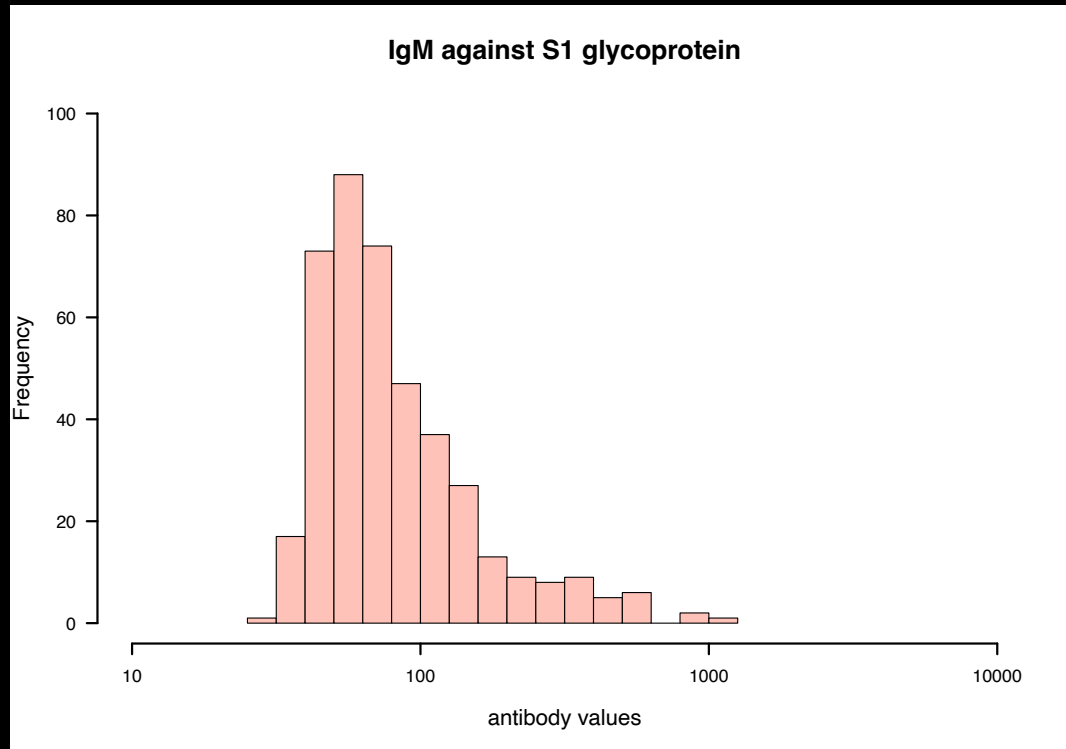


# Antibody data are intrinsically quantitative



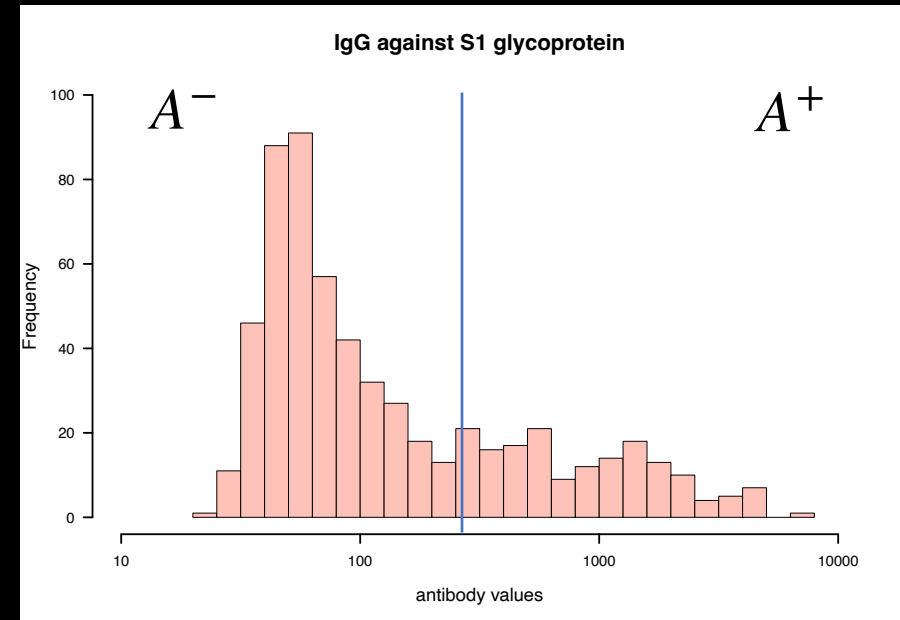
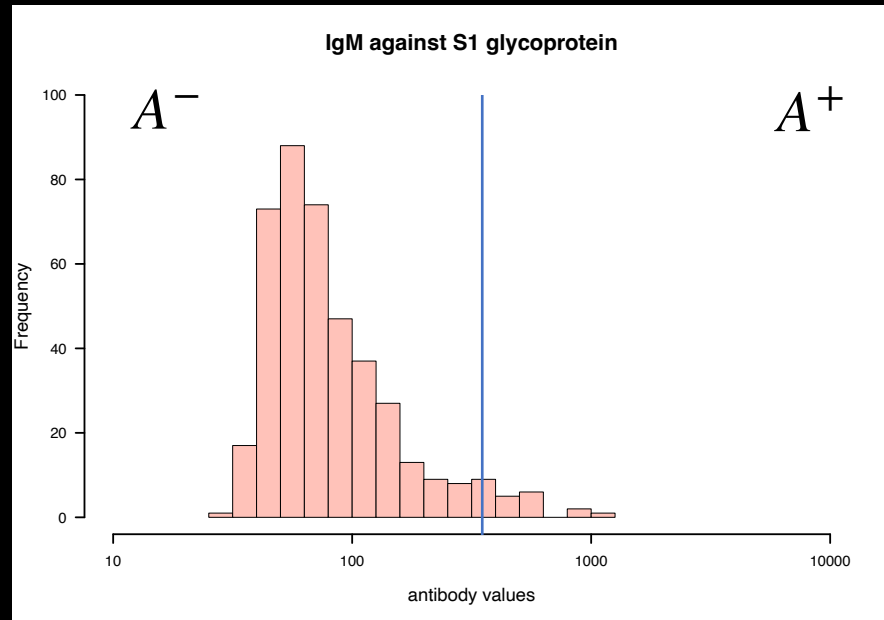
Rosado et al (2020). Serological signatures of SARS-CoV-2 infection: Implications for antibody-based diagnostics. medRxiv 2020.05.07.20093963.

# Who are the seropositive individuals?



Rosado et al (2020). Serological signatures of SARS-CoV-2 infection: Implications for antibody-based diagnostics. medRxiv 2020.05.07.20093963.

# How to determine the cut-off?



# Approaches to determine the cutoff

```
graph TD; A[Approaches to determine the cutoff] --> B[Use of a known seronegative population]; A --> C[Use of data under analysis only]; B --> D[European samples]; C --> E[Two-Gaussian mixture model]; D --> F[The 3-sigma rule]; E --> F;
```

Use of a known seronegative  
population

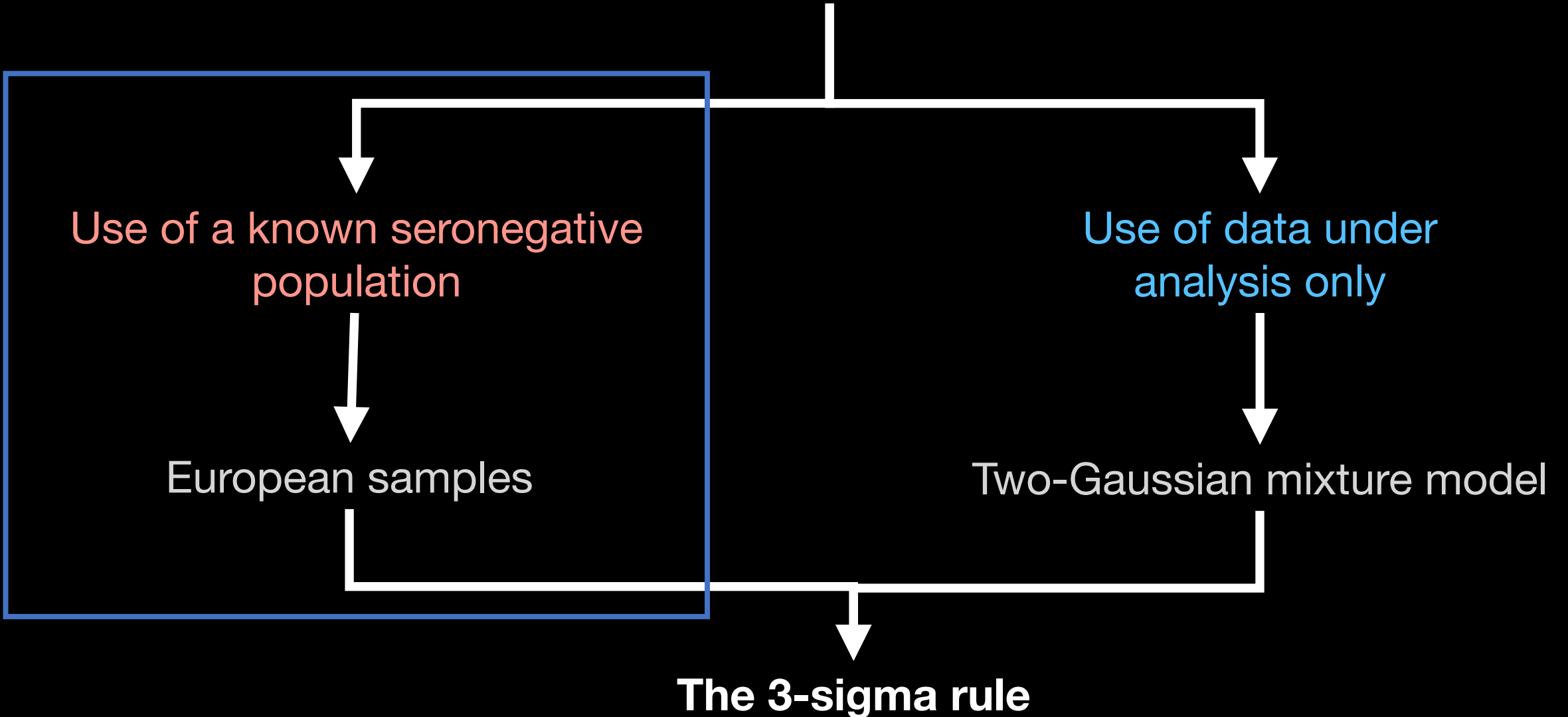
Use of data under  
analysis only

European samples

Two-Gaussian mixture model

**The 3-sigma rule**

## Approaches to determine the cutoff



## The 3-sigma rule

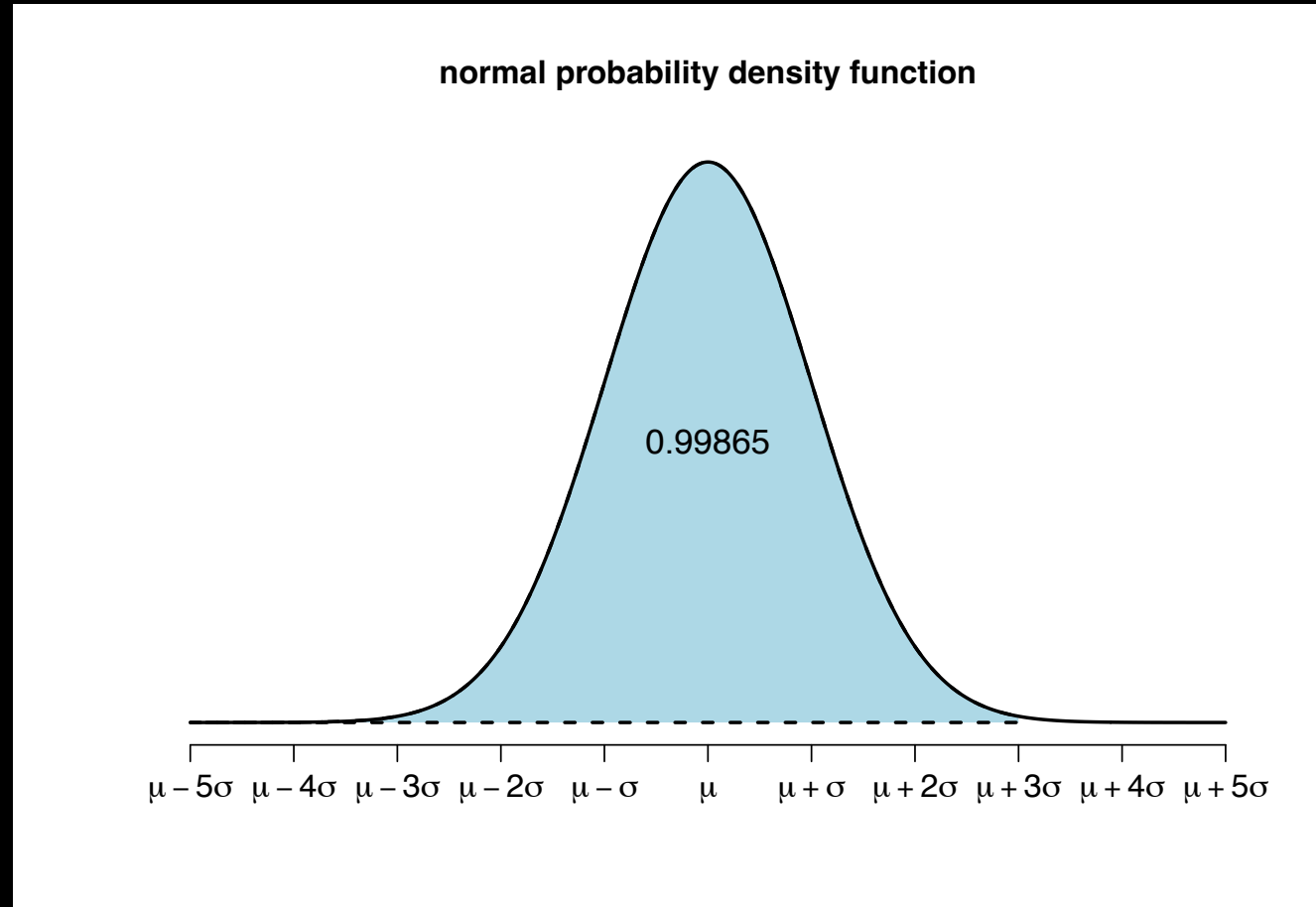
$$\mu_{A^-} = E[X|A^-]$$

$$\sigma_{A^-} = \sqrt{\text{Var}[X|A^-]}$$

Seronegative, if  $X_i \leq \mu_{A^-} + 3\sigma_{A^-}$

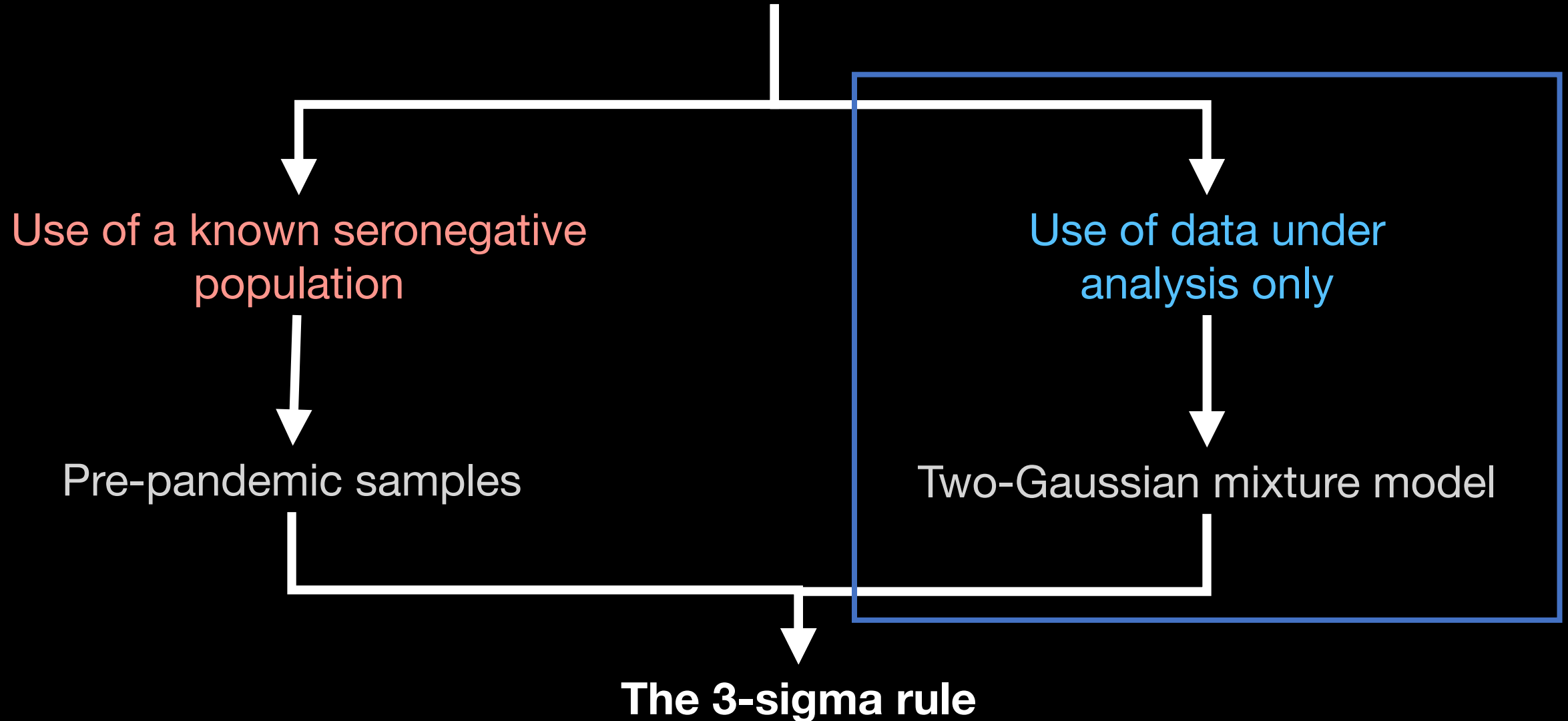
Seropositive, otherwise

# The link to the Normal distribution

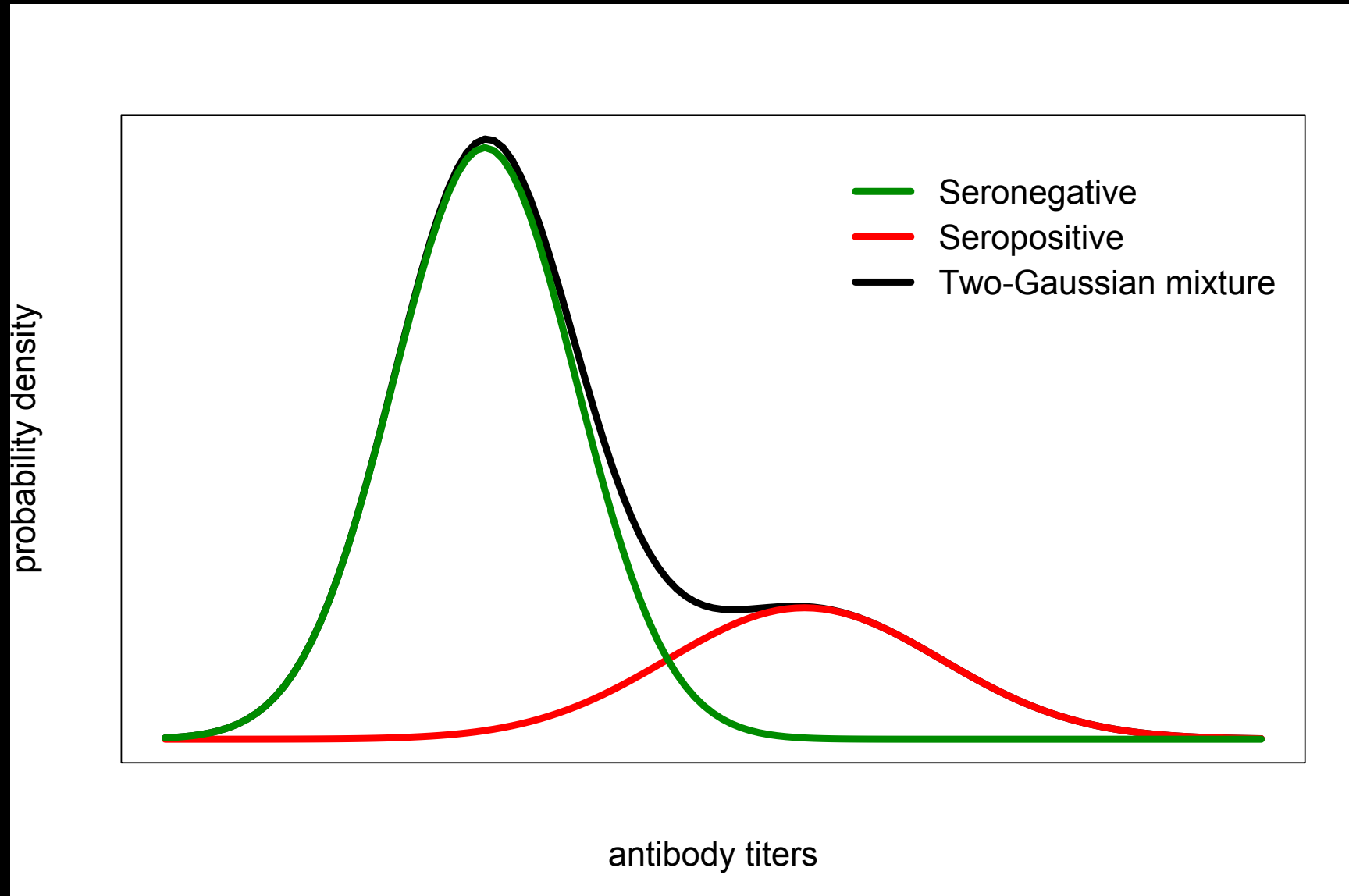




## Approaches to determine the cutoff



# Two-Gaussian mixture model



# Two-Gaussian mixture models

$$f_X(x) = (1 - \pi)f_{N(\mu_{S^-}, \sigma_{S^-})}(x) + \pi f_{N(\mu_{S^+}, \sigma_{S^+})}(x)$$

Definition of  $S^- \Rightarrow \mu_{S^-} < \mu_{S^+}$

In general:

$$f_X(x) = \sum_{i=1}^k \pi_i f_{N(\mu_i, \sigma_i)}(x) \quad \text{where} \quad \sum_{i=1}^k \pi_i = 1$$

# Estimation of the model by maximum likelihood method

## EM (Expectation-Maximization) Algorithm

1. Start with initial estimates for the parameters
2. E-Step - calculate the probability of each individual belonging to a given subpopulation according to estimates at 1.
3. M-Step - re-estimate the parameters using these probabilities and repeat the E-step with these new estimates
4. Stop with the increment in the log-likelihood is below a given tolerance error.

Calculate the cutoff for seropositivity according to  $\hat{\mu}_{S-}$  and  $\hat{\sigma}_{S-}$

Package mixtools

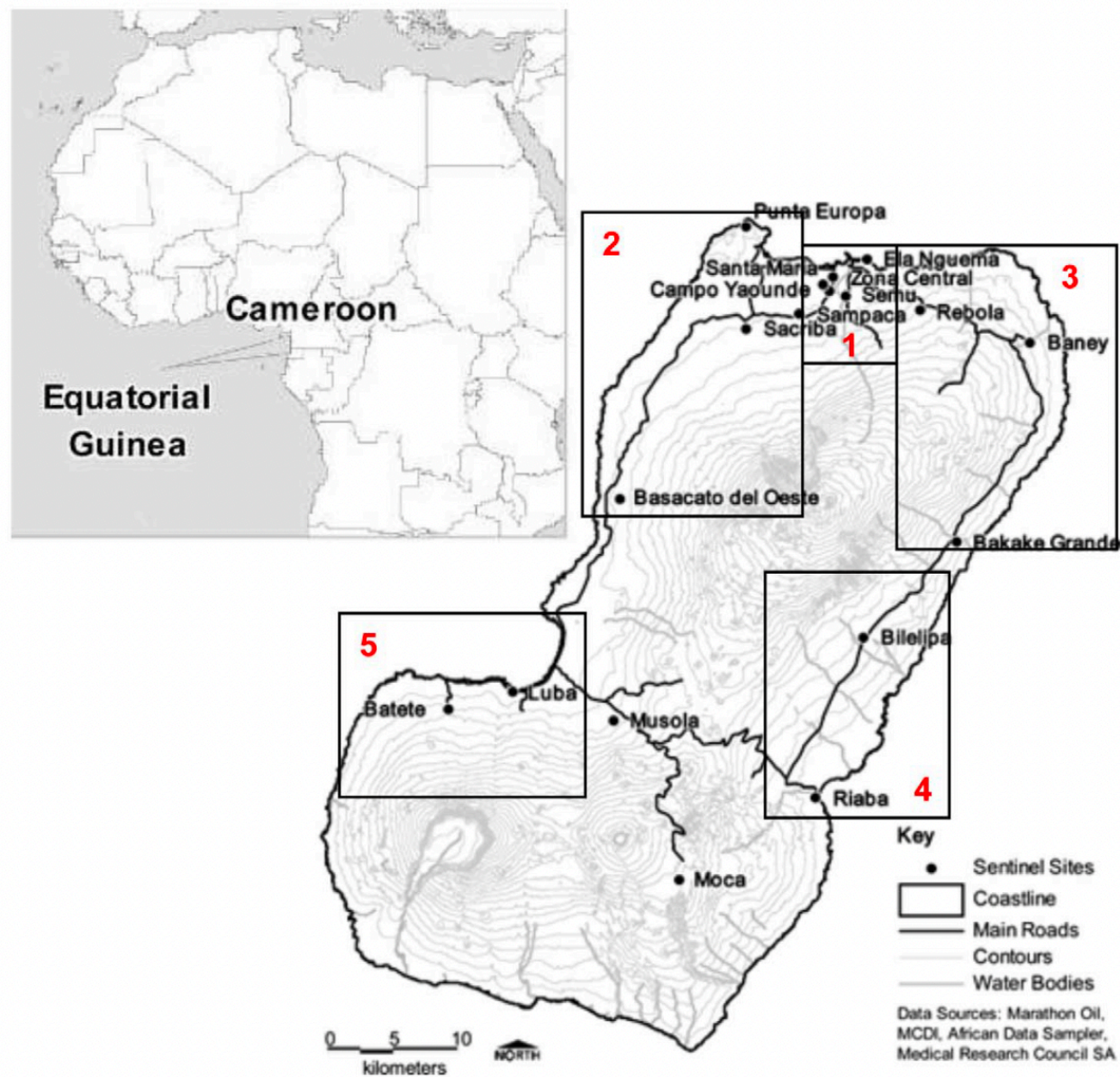


time!

# Serological Markers Suggest Heterogeneity of Effectiveness of Malaria Control Interventions on Bioko Island, Equatorial Guinea

**Jackie Cook<sup>1</sup>, Immo Kleinschmidt<sup>2</sup>, Christopher Schwabe<sup>3</sup>, Gloria Nseng<sup>4</sup>, Teun Bousema<sup>1</sup>, Patrick H. Corran<sup>1</sup>, Eleanor M. Riley<sup>1</sup>, Chris J. Drakeley<sup>1\*</sup>**

**1** Department of Immunology and Infection, London School of Hygiene and Tropical Medicine, London, United Kingdom, **2** Department of Infectious Disease Epidemiology, London School of Hygiene and Tropical Medicine, London, United Kingdom, **3** Medicinal Care Development International, Silver Spring, Maryland, United States of America, **4** Ministry of Health and Social Welfare, Malabo, Equatorial Guinea





**Table 1.** Demographic characteristics of the study population.

		% [n]						
		Malabo N = 2328	North West N = 1749	North East N = 1323	South East N = 700	South West N = 588	Other** N = 699	Total N = 7387
<b>Age (years)</b>	0–1	14.1 [324]	10.5 [182]	10.4 [137]	12.2 [85]	10.0 [58]	7.5 [52]	11.4 [838]
	1–5	21.1 [458]	18.0 [312]	19.8 [261]	14.6 [102]	16.8 [97]	15.2 [106]	18.6 [1363]
	5–15	26.3 [605]	30.6 [531]	30.1 [396]	21.0 [146]	24.0 [139]	28.7 [200]	27.5 [2017]
	15–90	38.6 [890]	41.0 [712]	39.8 [524]	52.2 [364]	49.2 [285]	48.6 [338]	42.5 [3113]
<b>Sex</b>	Female	61.2 [1410]	54.2 [932]	61.1 [805]	55.8 [389]	58.4 [338]	54.8 [382]	58.2 [4256]
<b>House recently sprayed<sup>1</sup></b>	Yes	74.2 [1580]	81.2 [1306]	85.6 [1076]	81.7 [519]	89.5 [477]	87.9 [574]	81.2 [5532]
<b>Slept under ITN<sup>2</sup></b>	Yes	82.6 [1629]	68.0 [988]	65.8 [797]	63.3 [404]	73.1 [385]	71.4 [449]	72.4 [4652]
<b>Parasite positive</b>	Yes	14.8 [300]	27.0 [374]	7.9 [94]	21.7 [135]	18.6 [97]	12.1 [75]	16.9 [1075]

<sup>1</sup>- within the previous 6 months.

<sup>2</sup>- on the night before the survey.

\*\*Moca and Musola kept separate due to their high altitude.

doi:10.1371/journal.pone.0025137.t001

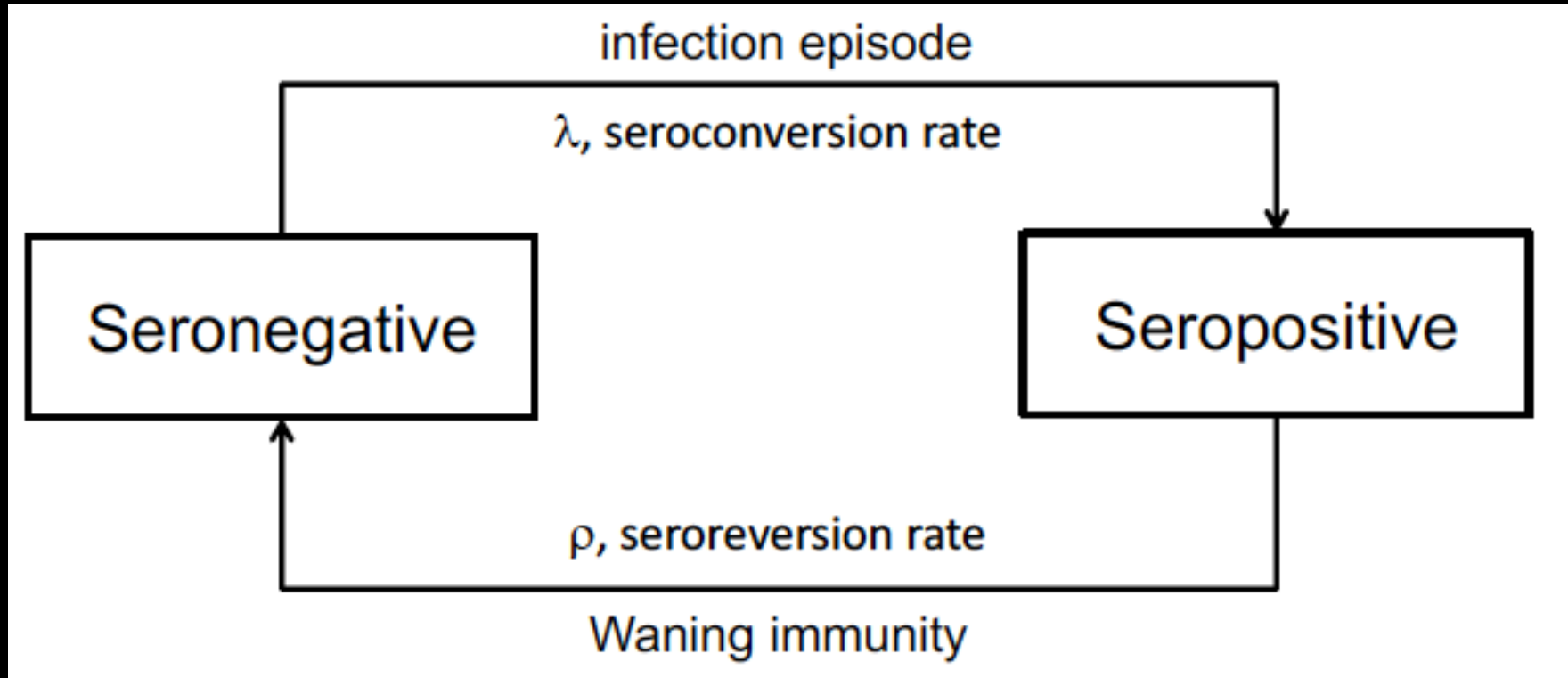


Variables

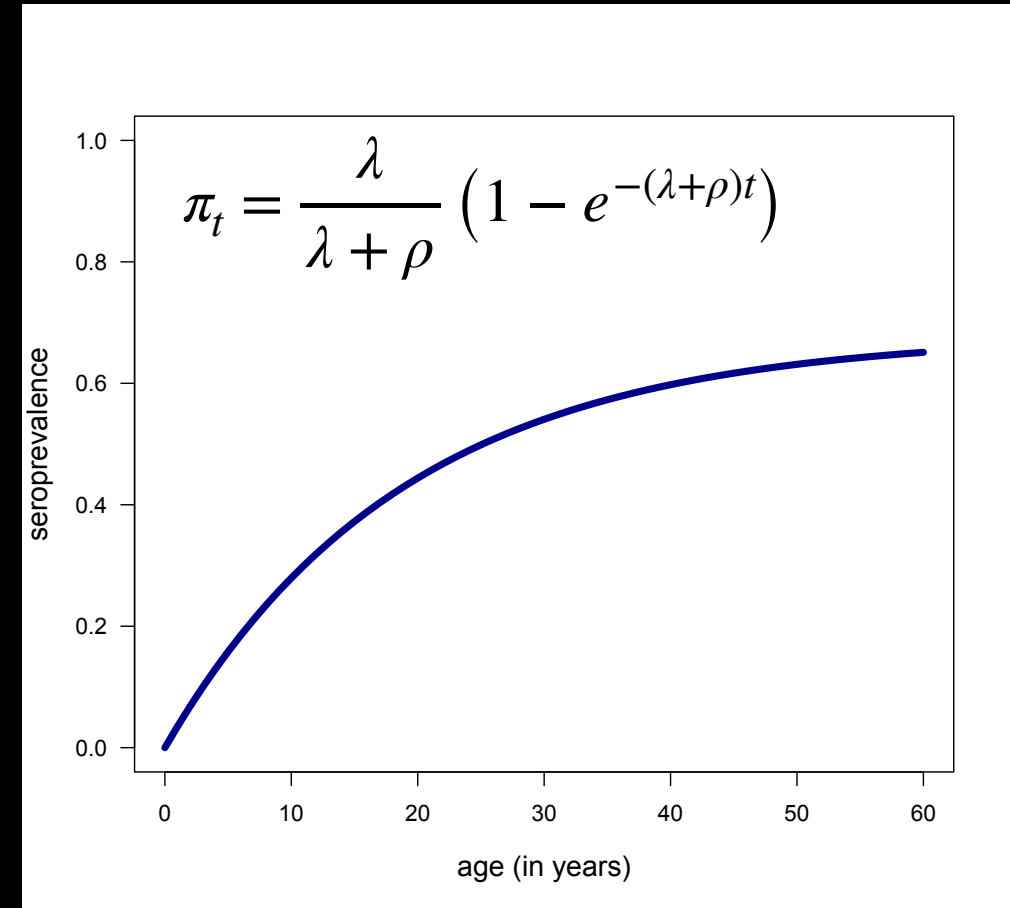
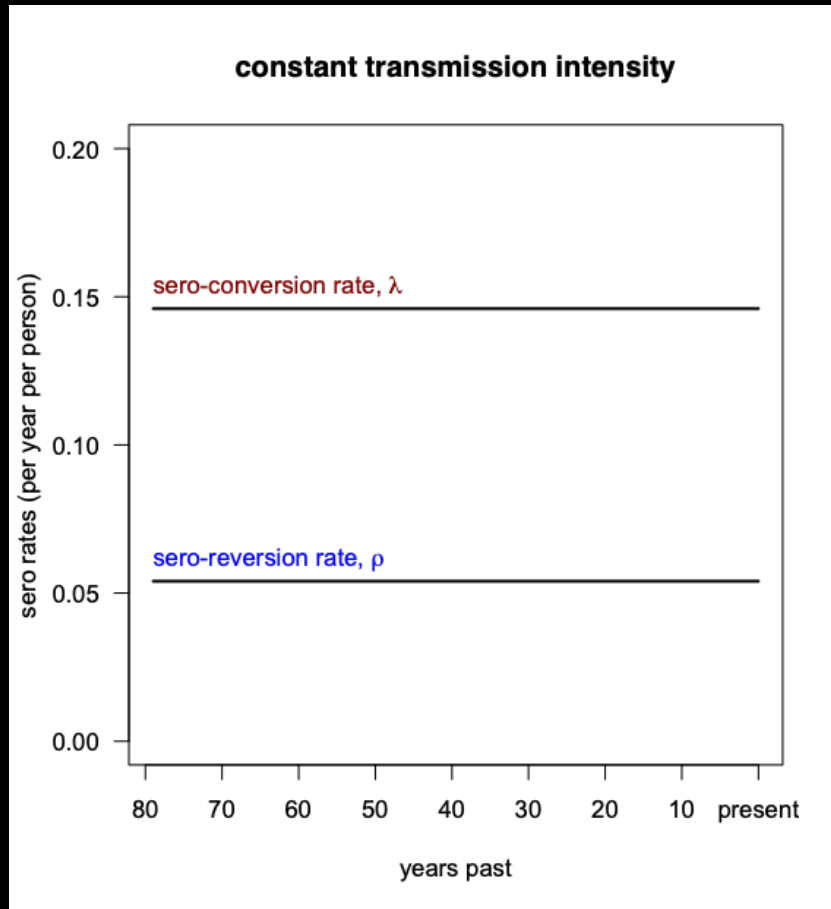
2.

Estimating seroconversion rate  
(using reversible catalytic models)

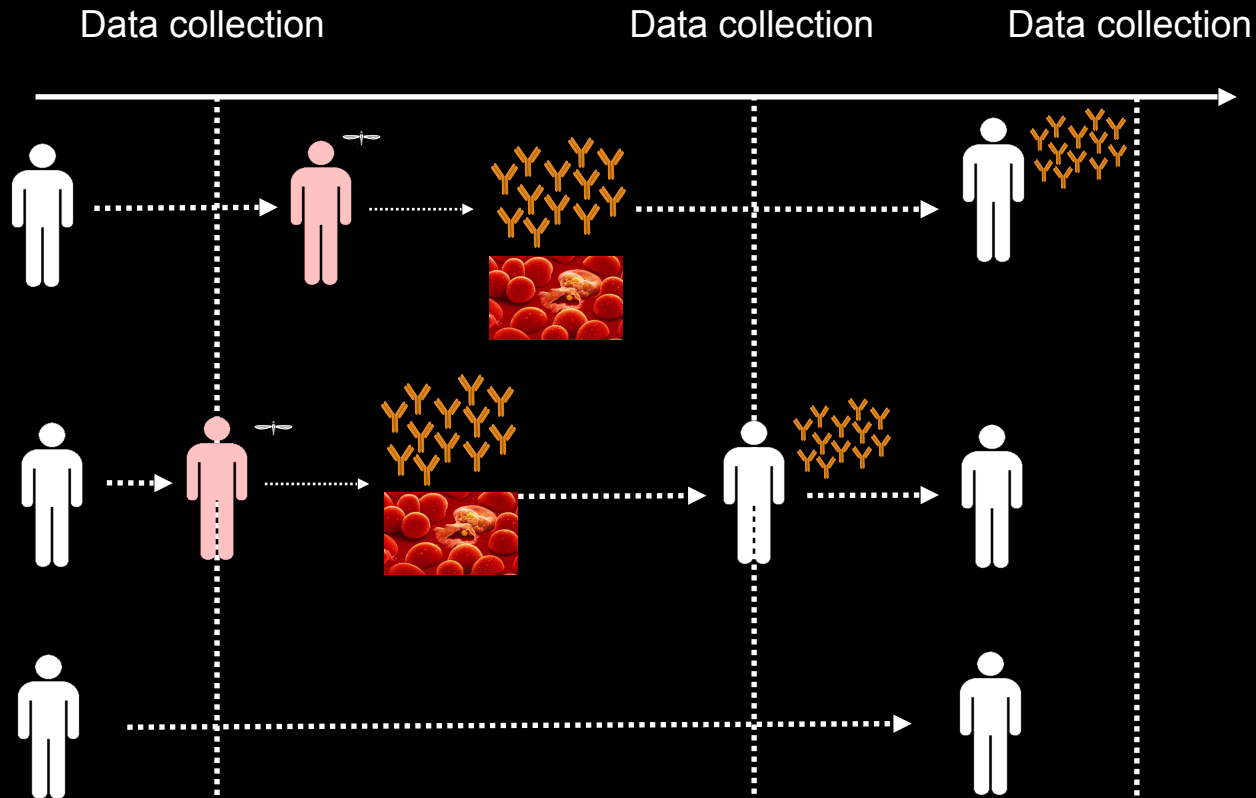
# Reversible catalytic models



# Constant transmission intensity



# Longitudinal surveys



**Statistical information: ++++**

Direct observation of serological transitions

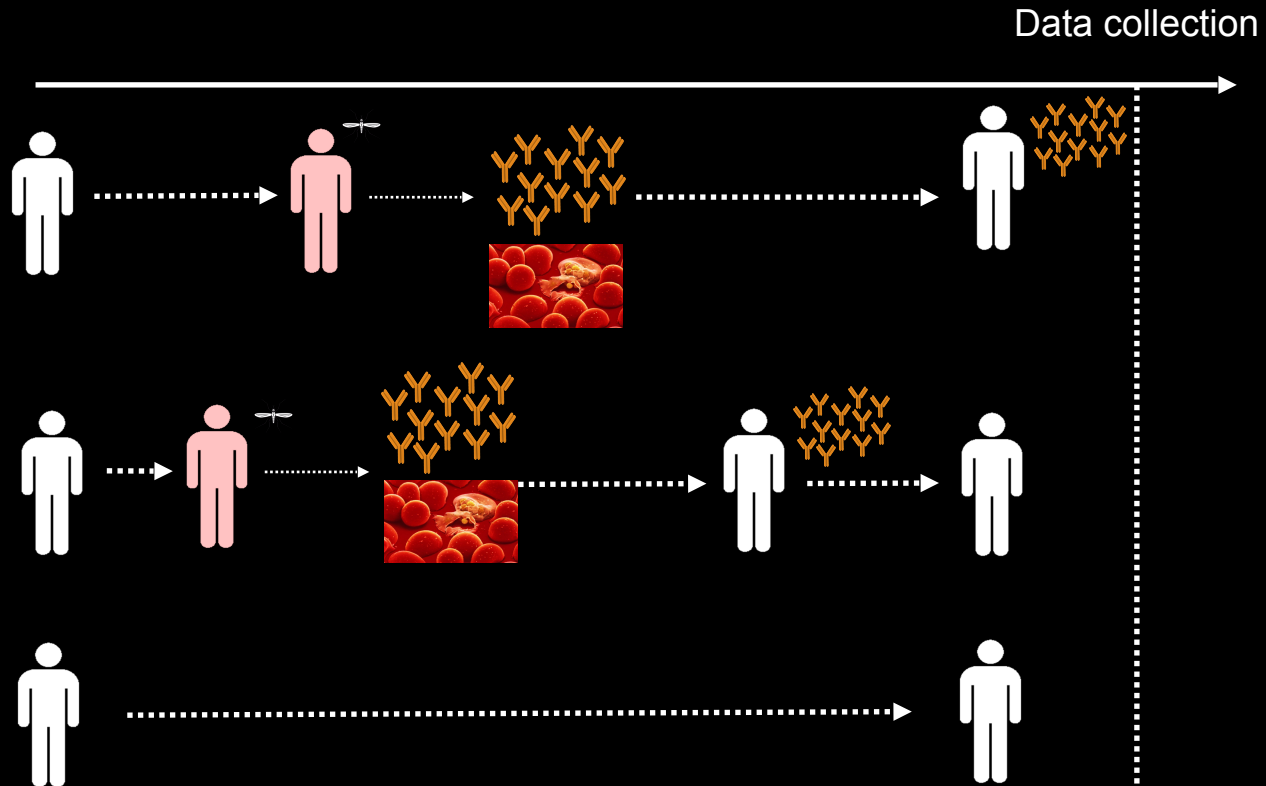
**Execution difficulty: ++++**

Time consuming

Sampling intensive

Participation adherence/drop-outs

# Cross-sectional surveys



**Statistical information: ++**

No direct observation of serological transitions  
Age as proxy of time

**Execution difficulty: ++**

Easy to engage participation  
Quick sampling

# Longitudinal versus cross-sectional surveys

Type of Study	Seroconversion rate	Seroreversion rate
Longitudinal	<b>0.021</b> (0.001-0.096)	<b>0.163</b> (0.001,0.729)
Cross-sectional	<b>0.023</b> (0.001,0.052)	<b>0.0001</b> (0.001,0.255)

Seroreversion rate is difficult to be estimated!  
So it is often fixed at 0 or an good estimate, say 0.017.



## Fixed seroreversion rate at 0

$$\rho = 0 \Rightarrow \pi_t = 1 - e^{-\lambda t}$$

$$\Rightarrow \log 1 - \pi_t = -\lambda t$$

$$\Rightarrow \log(-\log(1 - \pi_t)) = \log \lambda + \log t$$

Complementary log-log model



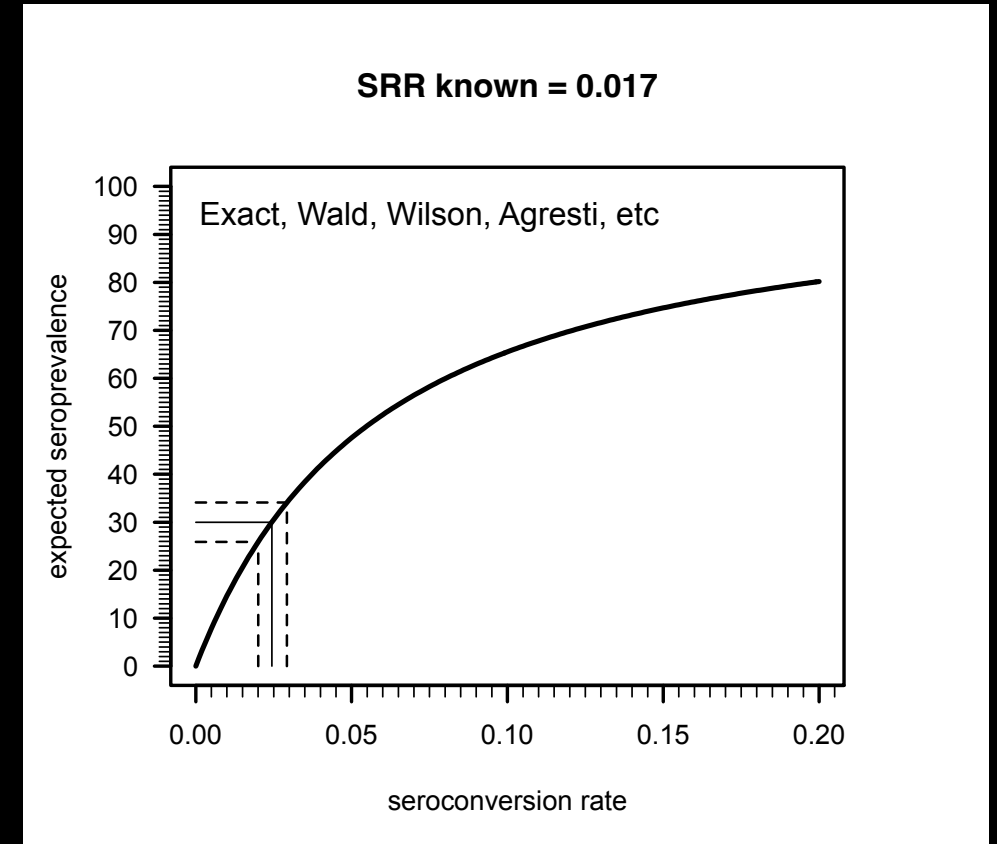
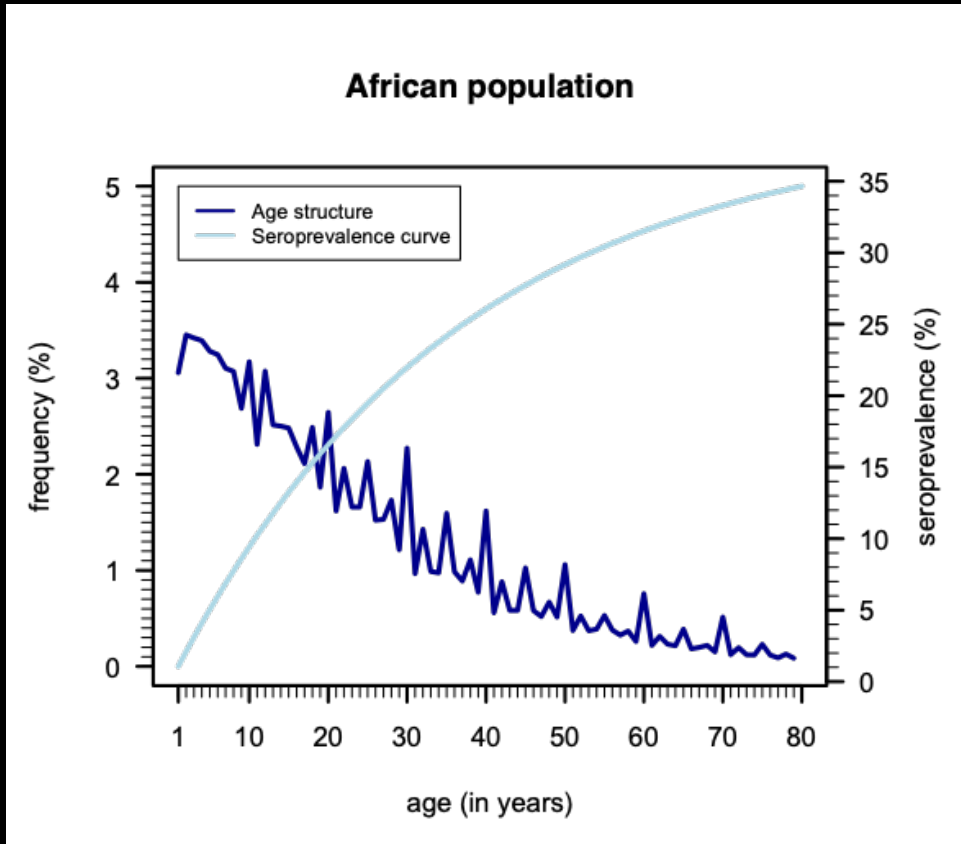


time!

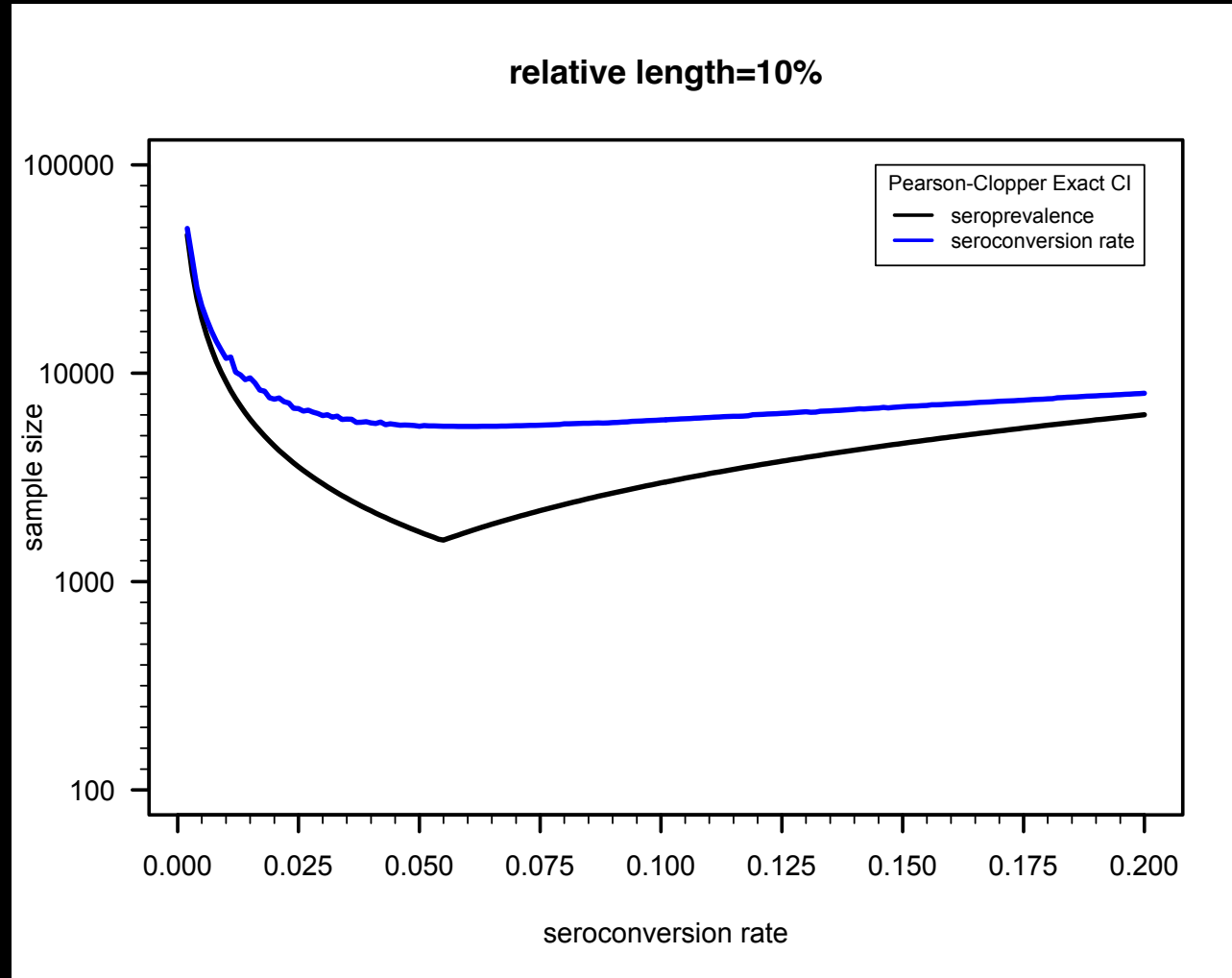
3.

Calculating sample size for controlling  
precision of seroconversion rate estimate

# Sample size calculation for seroconversion rate



# Sample size calculation for seroconversion rate



# Sample size calculation in practice

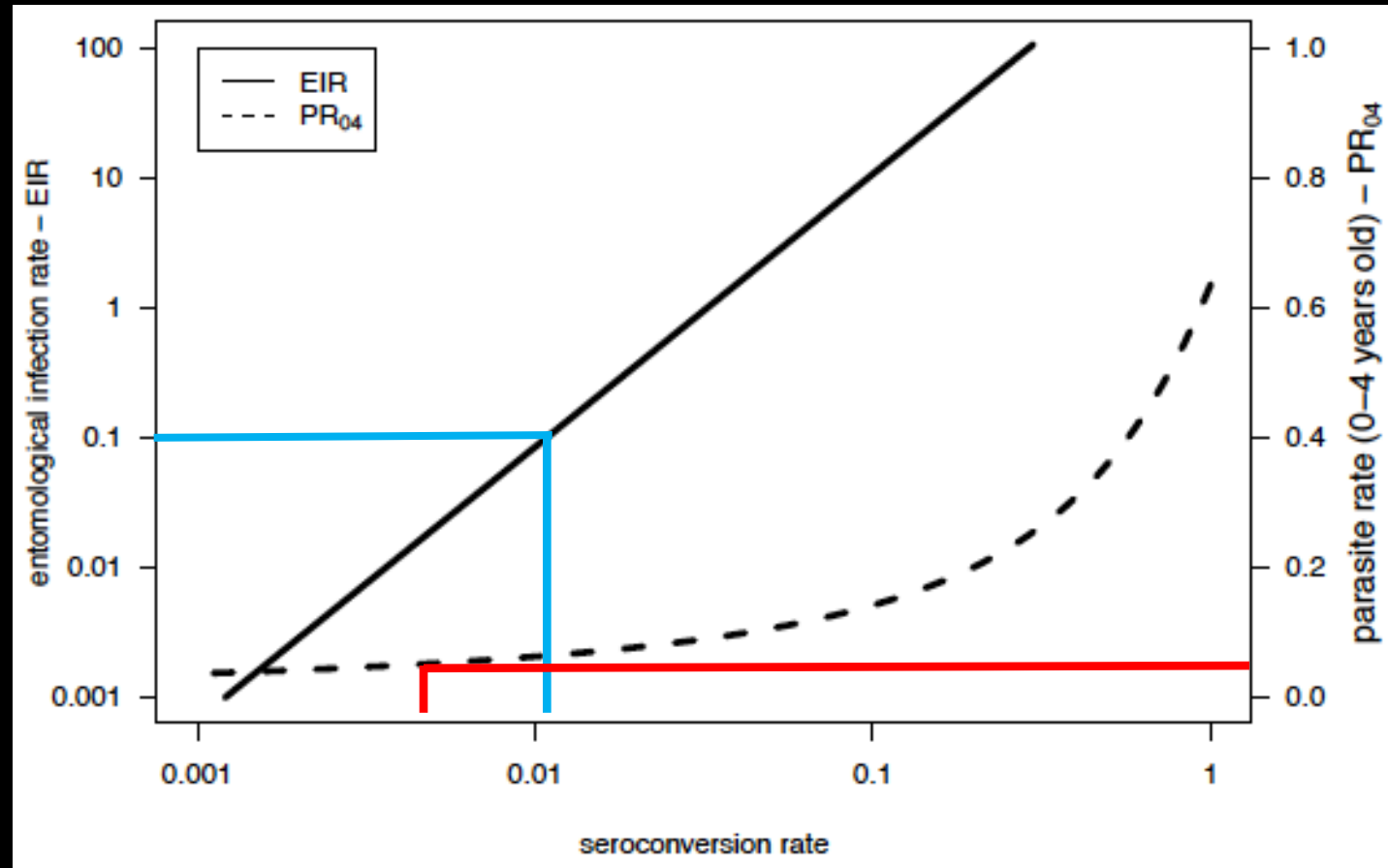
1. Desired precision
2. Antibody with known seroreversion rate
3. Transmission intensity of the population
4. Age structure associated with sampling scheme
5. Type of confidence interval to be used

# Identification of transmission intensity

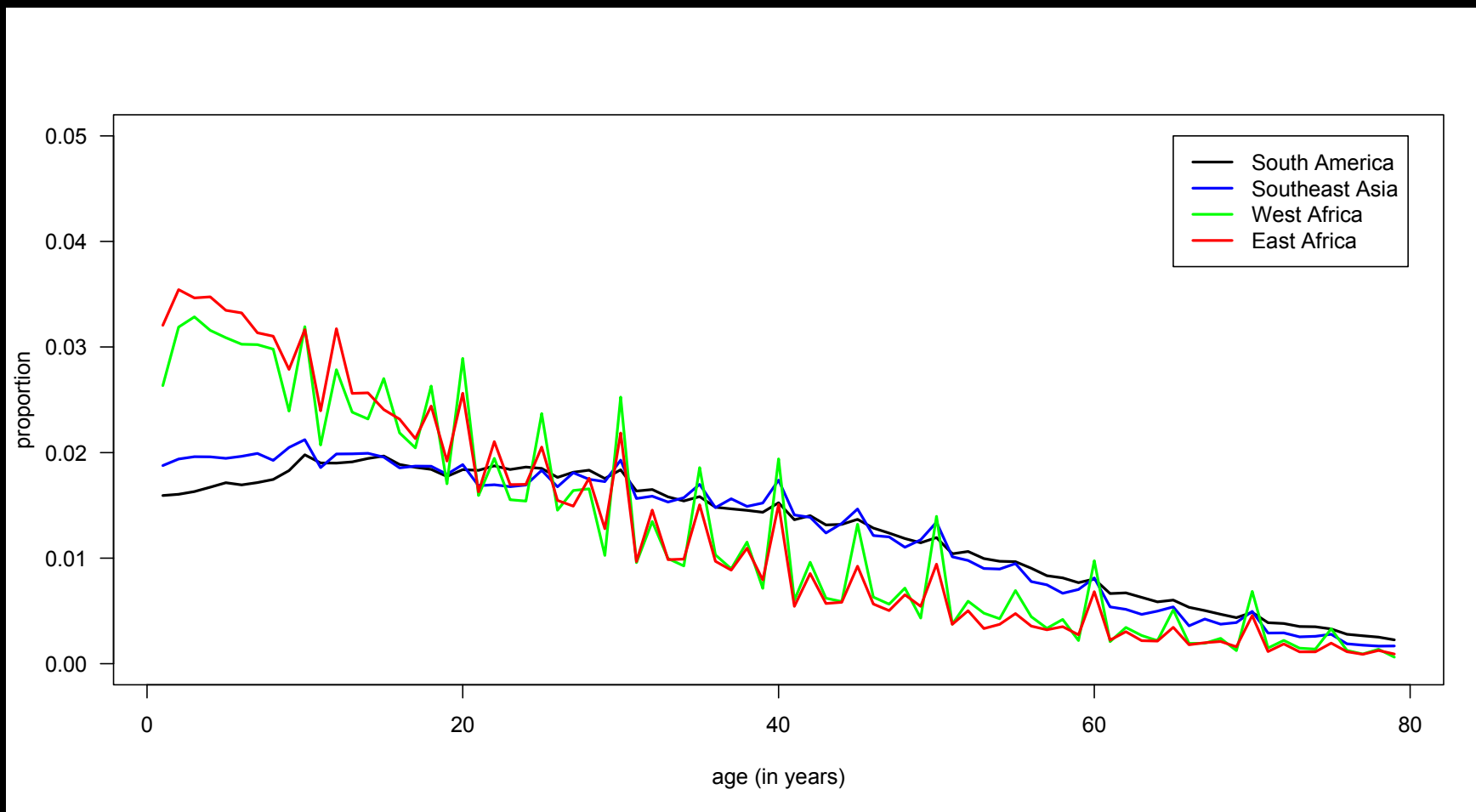
**Table 1 Expected relationship between EIR,  $PR_{04}$ , SCR and SP in African (AFR), Southeast Asian and South American (SEA + SA) populations where seroreversion rate was fixed at 0.017**

EIR	$PR_{04}$	SCR	Seroprevalence	
			AFR	SEA + SA
0.01	0.050	0.0036	0.057	0.073
0.10	0.073	0.0108	0.156	0.195
1.00	0.119	0.0324	0.365	0.437
10.0	0.231	0.0969	0.647	0.720
100.0	0.625	0.2900	0.860	0.896

# Identification of transmission intensity



# Identification of age structure





# Type of confidence interval

## Pearson-Clopper exact

Coverage higher than nominal confidence level

## Wald

Degenerate when  $x=0$  or  $x=n$

Overshooting

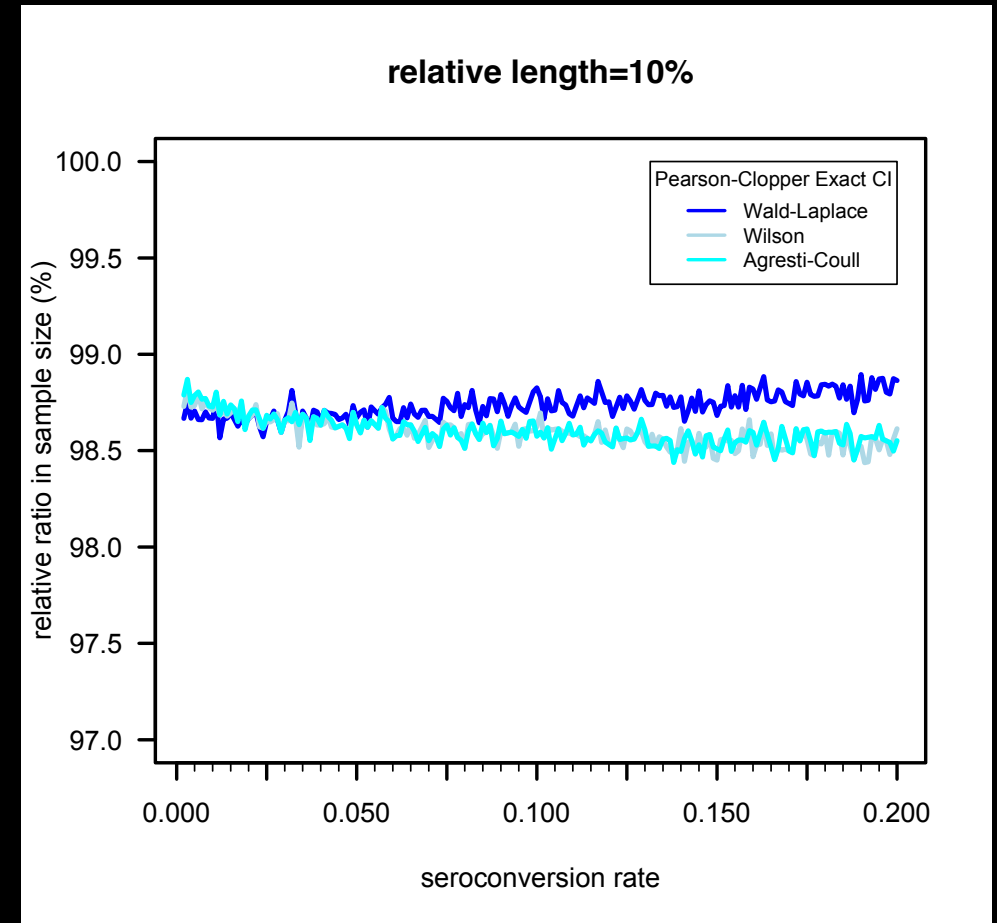
## Wilson

Good coverage in extreme probabilities

## Agresti-Coull

Overshooting

Better coverage than the exact CI





time!

# References

- Cook J, Kleinschmidt I, Schwabe C, et al. Serological markers suggest heterogeneity of effectiveness of malaria control interventions on Bioko Island, equatorial Guinea. PLoS One. 2011;6(9):e25137. doi:10.1371/journal.pone.0025137
- Sepúlveda N, Paulino CD, Drakeley C. Sample size and power calculations for detecting changes in malaria transmission using antibody seroconversion rate. Malar J. 2015;14:529. Published 2015 Dec 30. doi:10.1186/s12936-015-1050-3
- Sepúlveda N, Stresman G, White MT, Drakeley CJ. Current Mathematical Models for Analyzing Anti-Malarial Antibody Data with an Eye to Malaria Elimination and Eradication. J Immunol Res. 2015;2015:738030. doi:10.1155/2015/738030