Germination and how to estimate it; not a trivial task! (To germinate or not that is the question)

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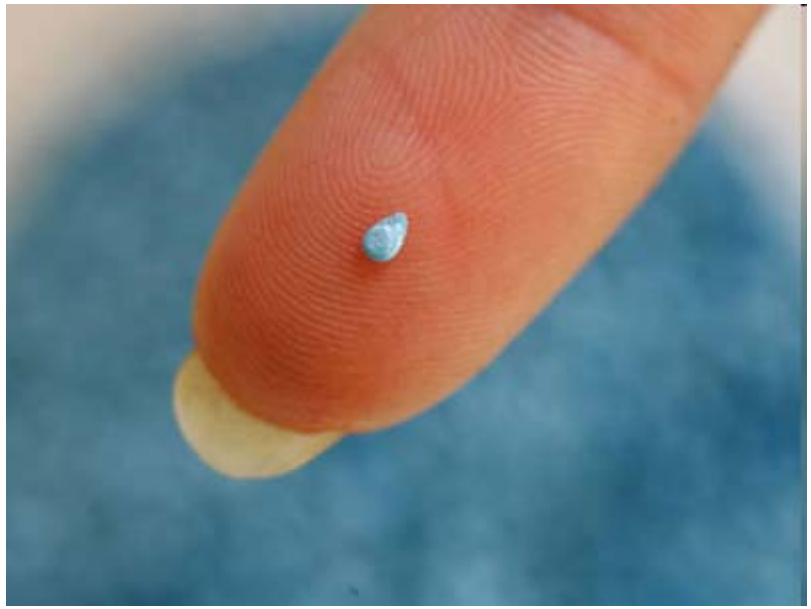
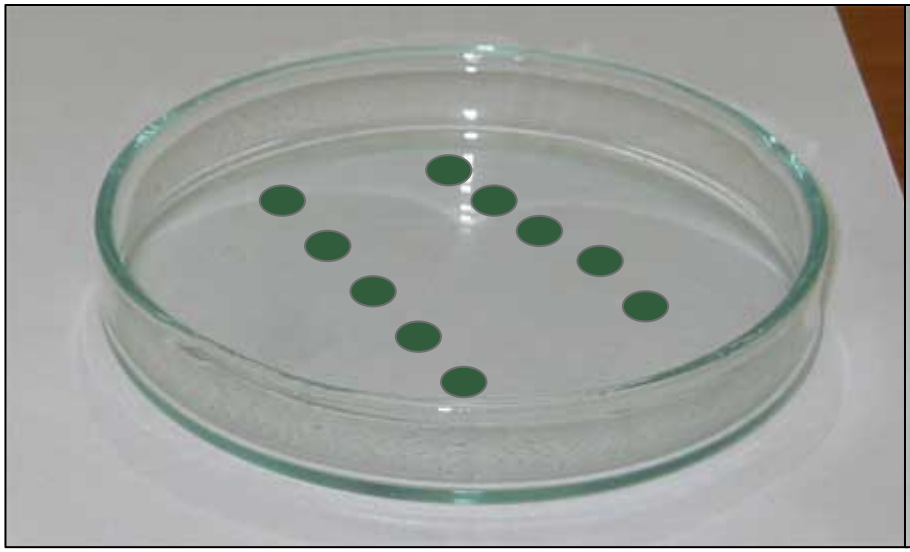
A single seed

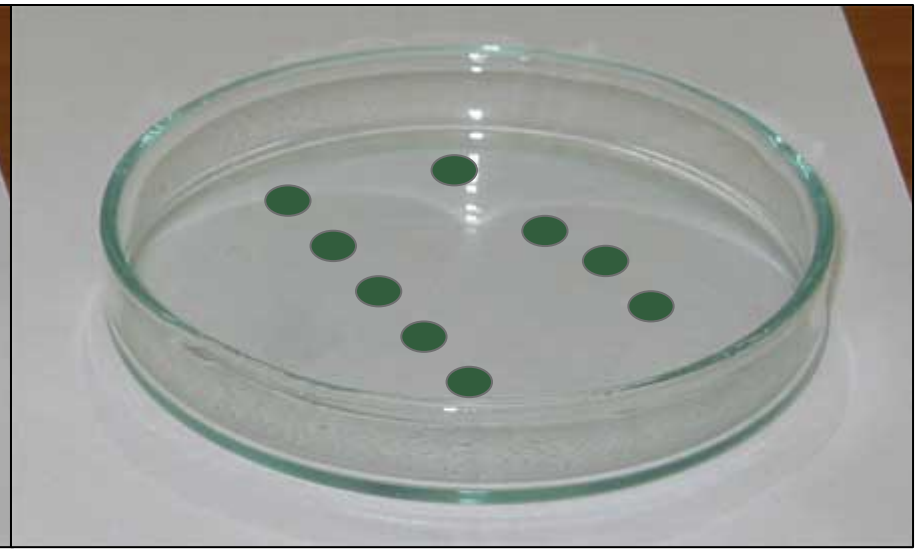


Does it germinate or not?
The are three ways to estimate it

Once counted the petridish is disposed of



1



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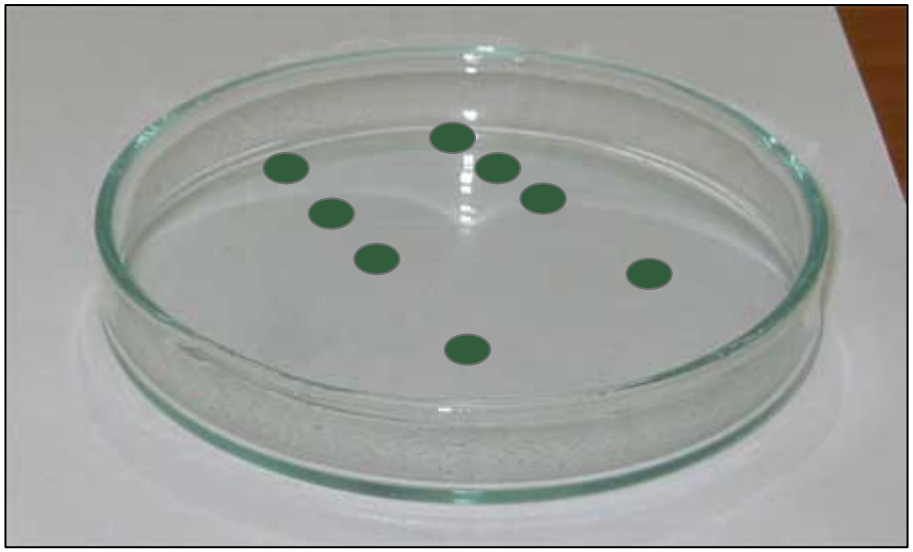

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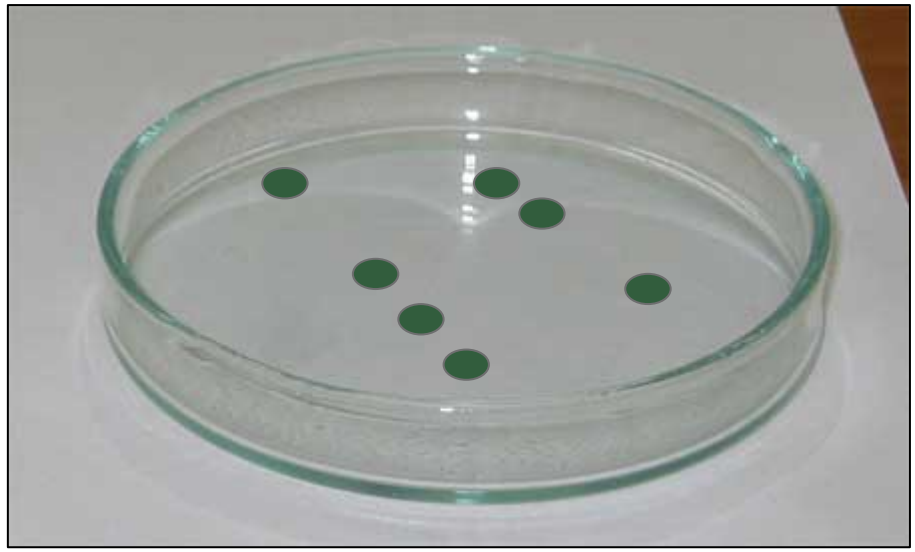

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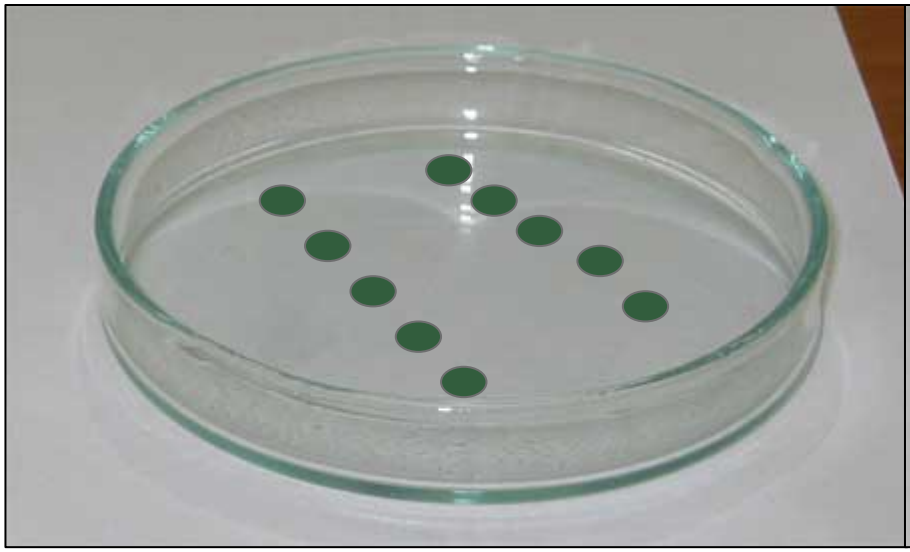
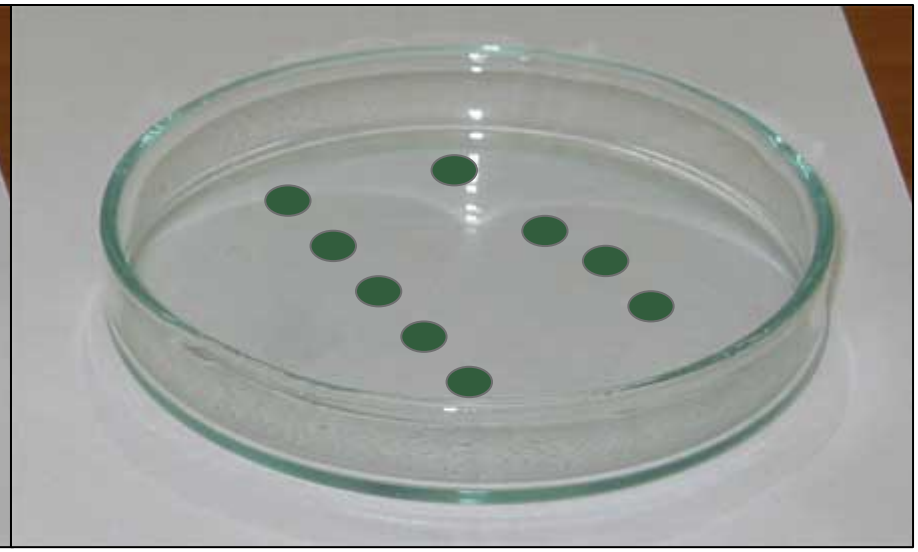
Data analysis straight forward

Time	Germinated	Total	Fraction
1	0	17	0,00
3	5	17	0,29
10	10	17	0,59

Once counted the petridish is recounted next time



1



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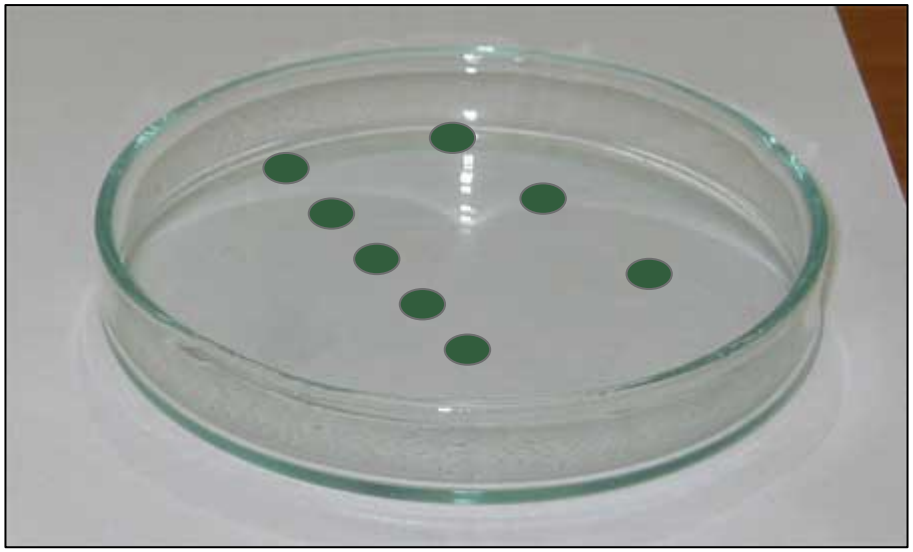

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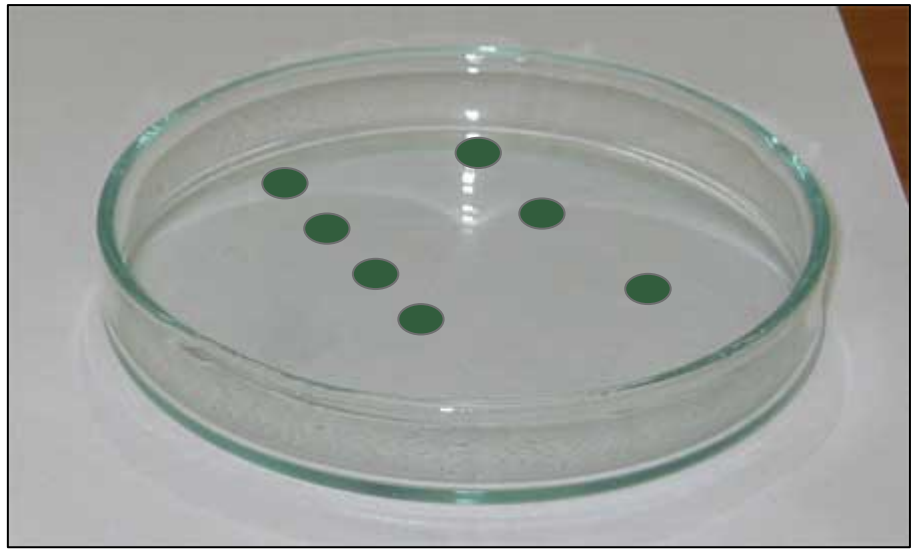

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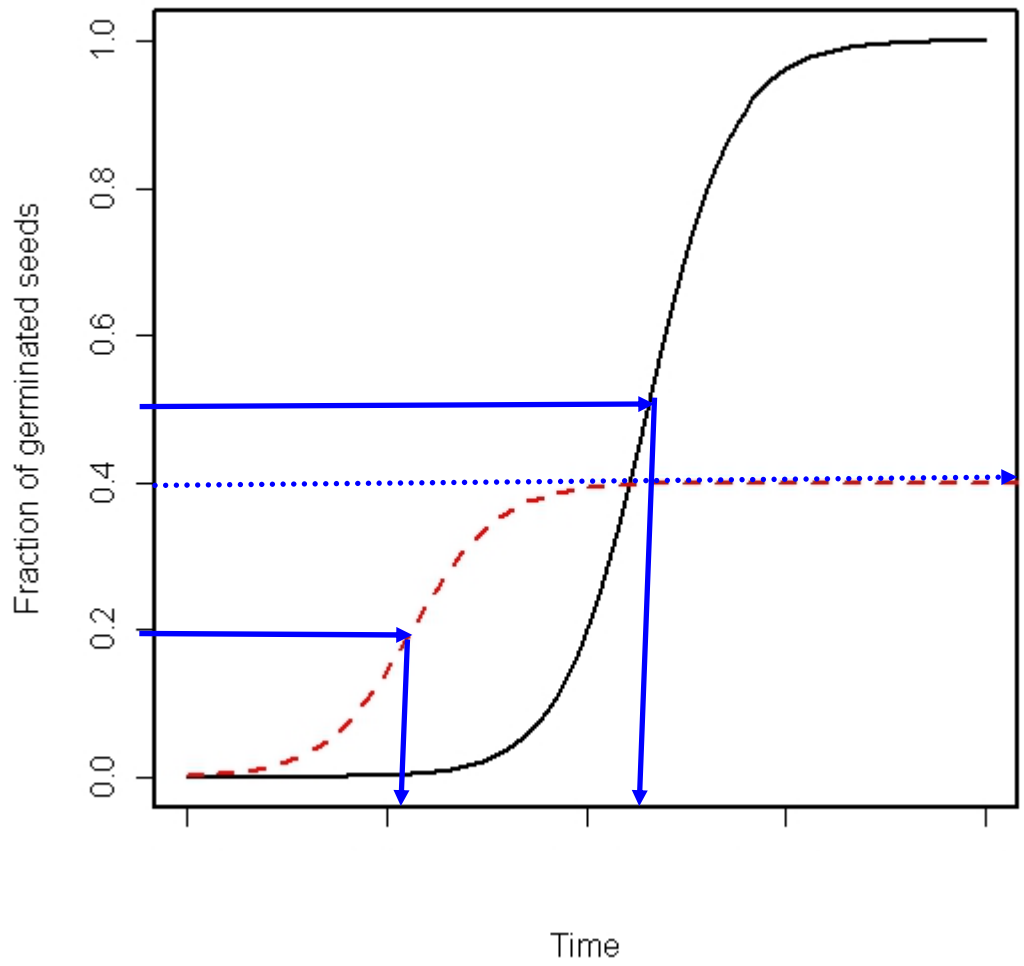
The not so good method

Time	Germinated	Total	Fraction
1	0	17	0,00
3	5	17	0,29
10	10	12 (17)	0,83

A total of 17 seeds are used in this small data example and 15 of these 17 seeds germinated and two seeds were right-censored at the end of the experiment, at day 10.

Start	End	Germinated
0	1	0
1	3	5
3	10	10
10	inf	2

Germination curves



Seed germination Curve

Logistic model

$$y = \frac{D}{1 + \left(\frac{z}{T_{50}} \right)^{b}}$$

$$y = \frac{D}{1 + \exp\{b \cdot [\log(z) - \log(T_{50})]\}}$$

y = Dependent variable (e.g., biomass)

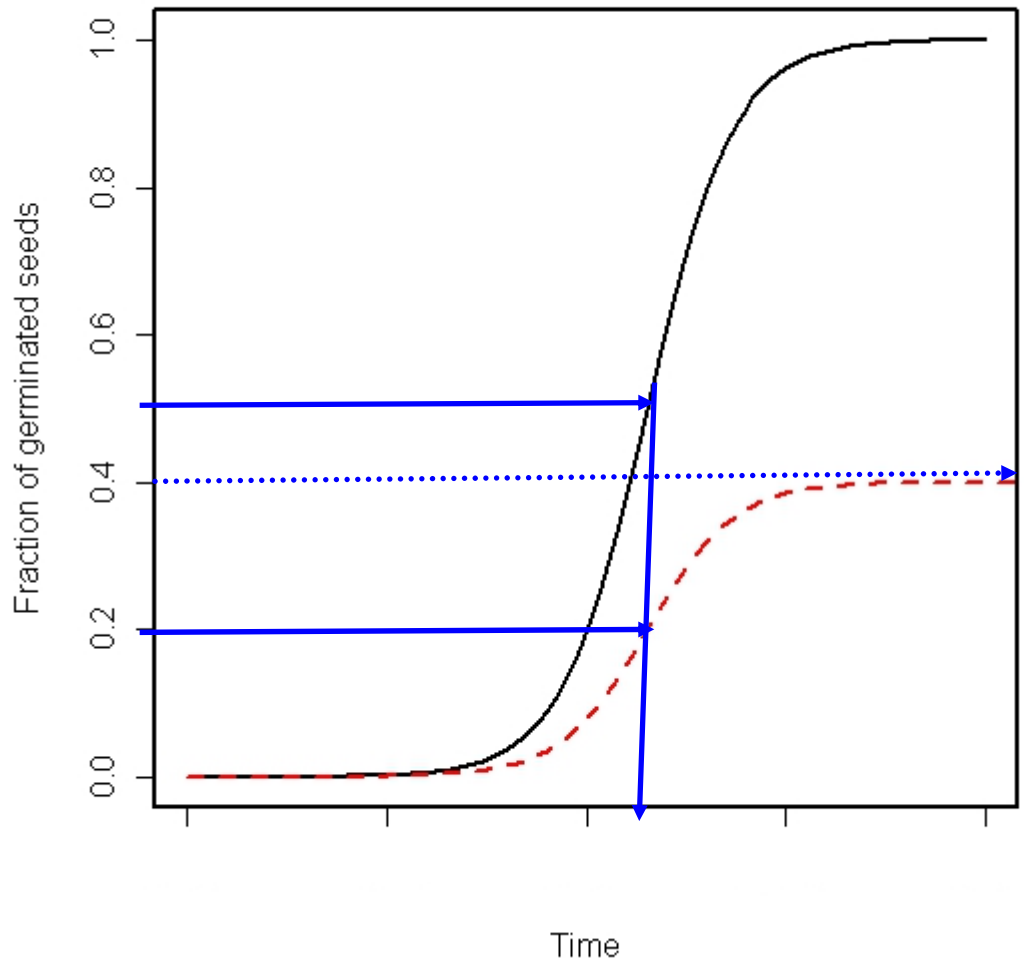
z = Independent variable (e.g., time)

D = Upper limit of *y*

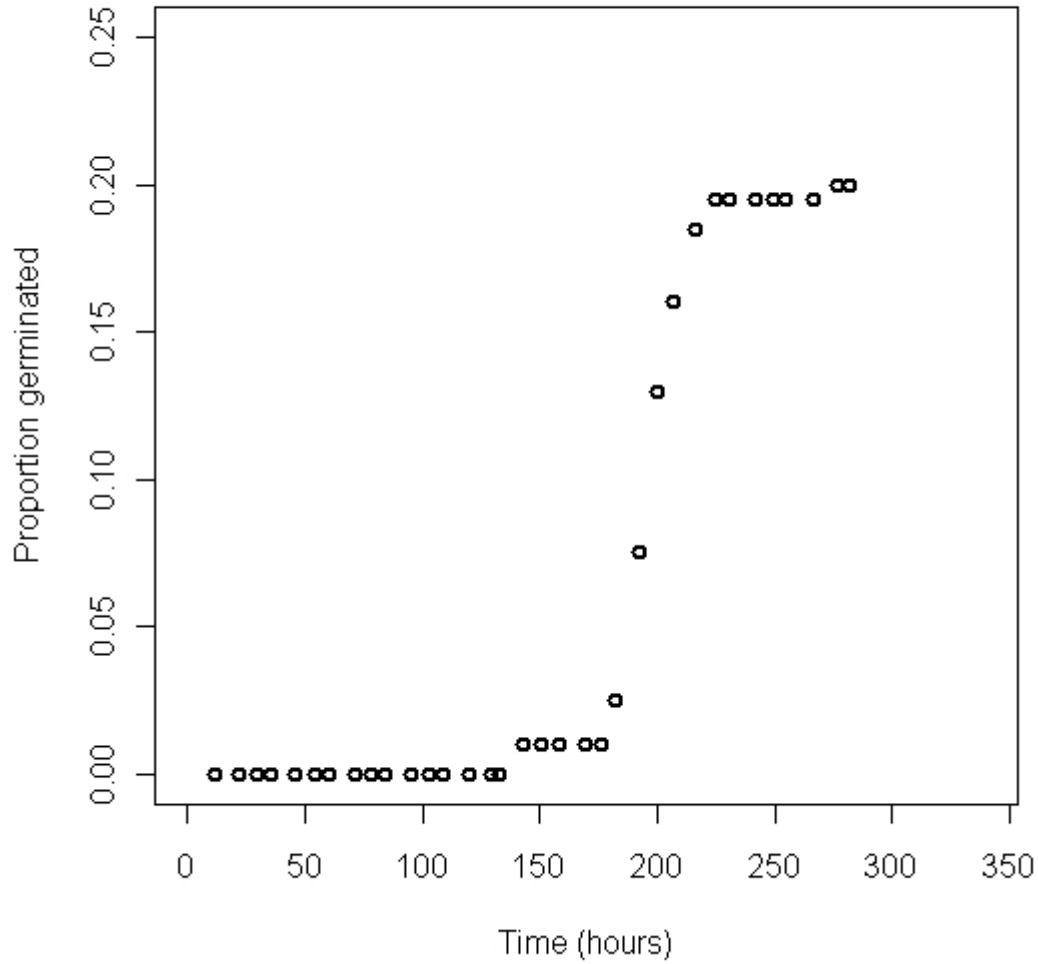
T_{50} = Time until half of the seeds have germinated relative to D

b = relative slope of curve around ED_{50}

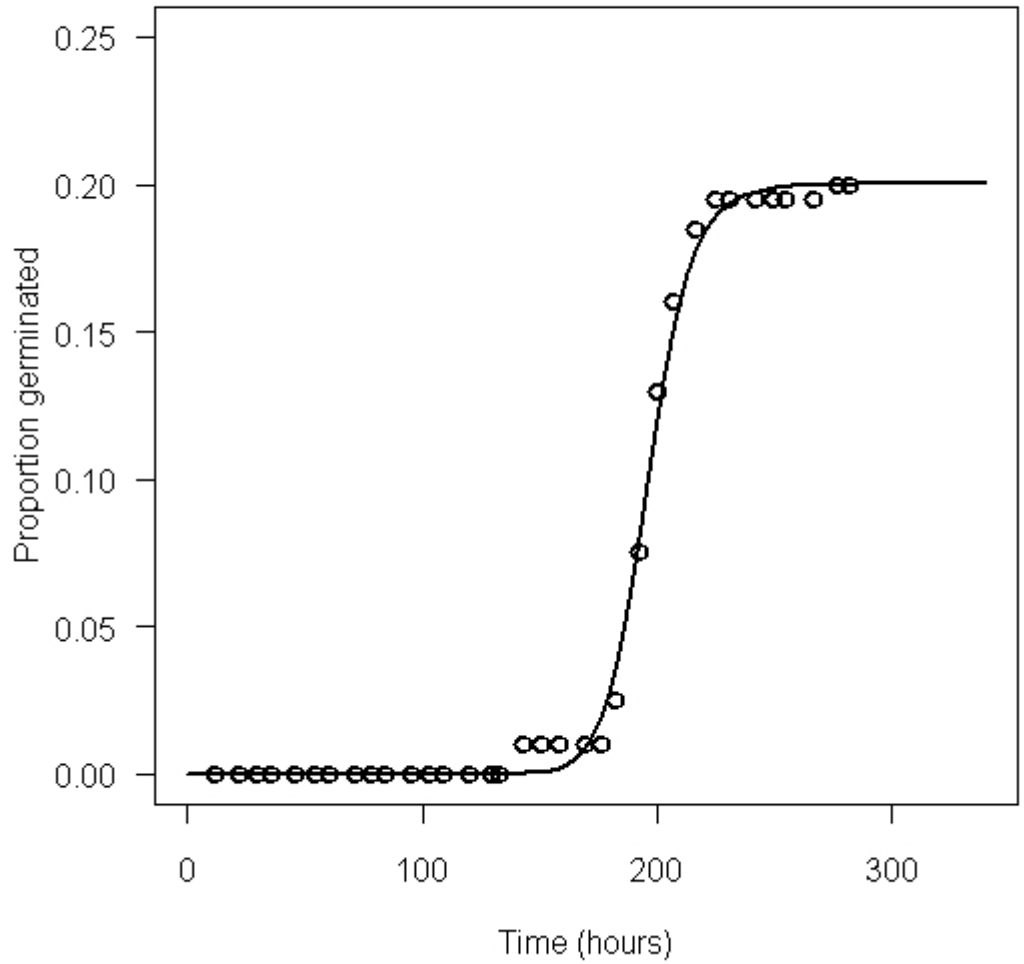
Germination curve



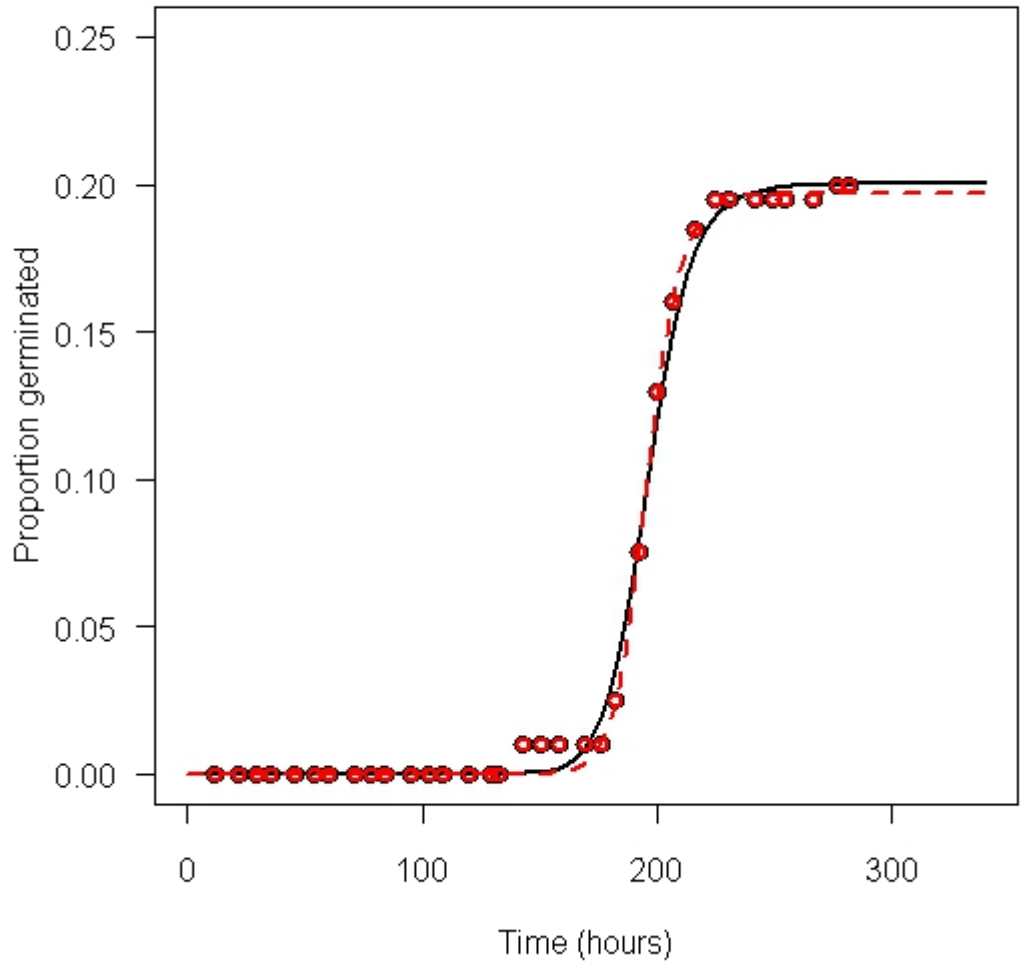
Germination curve *Stellaria media*



Germination curve *Stellaria media* (wrong model)



Germination curve *Stellaria media* (More correct model)



Wrong Model

	Estimate	Std. Error
Slope	-27.1	1.2
Upper Limit	0.197	0.001
T50	**196.**	**0.35**

Better Model

	Estimate	Std. Error
Slope	-20.8	2.9
Upper Limit	0.200	0.028
T50	**196.**	**2.51**

Various Tx S. media

	Estimate	Std. Error	Lower	Upper
Wrong model				
T10	181	0.71	179	182
T50	196	0.35	195	196
T90	212	0.85	210	214
Better model				
T10	176	3.49	169	183
T50	196	2.51	191	200
T90	217	4.27	209	226

Implications

Count and dispose the “dish” no problem do a logistic regression

Old method (logistic regression) too precise standard errors due to in appropriate assumptions

wrong inference when comparing parameters, say T50

More than 90% plus of all germination experiments published are probably using the wrong method (my guesstimate)