

Latex template for bioRxiv articles

First Author*,1, Second Author† and Third Author*,1,1

*Dept. of Plant Sciences and Center for Population Biology, University of California, Davis, CA, USA, [†]Some other Department, Some other place, CA, USA, [†]Genome Center, University of California, Davis, CA, USA

ABSTRACT Write your abstract in here Hello, here is some text without a meaning. This text should show what a printed text will look like at this place. If you read this text, you will get no information. Really? Is there no information? Is there a difference between this text and some nonsense like "Huardest gefburn"? Kjift – not at all! A blind text like this gives you information about the selected font, how the letters are written and an impression of the look. This text should contain all letters of the alphabet and it should be written in of the original language. There is no need for special content, but the length of words should match the language.

KEYWORDS Keyword one, keyword 2

Introduction

First part

A good introduction is very important. This is how you can Hufford *et al.* (2012) in line or as reference in the end (Bourne *et al.* 2017).

Second part

Hello, here is some text without a meaning. This text should show what a printed text will look like at this place. If you read this text, you will get no information. Really? Is there no information? Is there a difference between this text and some nonsense like "Huardest gefburn"? Kjift – not at all! A blind text like this gives you information about the selected font, how the letters are written and an impression of the look. This text should contain all letters of the alphabet and it should be written in of the original language. There is no need for special content, but the length of words should match the language.

Materials and Methods

This is an example table

Experiment 1

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Table 1 Parameters and variables

Variable	Description
N _{anc}	Population size at equilibrium
N_{final}	Population size after 0.1 * N_{anc} generations
$N_{bottlenck}$	Population size during bottleneck
ψ	Genetic background proportion
σ_m	Standard deviation of effect sizes of new mutations
V_S	Strength of stabilizing selection
V_{G0}	Genetic variance at equilibrium

Experiment 2 This is an example equation

$$w = exp[-\frac{(z - z_{opt})^2}{2V_c}]$$
 (1)

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Results

Here is a single column figure (Figure 1)

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¹ Dept. of Plant Sciences, University of California, Davis, CA, USA E-mail: corresponding@ucdavis.edu



Figure 1 Important figure Describe the figure

nonsense like "Huardest gefburn"? Kjift – not at all! A blind text like this gives you information about the selected font, how the letters are written and an impression of the look. This text should contain all letters of the alphabet and it should be written in of the original language. There is no need for special content, but the length of words should match the language.

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Discussion

Some more test

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another figure

This is a full size figure (Figure S1) just add stars to the figure

Acknowledgments

We acknowledge the support of our coffee maker that made this work possible

References

Bourne, P. E., J. K. Polka, R. D. Vale, and R. Kiley, 2017 Ten simple rules to consider regarding preprint submission. PLoS computational biology 13: e1005473.

Hufford, M. B., X. Xu, J. Van Heerwaarden, T. Pyhäjärvi, J.-M. Chia, et al., 2012 Comparative population genomics of maize domestication and improvement. Nature genetics 44: 808.



Supplement

Hello, here is some text without a meaning. This text should show what a printed text will look like at this place. If you read this text, you will get no information. Really? Is there no information? Is there a difference between this text and some nonsense like "Huardest gefburn"? Kjift – not at all! A blind text like this gives you information about the selected font, how the letters are written and an impression of the look. This text should contain all letters of the alphabet and it should be written in of the original language. There is no need for special content, but the length of words should match the language.



Figure S1 Supplemental figure Test test test



Table S1 Shrink a large table to fit the page

Parameter	Description
Adaptation	Trait related parameters
Time to optimum	Generations until new optimum is reached
Adaptation rate (haldane)	Adaptation rate until new optimum is reached. Calculated as $rate(h) = \frac{\frac{ln(x_2)}{sd}}{\frac{sd}{x_{12}}} - \frac{ln(x_1)}{\frac{sd}{x_{12}}}$
Final genetic variance	Genetic variance in the final generation
Fixations	Mutations that fix after the optimum shift
From new mutations (#)	Sum of fixed mutations in the final population that were already segregating before the optimum shift
From standing variation (#)	Sum of fixed mutations in the final population that arose after the optimum shift
Max. effect size	Maximal effect size of all fixations
Mean effect size	Mean effect size of all fixations
Mean effect size of negative fixations	Mean effect size of negative mutations
Mean effect size of positive fixations	Mean effect size of positive mutations
Mean emergence time	Mean generation when a mutation arose that fixed in the last 0.1 N generations
Mean fixation time	Mean generation in which a mutation fixed
Min. effect size	Minimal effect size of all fixations
Negative (#)	Sum of fixed mutations with negative effects in the final population
New/standing fixations	Ratio of mutations from new mutations vs. standing mutations
Proportion negative	Proportion of negative fixations from all mutations
Positive (#)	Sum of fixed mutations with positive effects in the final population
SD of effect sizes	Standard deviation of effect sizes of all fixations
SD of negative effect sizes	Standard deviation of effect sizes of negative fixations
SD of positive effect sizes	Standard deviation of effect sizes of positive fixations
Total (#)	Sum of fixed mutations in the final population
Sweeps	Mutations that fix faster than 99% of neutral fixations
Hard sweeps (#)	Sum of selective sweeps from new mutations
Proportion of hard sweeps	Porportion of hard selective sweeps of all selective sweeps
Proportion of sweeps from standing	Proportion of selective sweeps from stainding variation of all selection sweeps
Sweeps (#)	Sum of selective sweeps
Sweeps from standing variation (#)	Sum of selective sweeps from mutations that were already segregating before the optimum shift
Sweeps/fixations	Ratio of sweeps vs. fixations
Segregating sites	Mutations that segregate in the final generation
Max. effect size	Maximal effect size of segregating sites
Mean effect size	Mean effect size of segregating sites
Mean effect size of negative sites	Mean effect size of segregating sites with negative effects
Mean effect size of positive sites	Mean effect size of segregating sites with positive effects
Mean frequency of all sites	Mean allele frequency of segregating sites
Mean frequency of negative sites	Mean allele frequency of segregating sites with negative effects
Mean frequency of positive sites	Mean allele frequency of segregating sites with positive effects
Min. effect size	Minimal effect size of segregating sites
Negative (#)	Sum of segregating sites with negative effect
Positive (#)	Sum of segregating sites with positive effect
Proportion of negative sites	Proportion of segregating sites with negative effect of all segregating sites
Standard deviation of effect sizes	Standard deviation of effect sizes of all segregating sites
Total (#)	Sum segregating sites in the final generation

