Canalization of Litter Size in Sheep

Samira FATHALLAH

26/08/2013

Problems due to large variability of sheep litter size

Management technique

+

Genetic improvement

➔

Multiple incidence

⬇

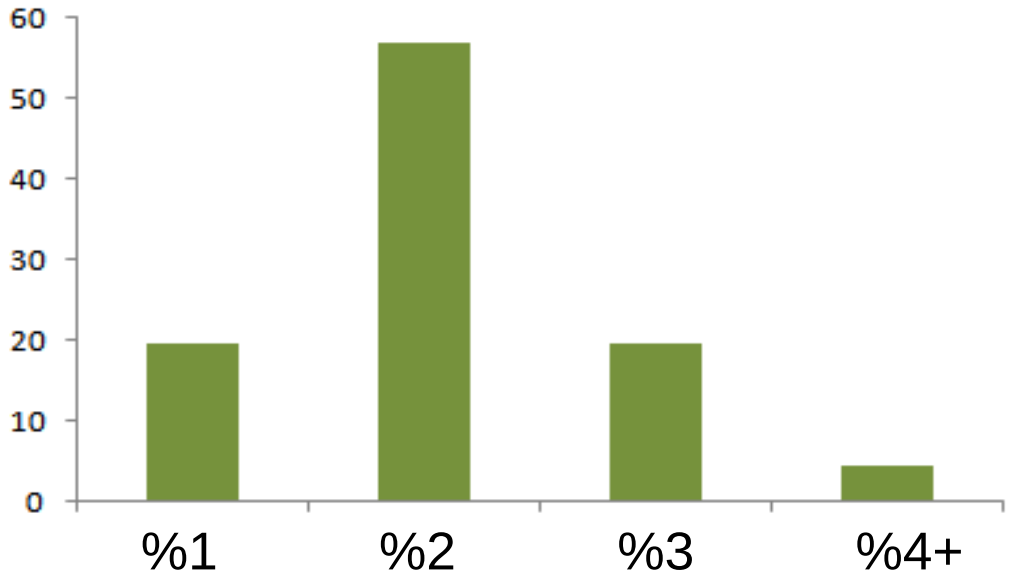
Mortality 20%

+

Economic costs

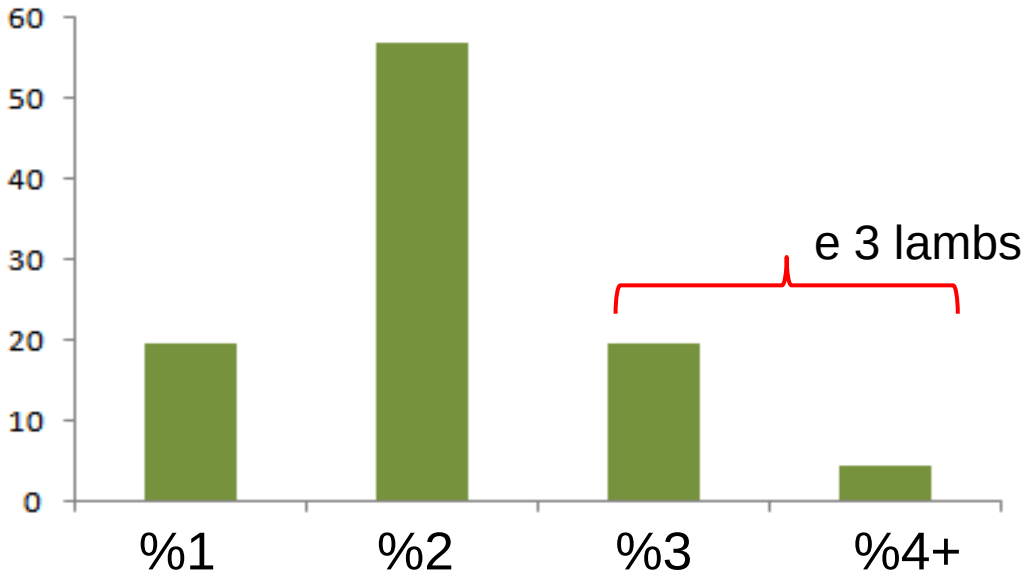
Distribution of litter size observed in Romane breed

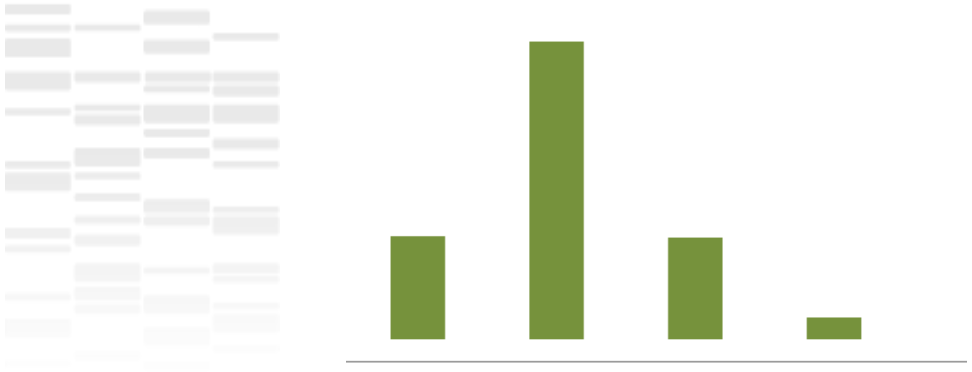
Records	154 780
Sires	1 620
Dams	22 492
Prolificacy	2.06



Distribution of litter size observed in Romane breed

Records	154 780
Sires	1 620
Dams	22 492
Prolificacy	2.06





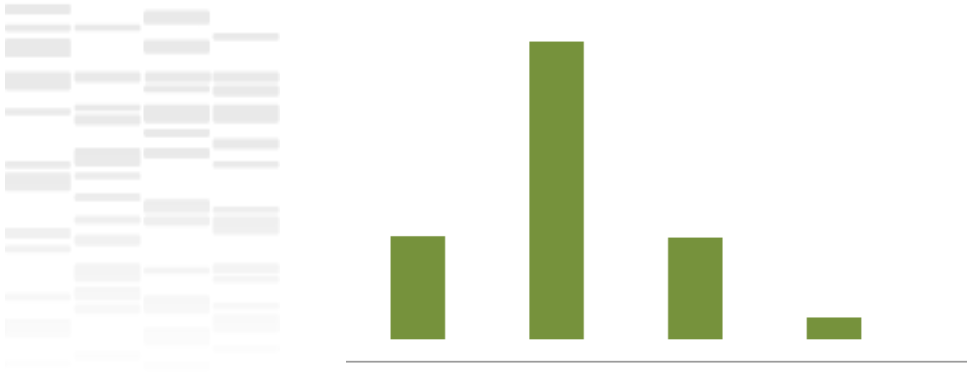
Litter size

a categorical variable
LS = 1, 2, 3,...n

continuous variable

classical canalization model
$\boldsymbol{y = \mu + u + f(\eta, v)\varepsilon}$

not suitable model: discrete variable

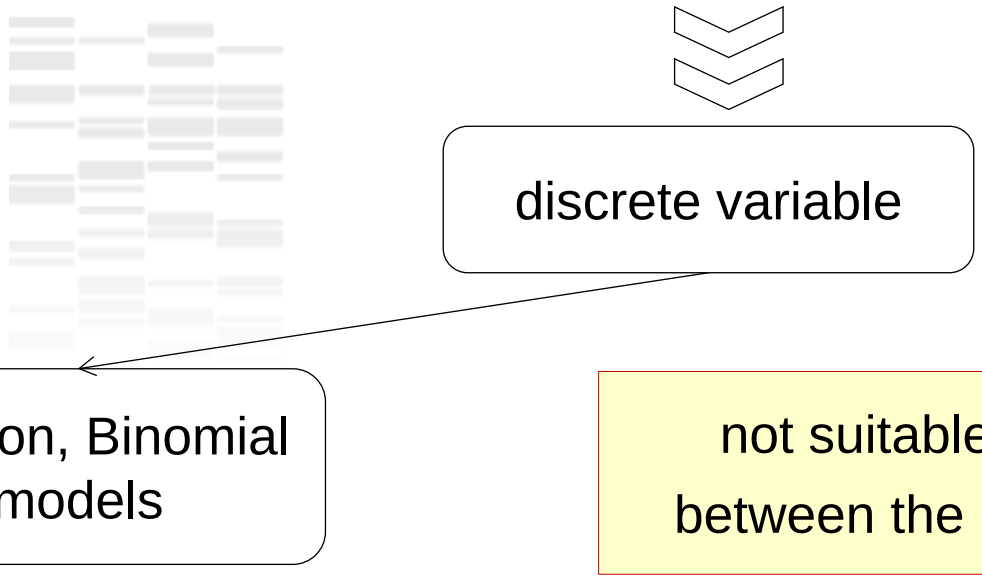


Litter size

a categorical variable
LS = 1, 2, 3,...n

continuous variable

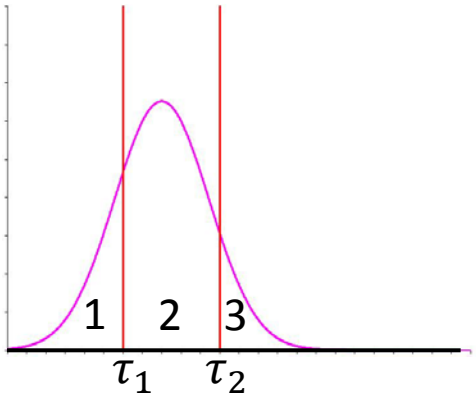
discrete variable


discrete variable
Poisson, Binomial models
not suitable model: dependence between the mean and the variance

discrete variable

~~Poisson, Binomial models~~

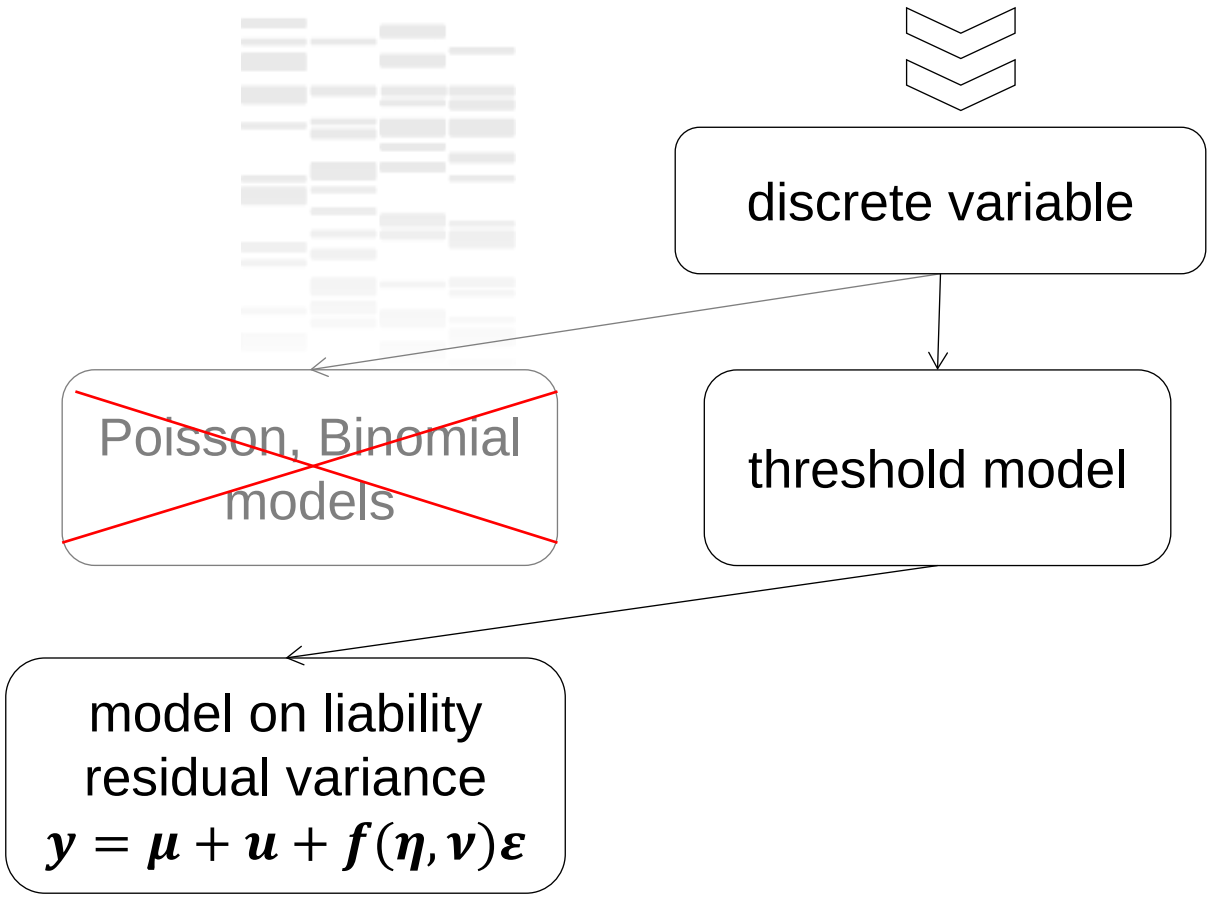
threshold model



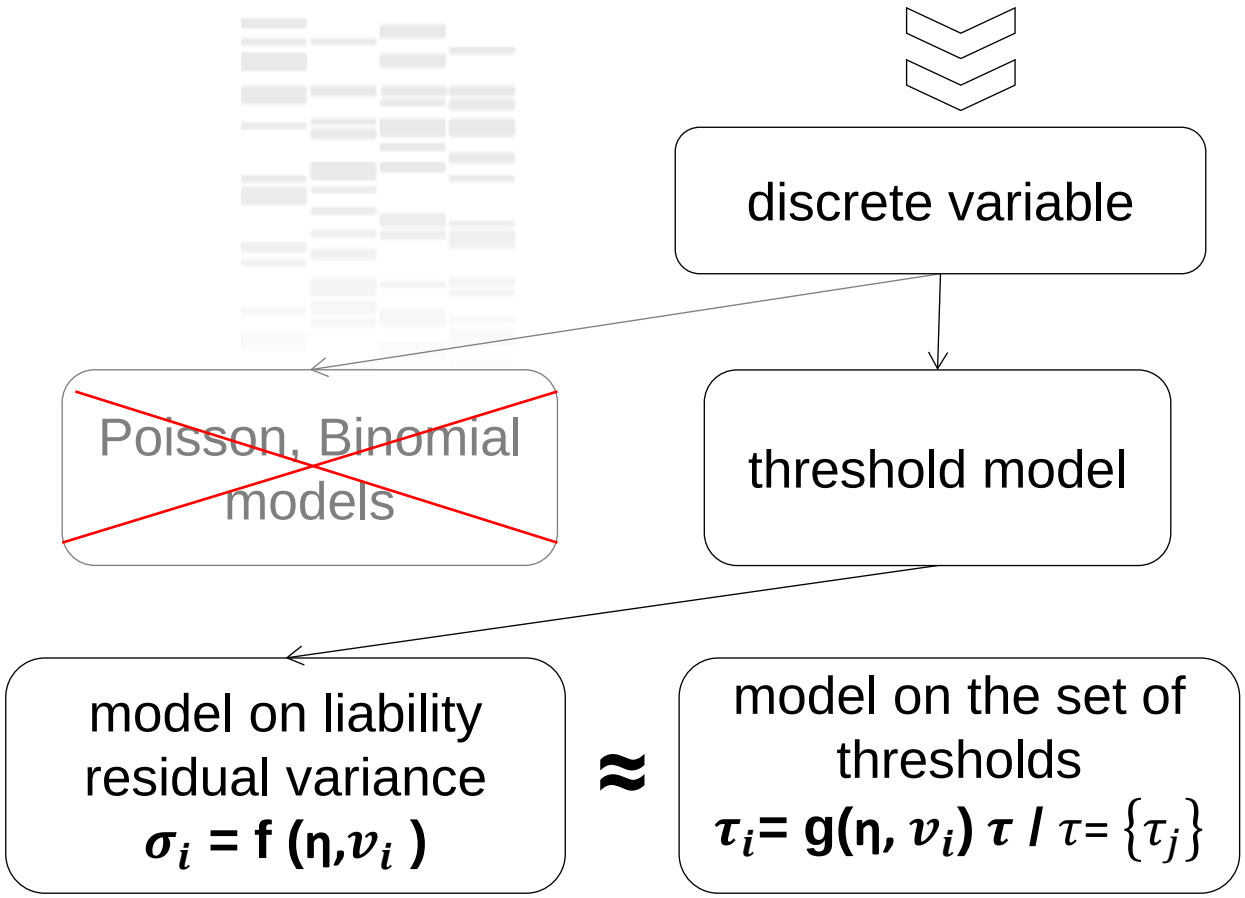
y: liability

$\tau = \{\tau_j\}$: set of thresholds

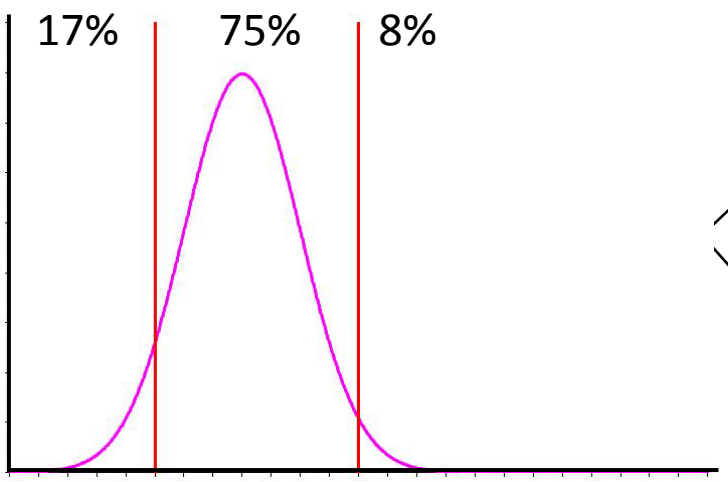
How can we model
the observed heterogeneous variability
using a threshold model?



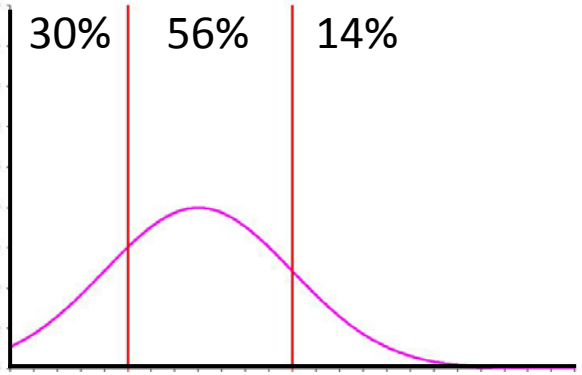
$$f = \begin{cases} Exp \text{ (San Cristobal } et\ al.\text{)} \\ Linear \text{ (Garcia } et\ al.\text{)} \\ Sqrt \text{ (Hill)} \end{cases}$$


discrete variable
Poisson, Binomial models
threshold model
model on liability residual variance
σ_i = f (η,v_i)
≈
model on the set of thresholds
τ_i= g(η, v_i) τ / τ= $\{\tau_j\}$

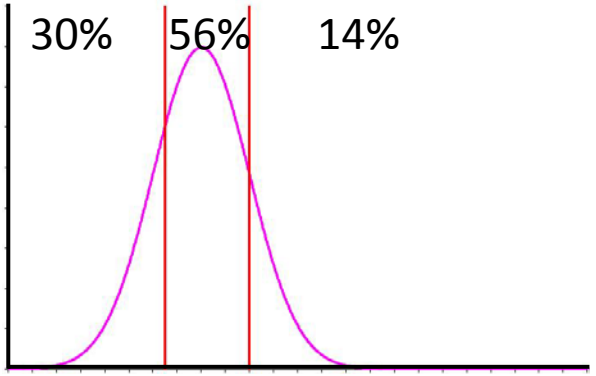
Model on the variance is equivalent to a model on the set of thresholds



$\mathcal{N}(0, 1.0)$ $\boldsymbol{\tau}$= {-1.5 2.0}

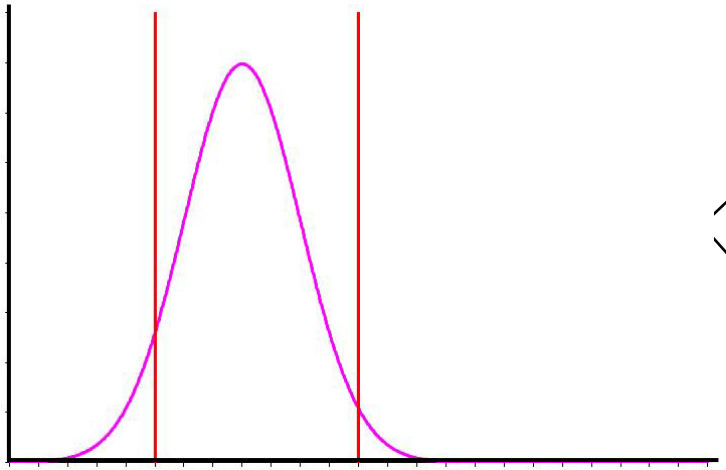


$\mathcal{N}(0, 4.0)$ $\boldsymbol{\tau}$= {-1.5 2.0}

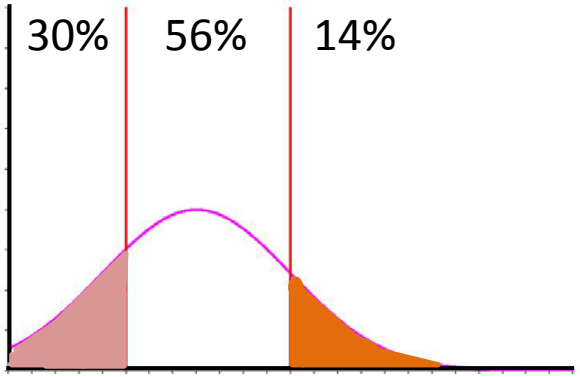


$\mathcal{N}(0, 1.0)$ $\boldsymbol{\tau}$= {-0.75 1.0}

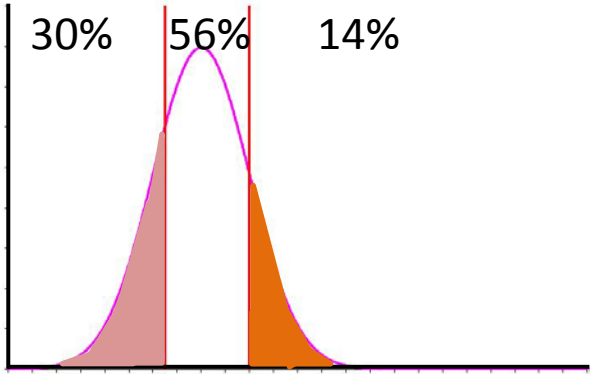
Model on the variance is equivalent to a model on the set of thresholds



$\mathcal{N}(0, 1.0)$ $\boldsymbol{\tau}$= {-1.5 2.0}

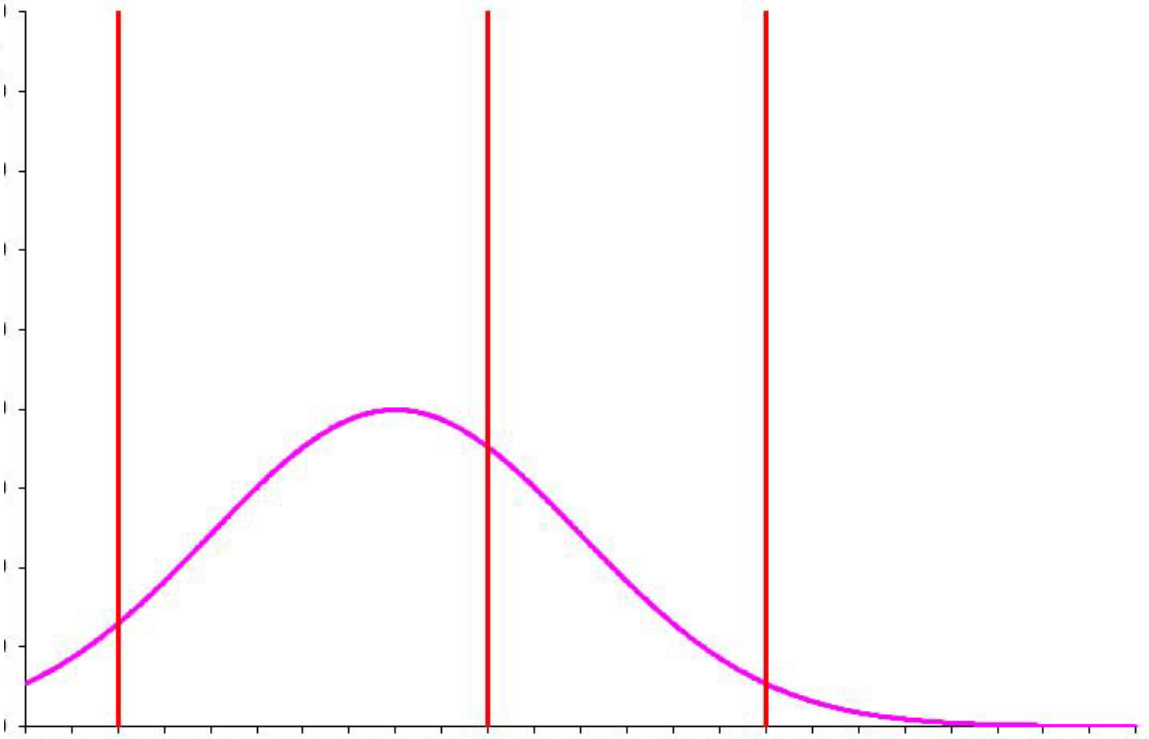


$\mathcal{N}(0, 4.0)$ $\boldsymbol{\tau}$= {-1.5 2.0}

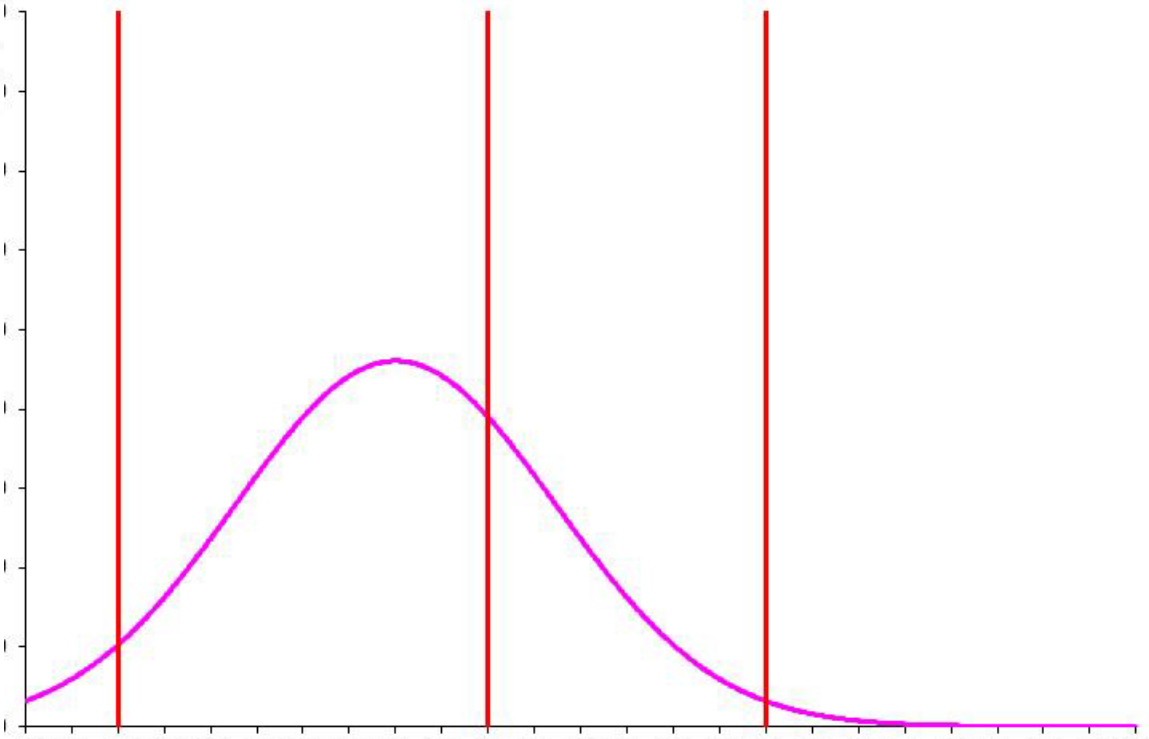


$\mathcal{N}(0, 1.0)$ $\boldsymbol{\tau}$= {-0.75 1.0}

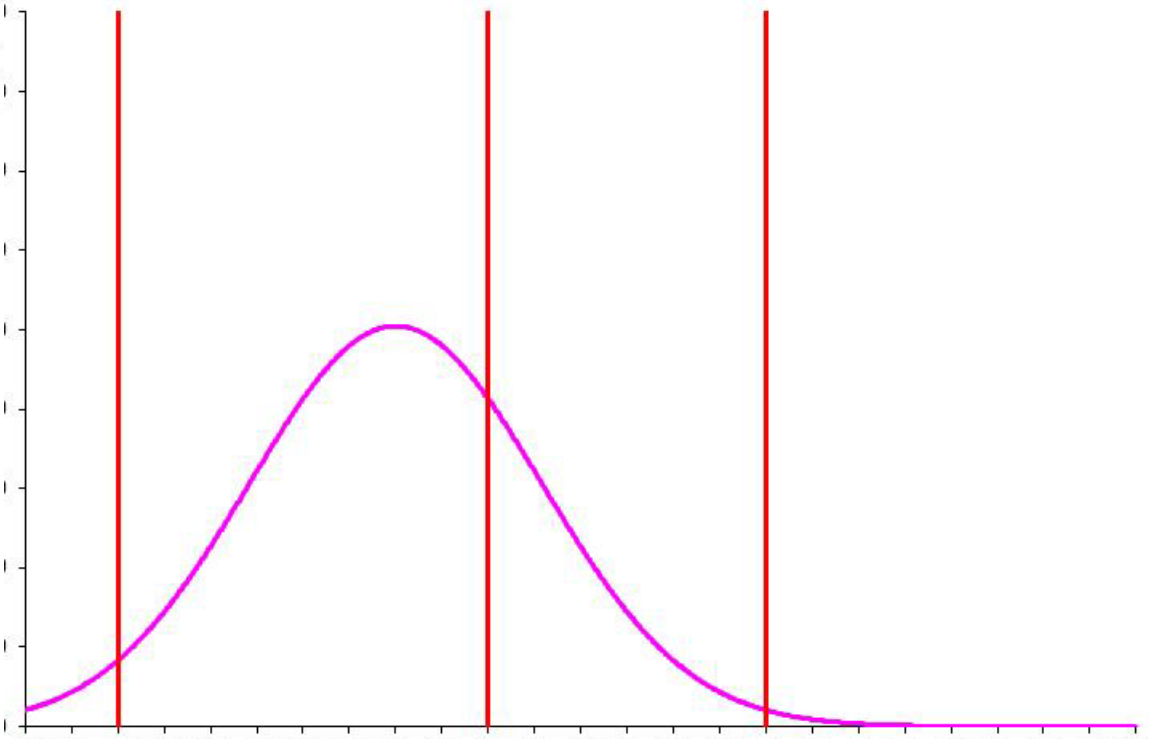
$\mathcal{N}(0, 4.0)$



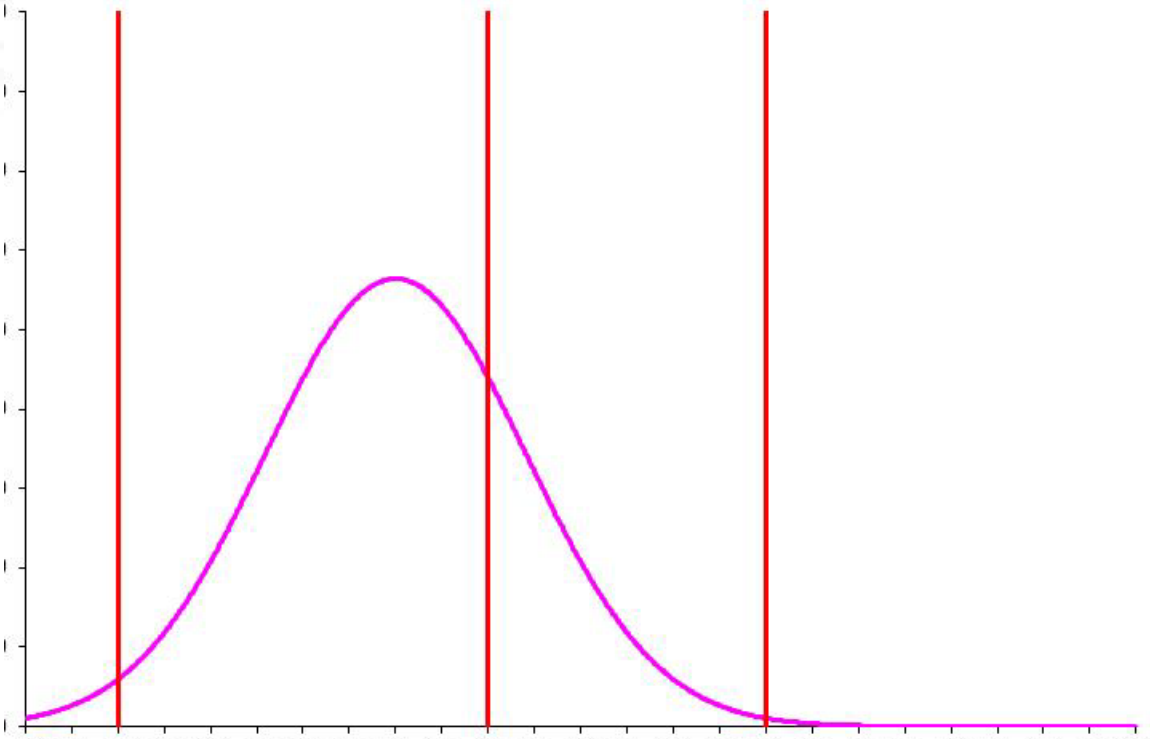
$\mathcal{N}(0, 3.0)$



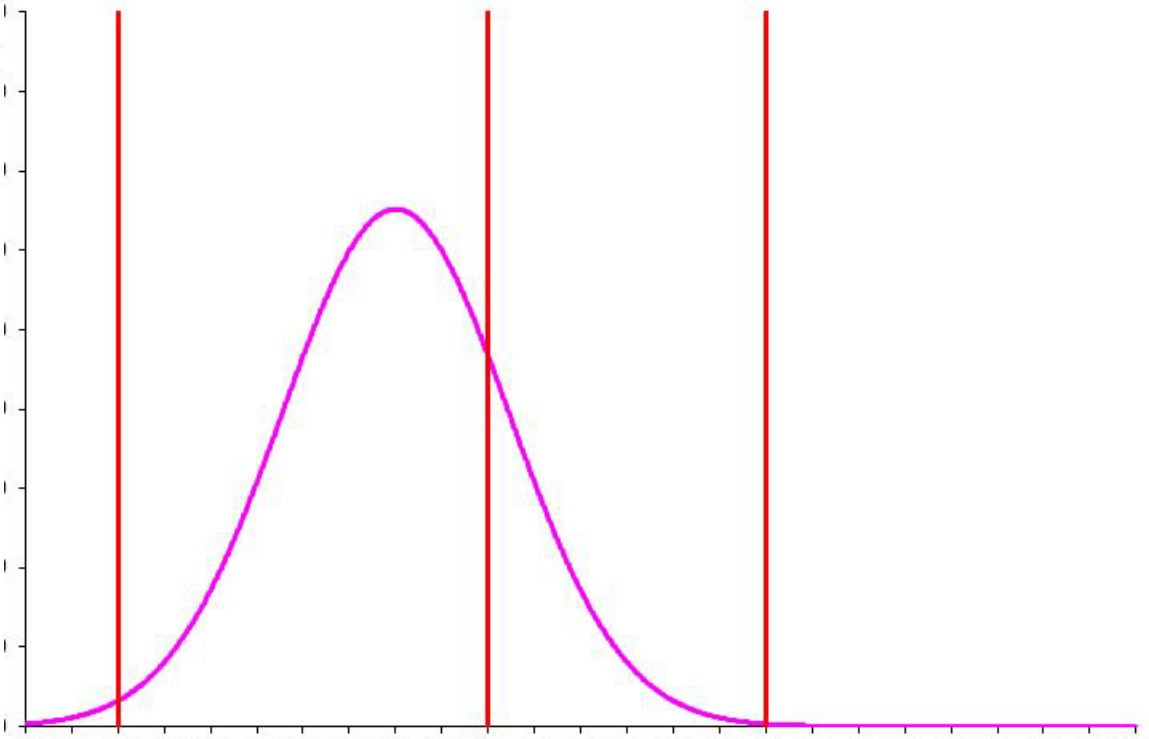
$\mathcal{N}(0, 2.5)$



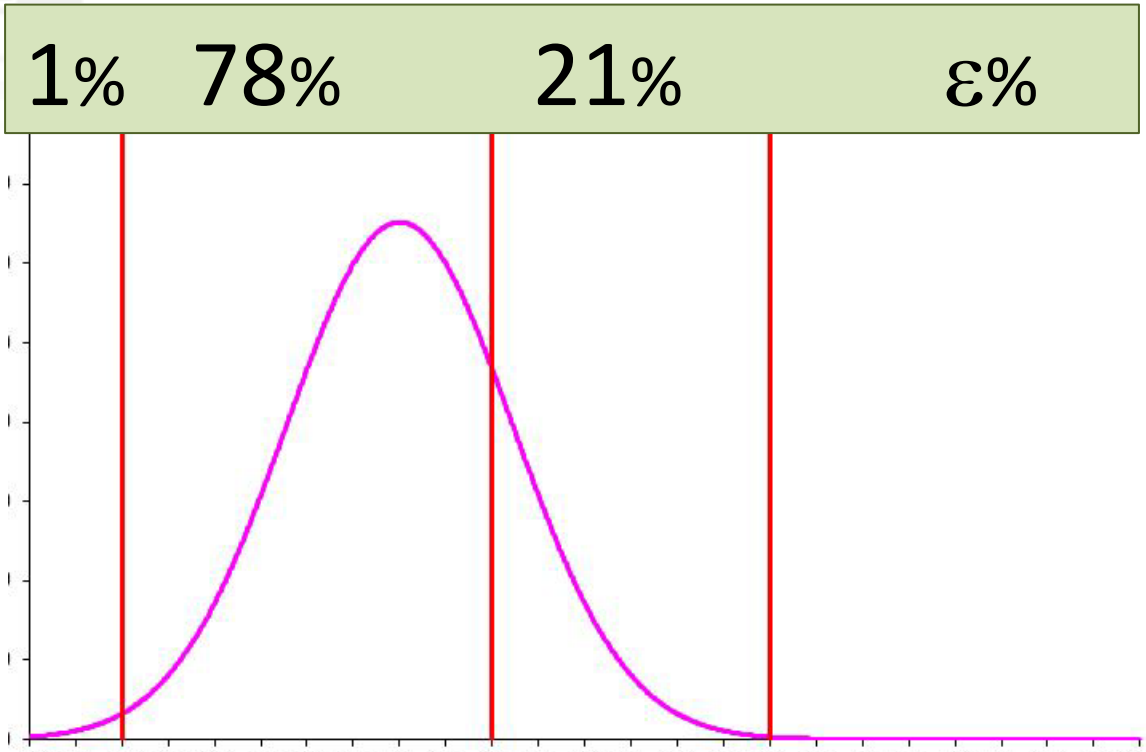
$\mathcal{N}(0, 2.0)$



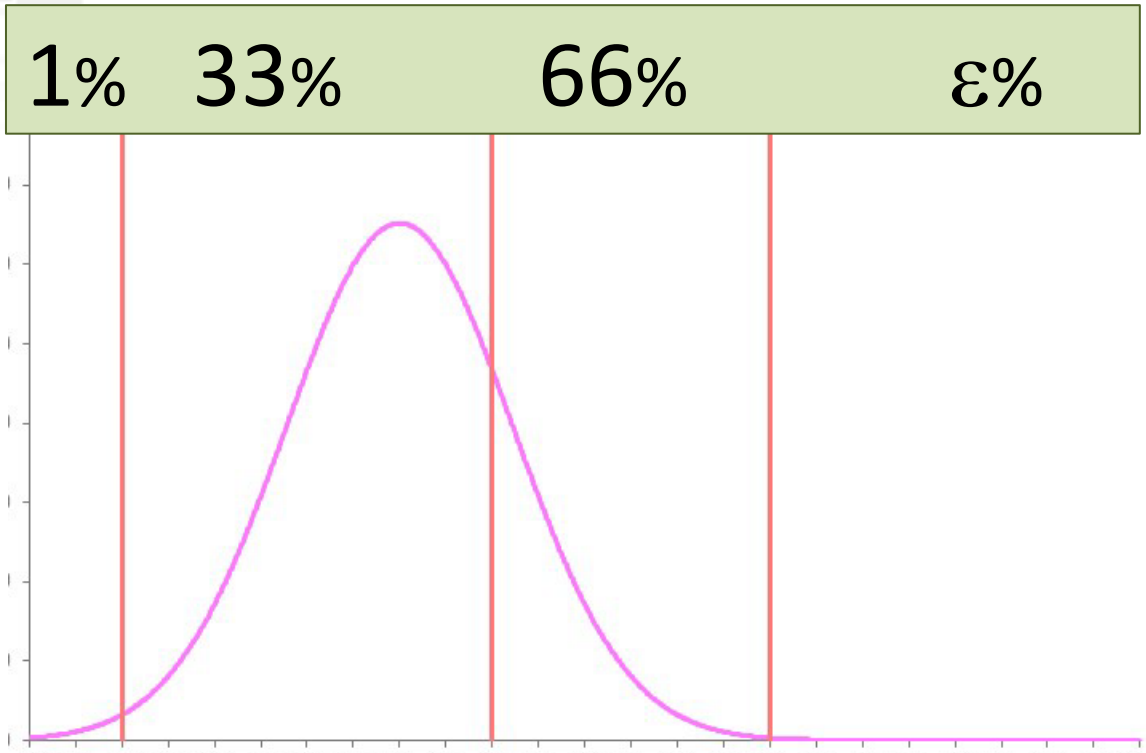
$\mathcal{N}(0, 1.5)$



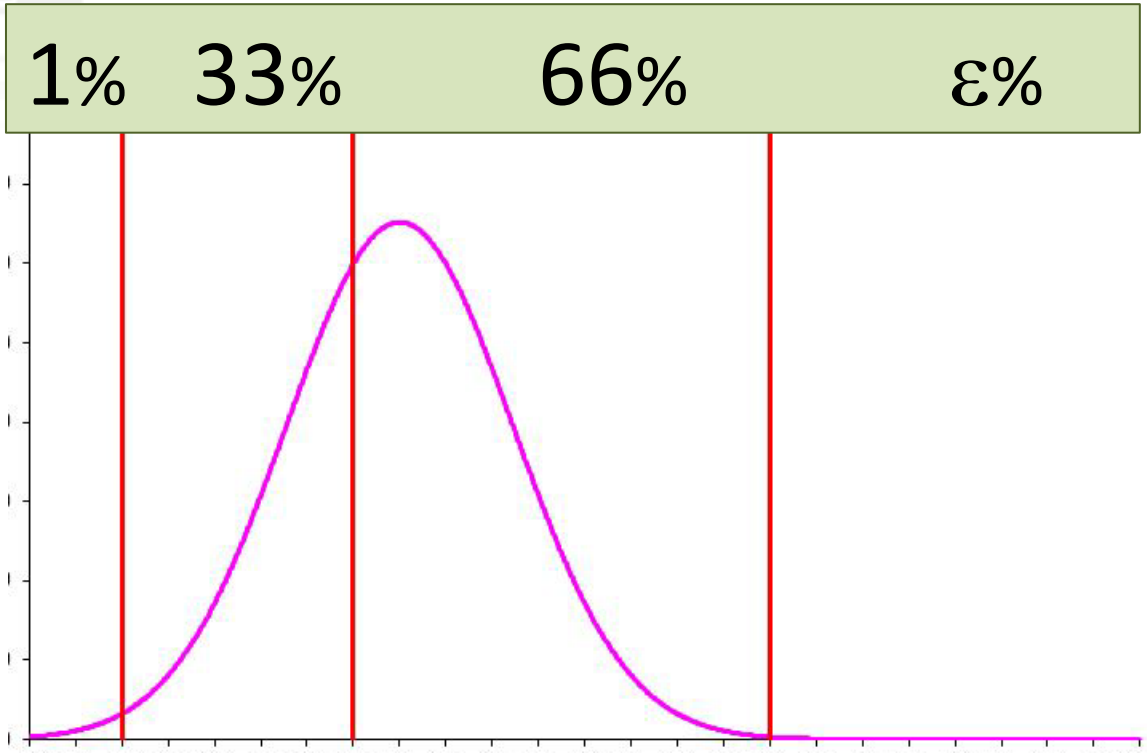
$\mathcal{N}(0, 1.5)$

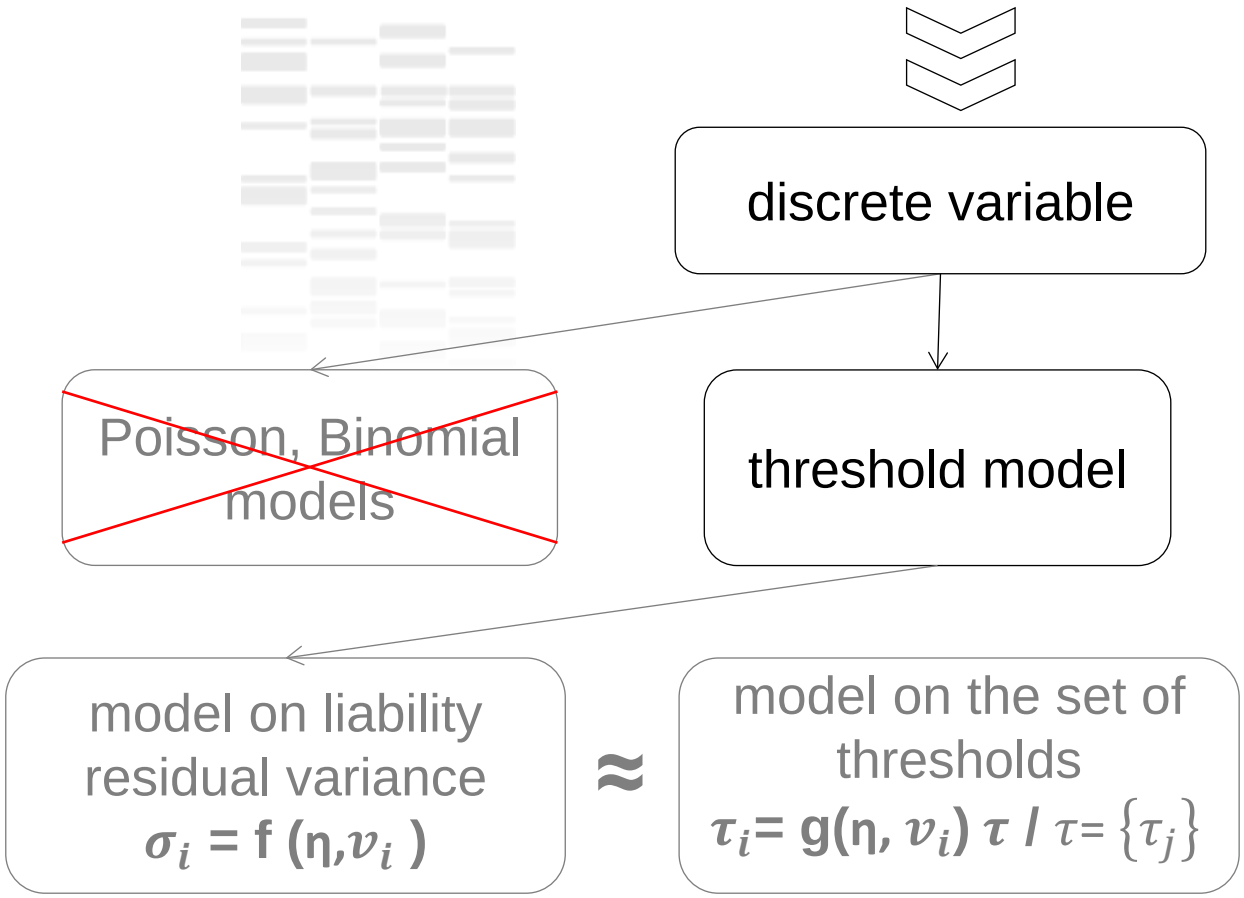


$\mathcal{N}(0, 1.5)$



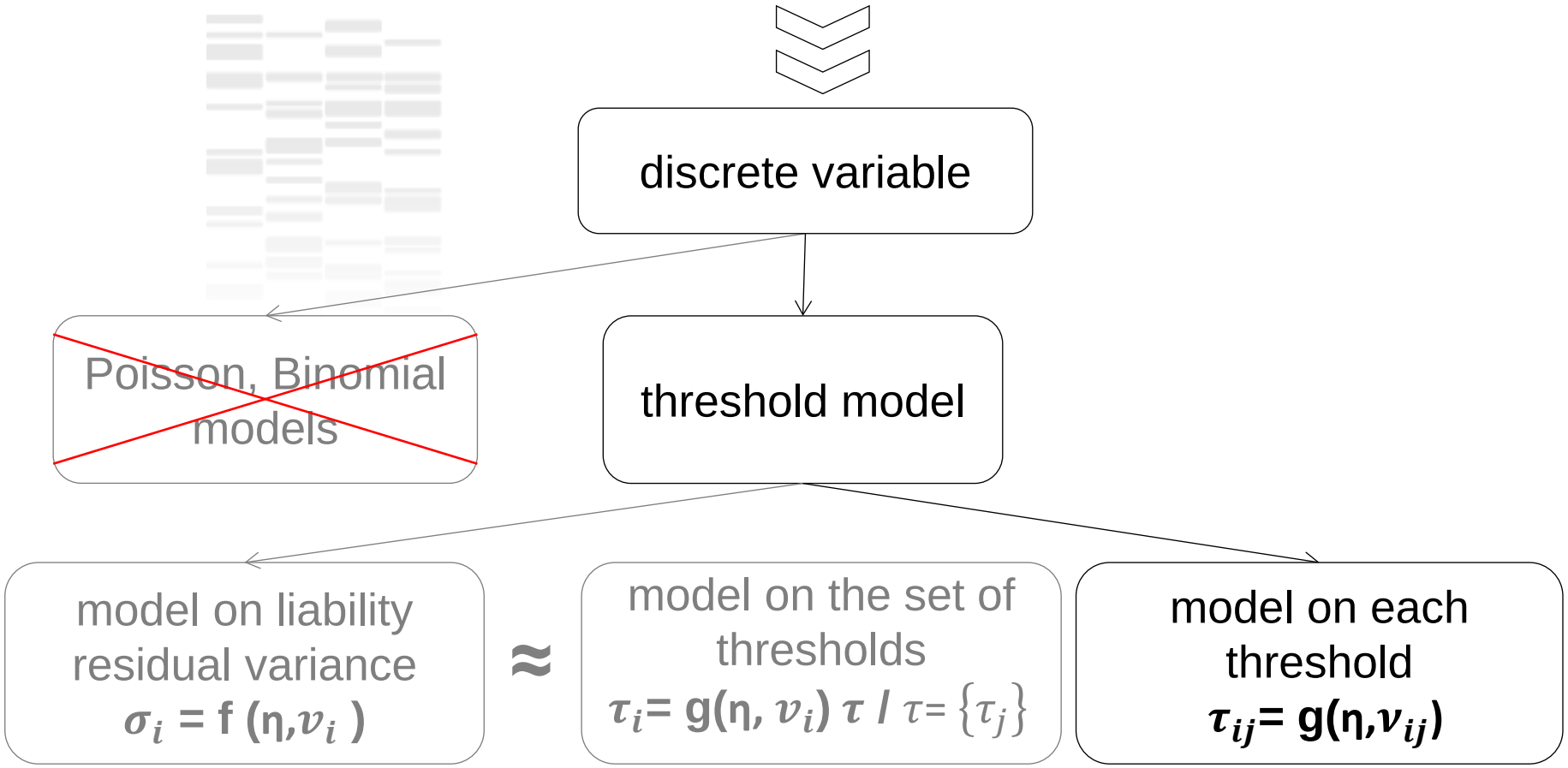
$\mathcal{N}(0, 1.5)$





not always suitable model:

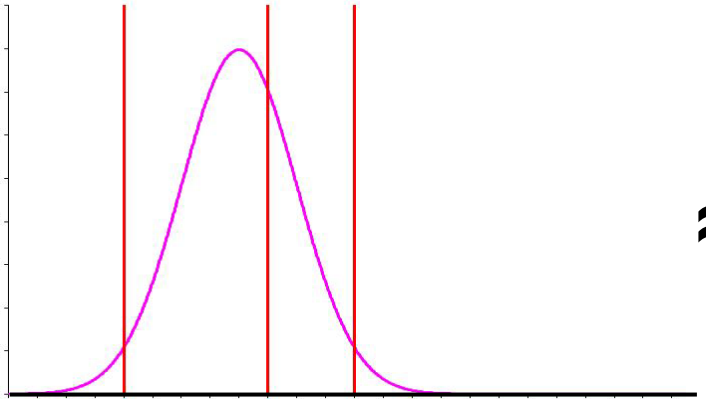
some objectives never reached



all objectives are possible

model on each threshold (N classes)

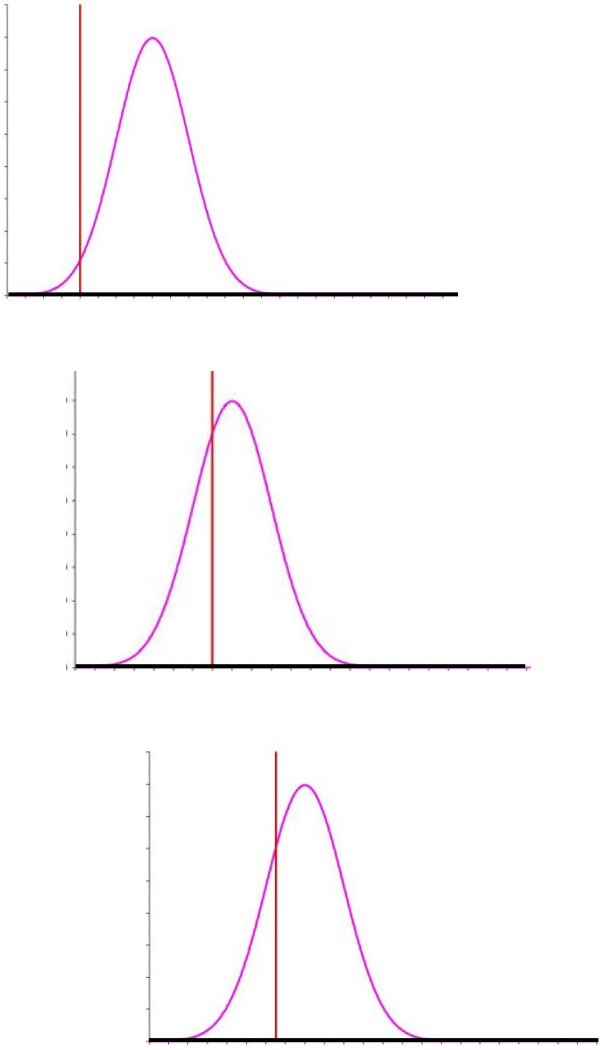
τ_{ij}= g(η,ν_{ij})



τ_{i1} τ_{i2} τ_{i3}

≈

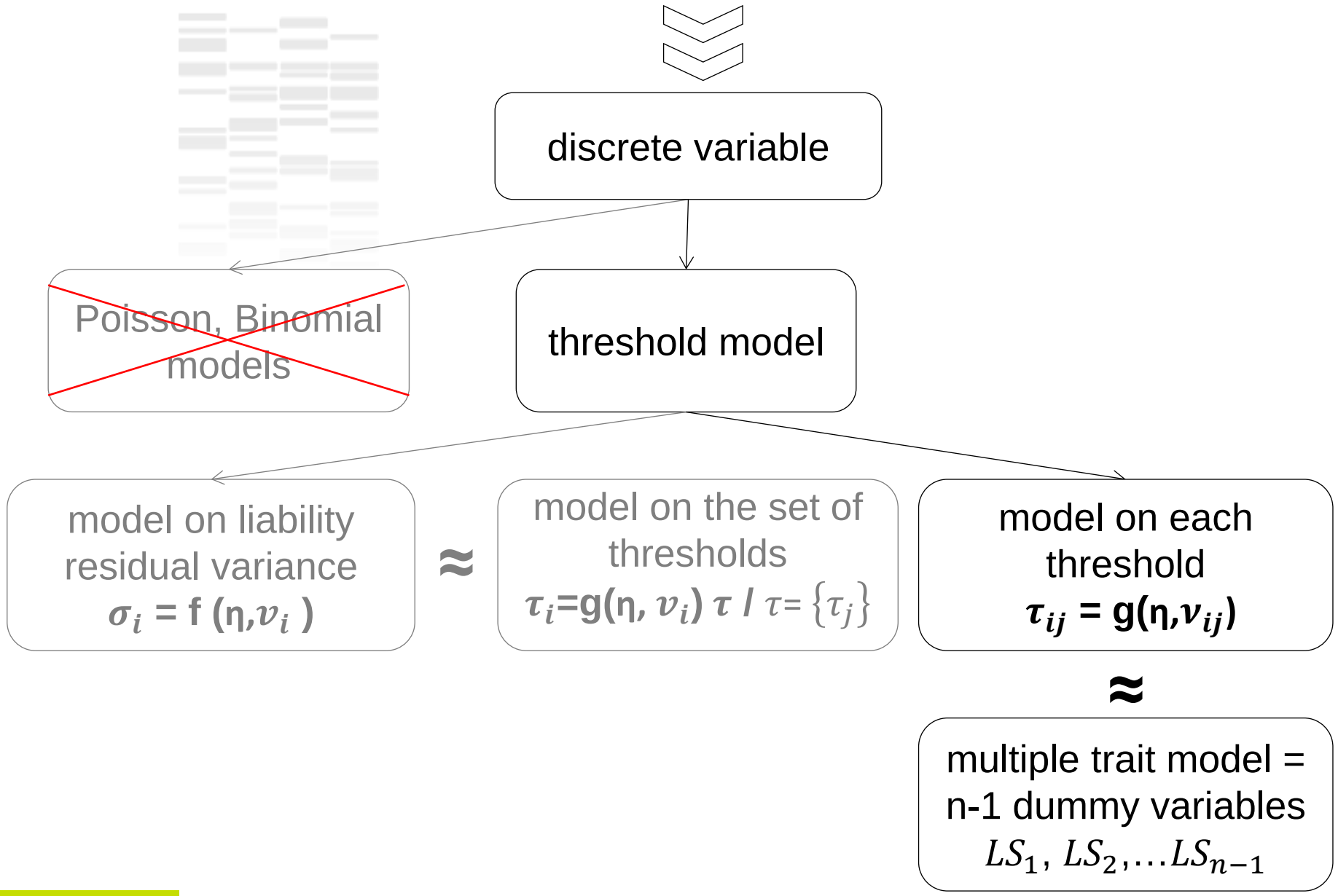
N-1 dummy variables



LS_1

LS_2

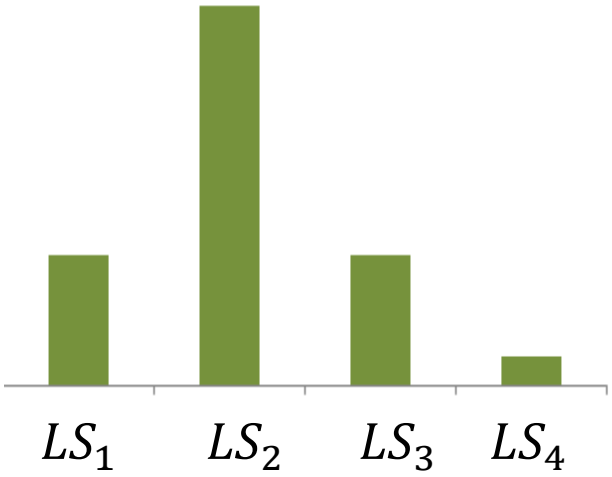
LS_3


discrete variable
Poisson, Binomial models
threshold model
model on liability residual variance
σ_i = f (η,ν_i)
≈
model on the set of thresholds
τ_i=g(η, ν_i) τ / τ= $\{\tau_j\}$
model on each threshold
τ_{ij} = g(η,ν_{ij})
≈
multiple trait model = n-1 dummy variables
LS_1, LS_2,…LS_{n-1}

Multiple trait model applied to the Romane breed

Heritability h^2 / Correlation for each trait (LS_1, LS_2, LS_3)

0.019 (0.002)	0.5 (0.002)	- 0.84 (0.001)
	0.024 (0.002)	- 0.88 (0.001)
		0.046 (0.003)



h^2 is not zero
r_g significant
' possibility to select these traits (LS_1, LS_2, LS_3)

Conclusions

Model on each threshold H multiple trait model

Model used for analyzing the twins → it works

Large number of parameters → lots of data

Extreme cases → convergence problems

Conclusions

Model on set of thresholds H model on liability residual variance

Software to be done

Take home message

- Model on each threshold H multiple trait model
- Model on set of thresholds H model on liability residual variance
- Software to be done