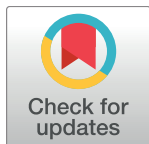


CORRECTION

Correction: Parameter estimation for multistage clonal expansion models from cancer incidence data: A practical identifiability analysis

Andrew F. Brouwer, Rafael Meza, Marisa C. Eisenberg

[Table 1](#) and [Figs 4, 5, 7, 8](#) and [10](#) are incorrect. There is an error in the value of the threshold used to calculate the confidence intervals. The authors have provided the corrected versions here.



OPEN ACCESS

Citation: Brouwer AF, Meza R, Eisenberg MC (2017) Correction: Parameter estimation for multistage clonal expansion models from cancer incidence data: A practical identifiability analysis. *PLoS Comput Biol* 13(7): e1005660. <https://doi.org/10.1371/journal.pcbi.1005660>

Published: July 17, 2017

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Table 1. Best-fit parameters and likelihood-based 95% confidence intervals. Best-fit parameters and likelihood-based 95% confidence intervals for the fits of the two-, three-, and four-stage clonal expansion models (with parameterizations using only practically identifiable parameter combinations and given in Eqs. (2), (9), and (11) respectively) to age-specific incidence of pancreatic cancer.

Model	Parameter combination	Value	Likelihood-based 95% CI
Two-stage			
	$p_2 = \frac{1}{2}(-(\alpha - \beta - \mu_1) - \sqrt{(\alpha - \beta - \mu_1)^2 - 4\alpha\mu_1})$	-1.29E-1	(-1.32E-1, -1.26E-1)
	$q_2 = \frac{1}{2}(-(\alpha - \beta - \mu_1) + \sqrt{(\alpha - \beta - \mu_1)^2 - 4\alpha\mu_1})$	6.21E-6	(5.58E-6, 6.88E-6)
	$r_2 = \nu\lambda/\alpha$	1.50E-2	(1.38E-2, 1.65E-2)
Three-stage			
	$p_3 = \frac{1}{2}(-(\alpha - \beta - \mu_2) - \sqrt{(\alpha - \beta - \mu_2)^2 - 4\alpha\mu_2})$	-1.38E-1	(-1.42E-1, -1.34E-1)
	$q_3 = \frac{1}{2}(-(\alpha - \beta - \mu_2) + \sqrt{(\alpha - \beta - \mu_2)^2 - 4\alpha\mu_2})$	1.57E-5	(1.38E-5, 1.76E-5)
	$r_3 = \sqrt{\nu\lambda\mu_1/\alpha}$	2.35E-2	(2.23E-2, 2.49E-2)
Four-stage			
	$p_4 = \frac{1}{2}(-(\alpha - \beta - \mu_3) - \sqrt{(\alpha - \beta - \mu_3)^2 - 4\alpha\mu_3})$	-1.50E-1	(-1.57E-1, -1.43E-1)
	$q_4 = \frac{1}{2}(-(\alpha - \beta - \mu_3) + \sqrt{(\alpha - \beta - \mu_3)^2 - 4\alpha\mu_3})$	4.59E-5	(3.90E-5, 5.32E-5)
	$r_3 = (\nu\lambda\mu_1\mu_2/\alpha)^{1/3}$	2.66E-2	(2.54E-2, 2.80E-2)

<https://doi.org/10.1371/journal.pcbi.1005660.t001>

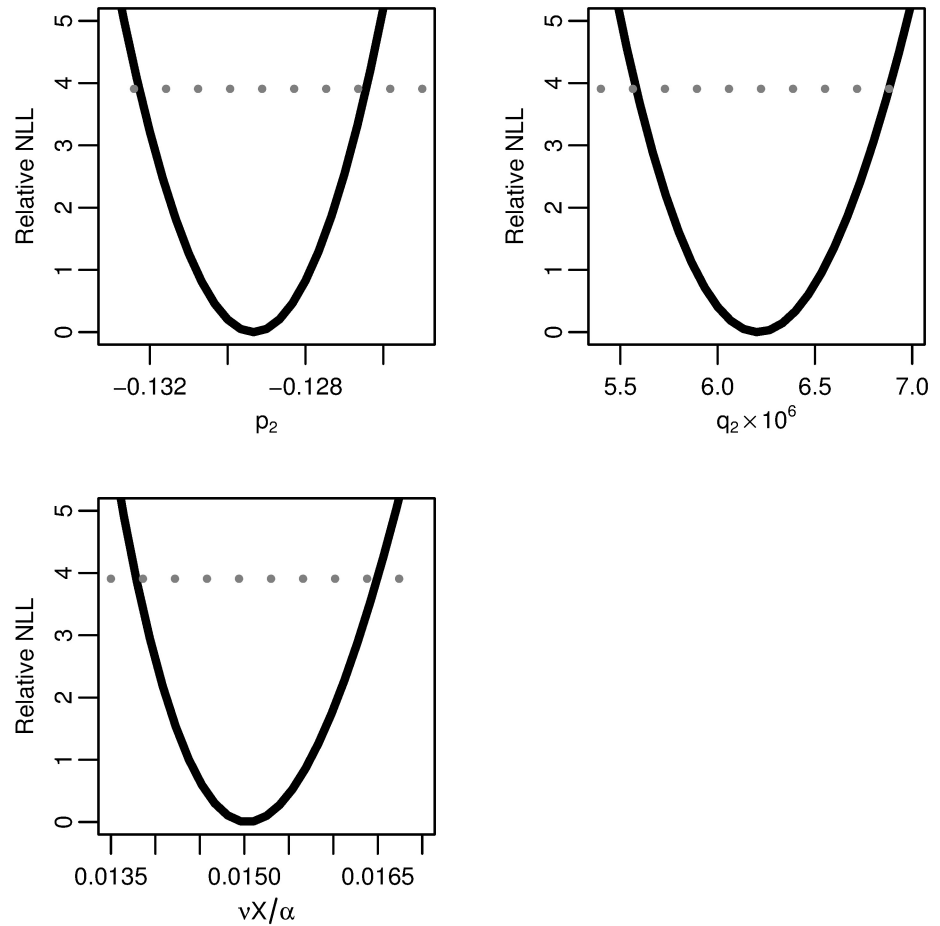


Fig 4. Two-stage model profile likelihoods. Profiles of the relative negative log-likelihood (NLL) of the two-stage clonal expansion model as each of the parameter combinations p_2 , q_2 , and vX/α are varied while the remaining parameters are fit. The gray dotted line gives the $\alpha = 0.05$ threshold for simultaneous confidence intervals based on the relative negative log-likelihood. All three parameters are identifiable.

<https://doi.org/10.1371/journal.pcbi.1005660.g001>

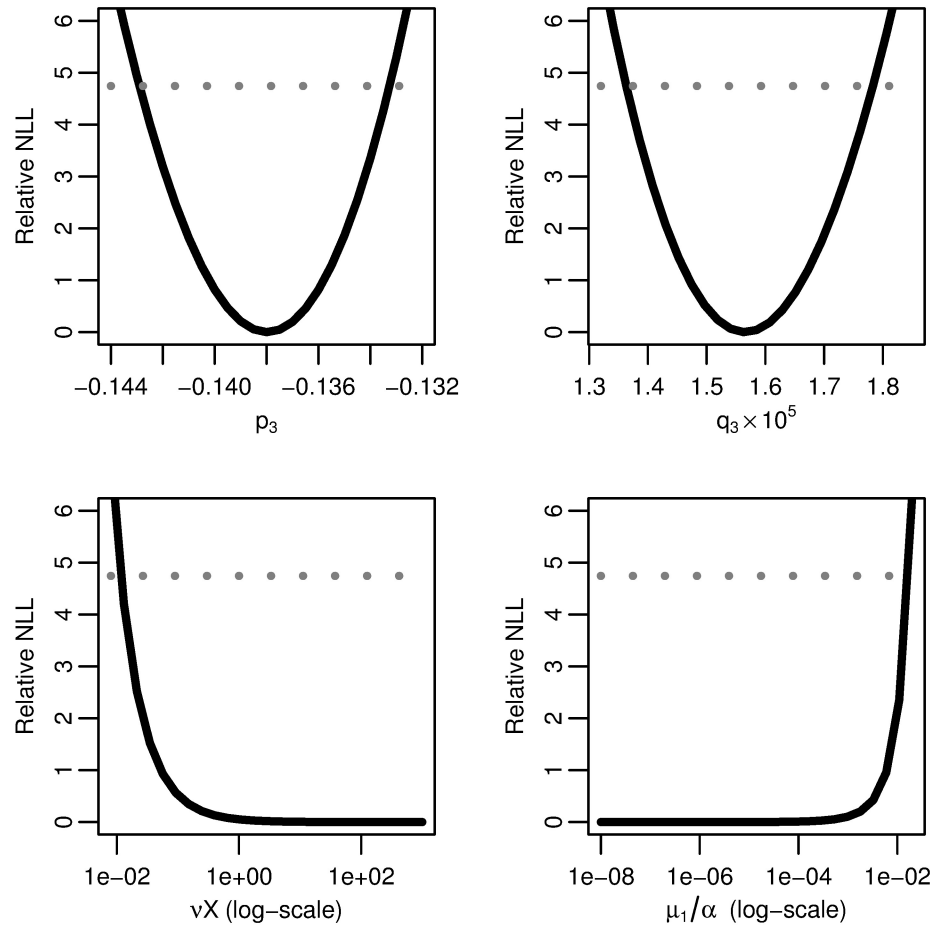


Fig 5. Three-stage model profile likelihoods. Profiles of the relative negative log-likelihood (NLL) of the three-stage clonal expansion model as each of parameter combinations p_3 , q_3 , vX , and μ_1/α are varied while the remaining parameters are fit. The gray dotted line gives the $\alpha = 0.05$ threshold for simultaneous confidence intervals based on the relative negative log-likelihood. Parameter combinations p_3 and p_4 are identifiable, while vX and μ_1/α are practically unidentifiable.

<https://doi.org/10.1371/journal.pcbi.1005660.g002>

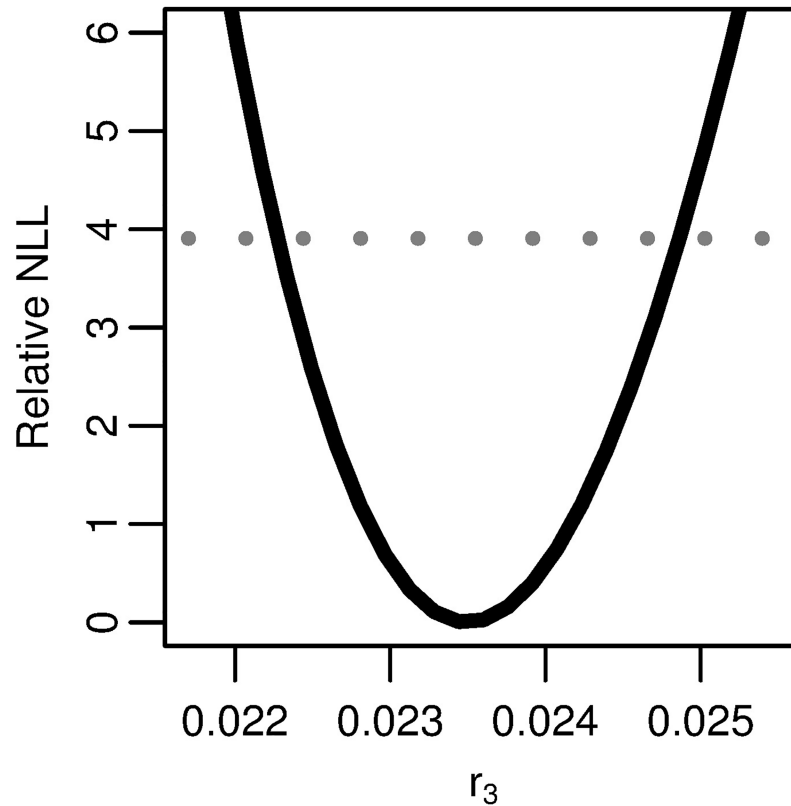


Fig 7. Profile likelihood for the reparameterized combination of the three-stage model. Profile of the relative negative log-likelihood (NLL) as the parameter $r_3 = \sqrt{vX\mu 1/\alpha}$ varied while the remaining parameters are fit in the three-stage clonal expansion model. The gray dotted line gives the $\alpha = 0.05$ threshold for simultaneous confidence intervals based on the relative negative log-likelihood. Parameter combination r_3 is identifiable.

<https://doi.org/10.1371/journal.pcbi.1005660.g003>

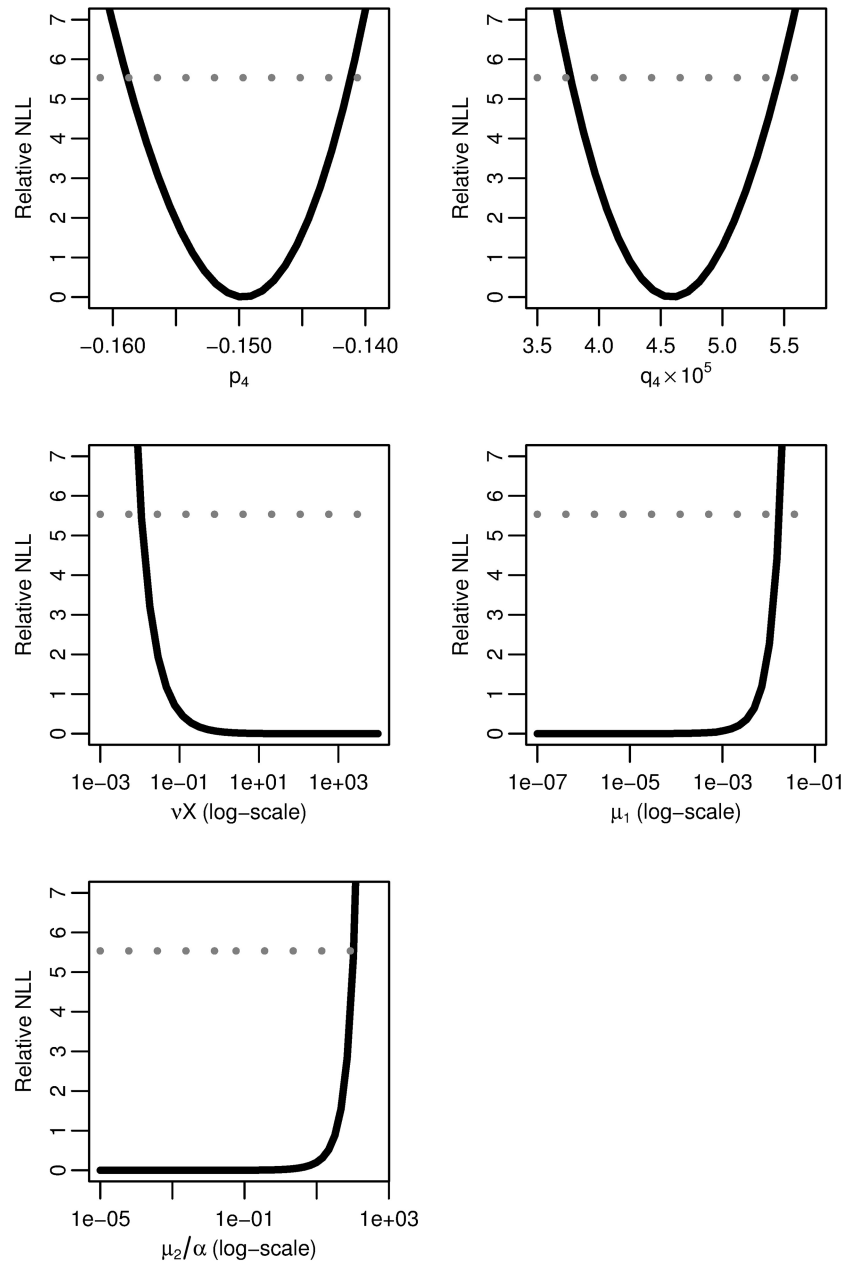


Fig 8. Four-stage model profile likelihoods. Profiles of the relative negative log-likelihood (NLL) of the four-stage clonal expansion model as each of parameter combinations p_4 , q_4 , vX , μ_1 , and μ_2/α are varied while the remaining parameters are fit. The gray dotted line gives the $\alpha = 0.05$ threshold for simultaneous confidence intervals based on the relative negative log-likelihood. Parameter combinations p_4 and q_4 are identifiable, while vX , μ_1 , and μ_2/α are practically unidentifiable.

<https://doi.org/10.1371/journal.pcbi.1005660.g004>

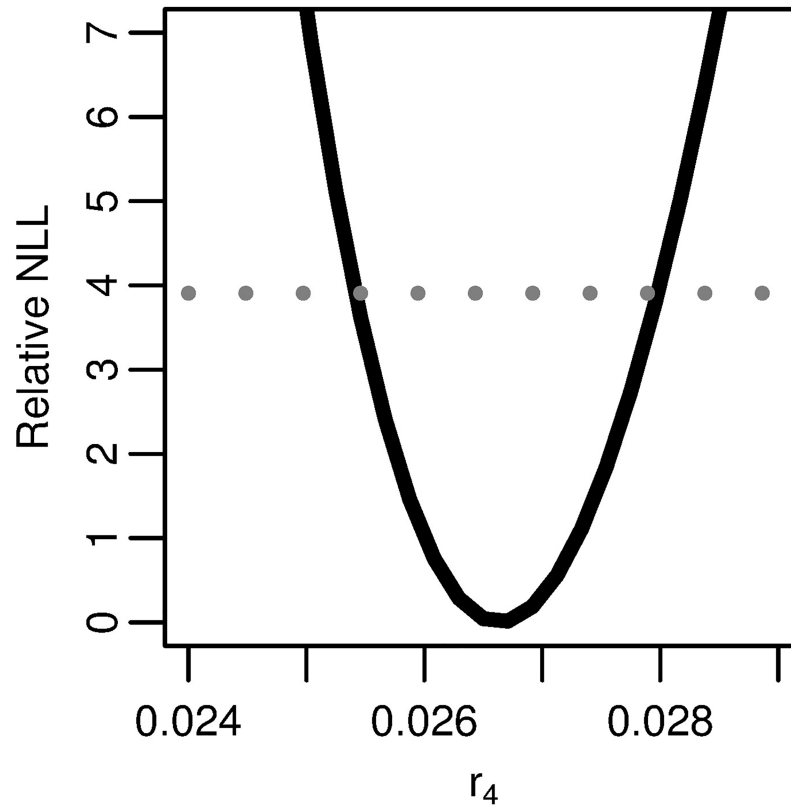


Fig 10. Profile likelihood for the reparameterized combination of the four-stage model. Profile of the relative negative log-likelihood (NLL) as the parameter $r_4 = (vX\mu_1\mu_2/\alpha)^{1/3}$ is varied while the remaining parameters are fit in the four stage clonal expansion model. The gray dotted line gives the $\alpha = 0.05$ threshold for simultaneous confidence intervals based on the relative negative log-likelihood. Parameter combination r_4 is identifiable.

<https://doi.org/10.1371/journal.pcbi.1005660.g005>

Reference

1. Brouwer AF, Meza R, Eisenberg MC (2017) Parameter estimation for multistage clonal expansion models from cancer incidence data: A practical identifiability analysis. *PLOS Computational Biology* 13(3): e1005431. <https://doi.org/10.1371/journal.pcbi.1005431> PMID: 28288156