

Template for preparing your submission to *GENETICS* using Overleaf

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1 ABSTRACT The abstract should be written for people who may not read the entire paper, so it must stand on its own. The
 2 impression it makes usually determines whether the reader will go on to read the article, so the abstract must be engaging,
 3 clear, and concise. In addition, the abstract may be the only part of the article that is indexed in databases, so it must accurately
 4 reflect the content of the article. A well-written abstract is the most effective way to reach intended readers, leading to more
 5 robust search, retrieval, and usage of the article.
 6 Please see additional guidelines notes on preparing your abstract below.

7 KEYWORDS Keyword; Keyword2; Keyword3; ...

1 This *Genetics* journal template is provided to help you write
 2 your work in the correct journal format. Instructions for
 3 use are provided below. Note that by default line numbers are
 4 present to aid reviewers and editors in reading and comment-
 5 ing on your manuscript. To remove line numbers, remove the
 6 `lineno` option from the `\documentclass` declaration.

7 Guide to using this template in Overleaf

8 This template is provided to help you prepare your article for
 9 submission to the *Genetics*.

10 Author Affiliations

11 For the authors' names, indicate different affiliations with the
 12 symbols: *, †, ‡, §. After four authors, the symbols double, triple,
 13 quadruple, and so forth as required.

14 Your Abstract

15 In addition to the guidelines provided in the example abstract
 16 above, your abstract should:

- 17** • provide a synopsis of the entire article;

- begin with the broad context of the study, followed by specific background for the study; 18
- describe the purpose, methods and procedures, core findings and results, and conclusions of the study; 19
- emphasize new or important aspects of the research; 20
- engage the broad readership of *GENETICS* and be understandable to a diverse audience (avoid using jargon); 21
- be a single paragraph of less than 250 words; 22
- contain the full name of the organism studied; 23
- NOT contain citations or abbreviations. 24

28 Introduction

29 For the introduction, authors should be mindful of the broad
 30 readership of the journal. The introduction should set the stage
 31 for the importance of the work to a generalist reader and draw
 32 the reader in to the specific study. The scope and impact of the
 33 work should be clearly stated.

34 In individual organisms where a mutant is being studied,
 35 the rationale for the study of that mutant must be clear to a
 36 geneticist not studying that particular organism. Similarly, study
 37 of particular phenotypes should be justified broadly and not on
 38 the basis of interest for that organism alone. General background
 39 on the importance of the genetic pathway and/or phenotype
 40 should be provided in a single, well-reasoned paragraph near
 41 the beginning of the introduction.

42 Authors are encouraged to:

- cite the supporting literature completely rather than select a subset of citations; 43

doi: 10.1534/genetics.XXX.XXXXXX

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¹These authors contributed equally to this work.

²These authors contributed equally to this work.

³Corresponding author: Please insert the affiliation correspondence address and email for the corresponding author. The corresponding author should be marked with the relevant number in the author list, as shown in the example.

- 1 • provide important background citations, including relevant
- 2 review papers (to help orient the non-specialist reader);
- 3 • to cite similar work in other organisms.

4 **Materials and Methods**

5 Manuscripts submitted to *GENETICS* should contain a clear de-
 6 scription of the experimental design in sufficient detail so that
 7 the experimental analysis could be repeated by another scientist.
 8 If the level of detail necessary to explain the protocol goes be-
 9 yond two paragraphs, give a short description in the main body
 10 of the paper and prepare a detailed description for supporting
 11 information. For example, details would include indicating how
 12 many individuals were used, and if applicable how individuals
 13 or groups were combined for analysis. If working with mutants
 14 indicate how many independent mutants were isolated. If work-
 15 ing with populations indicate how samples were collected and
 16 whether they were random with respect to the target population.

17 **Statistical Analysis**

18 It is important to indicate what statistical analysis has been per-
 19 formed; not just the name of the software and options selected,
 20 but the method and model applied. In the case of many genes
 21 being examined simultaneously, or many phenotypes, a multi-
 22 ple comparison correction should be used to control the type I
 23 error rate, or a rationale for not applying a correction must be
 24 provided. The type of correction applied should be clearly stated.
 25 It should also be clear whether the p-values reported are raw, or
 26 after correction. Corrected p-values are often appropriate, but
 27 raw p-values should be available in the supporting materials so
 28 that others may perform their own corrections. In large scale
 29 data exploration studies (e.g. genome wide expression studies) a
 30 clear and complete description of the replication structure must
 31 be provided.

32 **Data Availability**

33 At the end of the Materials and Methods section, include a
 34 statement on reagent and data availability. Please read the Data
 35 and Reagent Policy before writing the statement. Make sure to
 36 list the accession numbers or DOIs of any data you have placed
 37 in public repositories. List the file names and descriptions of
 38 any data you will upload as supplemental information. The
 39 statement should also include any applicable IRB numbers. You
 40 may include specifications for how to properly acknowledge or
 41 cite the data.

42 For example: Strains are available upon request. File S1
 43 contains detailed descriptions of all supplemental files. File
 44 S2 contains SNP ID numbers and locations. File S3 contains
 45 genotypes for each individual. Sequence data are available at
 46 GenBank and the accession numbers are listed in File S3. Gene
 47 expression data are available at GEO with the accession number:
 48 GDS1234. Code used to generate the simulated data is provided
 49 in file S4.

50 **Results and Discussion**

51 The results and discussion should not be repetitive. The results
 52 section should give a factual presentation of the data and all
 53 tables and figures should be referenced; the discussion should
 54 not summarize the results but provide an interpretation of the
 55 results, and should clearly delineate between the findings of
 56 the particular study and the possible impact of those findings
 57 in a larger context. Authors are encouraged to cite recent work

relevant to their interpretations. Present and discuss results
 only once, not in both the Results and Discussion sections. It is
 sometimes acceptable to combine results and discussion. The
 text should be as succinct as possible. Heed Strunk and White's
 dictum: "Omit needless words!"

63 **Additional guidelines**

64 **Numbers**

65 In the text, write out numbers nine or less except as part of a date,
 66 a fraction or decimal, a percentage, or a unit of measurement.
 67 Use Arabic numbers for those larger than nine, except as the first
 68 word of a sentence; however, try to avoid starting a sentence
 69 with such a number.

70 **Units**

71 Use abbreviations of the customary units of measurement only
 72 when they are preceded by a number: "3 min" but "several
 73 minutes". Write "percent" as one word, except when used with
 74 a number: "several percent" but "75%." To indicate temperature
 75 in centigrade, use ° (for example, 37°); include a letter after
 76 the degree symbol only when some other scale is intended (for
 77 example, 45°K).

78 **Nomenclature and Italicization**

79 Italicize names of organisms even when when the species is
 80 not indicated. Italicize the first three letters of the names of
 81 restriction enzyme cleavage sites, as in HindIII. Write the names
 82 of strains in roman except when incorporating specific genotypic
 83 designations. Italicize genotype names and symbols, including
 84 all components of alleles, but not when the name of a gene is the
 85 same as the name of an enzyme. Do not use "+" to indicate wild
 86 type. Carefully distinguish between genotype (italicized) and
 87 phenotype (not italicized) in both the writing and the symbolism.

88 **Cross References**

89 Use the `\nameref` command with the `\label` command to insert
 90 cross-references to section headings. For example, a `\label` has
 91 been defined in the section [Materials and Methods](#).

92 **In-text Citations**

93 Add citations using the `\citep{}` command, for example ([Ne-
 94 her and Hallatschek 2013](#)) or for multiple citations, ([Neher and
 95 Hallatschek 2013](#); [Rödelsperger et al. 2014](#); [Falush et al. 2016](#))

96 **Examples of Article Components**

97 The sections below show examples of different header levels,
 98 which you can use in the primary sections of the manuscript
 99 (Results, Discussion, etc.) to organize your content.

100 **First level section header**

101 Use this level to group two or more closely related headings in a
 102 long article.

103 **Second level section header**

104 Second level section text.

105 **Third level section header:** Third level section text. These head-
 106 ings may be numbered, but only when the numbers must be
 107 cited in the text.

1 Figures and Tables

2 Figures and Tables should be labelled and referenced in the
3 standard way using the `\label{}` and `\ref{}` commands.

4 Sample Figure

5 Figure 1 shows an example figure.

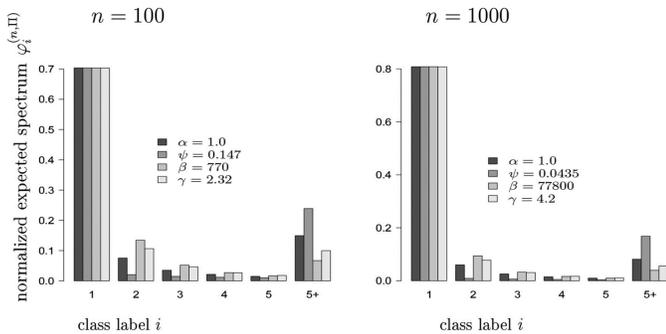


Figure 1 Example figure from [10.1534/genetics.114.173807](https://doi.org/10.1534/genetics.114.173807).

Please include your figures in the manuscript for the review process. You can upload figures to Overleaf via the Project menu. Upon acceptance, we'll ask for your figure files to be uploaded in any of the following formats: TIFF (.tiff), JPEG (.jpg), Microsoft PowerPoint (.ppt), EPS (.eps), or Adobe Illustrator (.ai). Images should be a minimum of 300 dpi in resolution and 500 dpi minimum if line art images. RGB, CMYK, and Grayscale are all acceptable. Halftones should be high contrast with sharp detail, because some loss of detail and contrast is inevitable in the production process. Figures should be 10-20 cm in width and 1-25 cm in height. Graph axes must be exactly perpendicular and all lines of equal density. Label multiple figure parts with A, B, etc. in bolded type, and use Arrows and numbers to draw attention to areas you want to highlight. Legends should start with a brief title and should be a self-contained description of the content of the figure that provides enough detail to fully understand the data presented. All conventional symbols used to indicate figure data points are available for typesetting; unconventional symbols should not be used. Italicize all mathematical variables (both in the figure legend and figure), genotypes, and additional symbols that are normally italicized.

6 Sample Video

7 Figure 2 shows how to include a video in your manuscript.

8 Sample Table

9 Table 1 shows an example table. Avoid shading, color type,
10 line drawings, graphics, or other illustrations within tables. Use
11 tables for data only; present drawings, graphics, and illustrations
12 as separate figures. Histograms should not be used to present
13 data that can be captured easily in text or small tables, as they
14 take up much more space.

15 Tables numbers are given in Arabic numerals. Tables should
16 not be numbered 1A, 1B, etc., but if necessary, interior parts of
17 the table can be labeled A, B, etc. for easy reference in the text.

18 Sample Equation

Let X_1, X_2, \dots, X_n be a sequence of independent and identically distributed random variables with $E[X_i] = \mu$ and $\text{Var}[X_i] =$

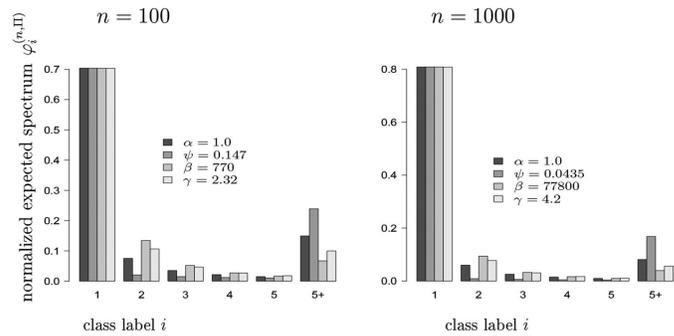


Figure 2 Example movie (the figure file above is used as a placeholder for this example). *GENETICS* supports video and movie files that can be linked from any portion of the article - including the abstract. Acceptable formats include .asf, avi, .wav, and all types of Windows Media files.

$\sigma^2 < \infty$, and let

$$S_n = \frac{X_1 + X_2 + \dots + X_n}{n} = \frac{1}{n} \sum_i^n X_i \quad (1)$$

denote their mean. Then as n approaches infinity, the random variables $\sqrt{n}(S_n - \mu)$ converge in distribution to a normal $\mathcal{N}(0, \sigma^2)$.

Literature Cited

Falush, D., L. van Dorp, and D. Lawson, 2016 A tutorial on how (not) to over-interpret STRUCTURE/ADMIXTURE bar plots. bioRxiv. <http://www.biorxiv.org/content/early/2016/07/28/066431>.

Neher, R. A. and O. Hallatschek, 2013 Genealogies of rapidly adapting populations. *Proceedings of the National Academy of Sciences* **110**: 437–442.

Rödelsperger, C., R. A. Neher, A. M. Weller, G. Eberhardt, H. Witte, *et al.*, 2014 Characterization of genetic diversity in the nematode *pristionchus pacificus* from population-scale resequencing data. *Genetics* **196**: 1153–1165.

Table 1 Students and their grades

Student	Grade ^a	Rank	Notes
Alice	82%	1	Performed very well.
Bob	65%	3	Not up to his usual standard.
Charlie	73%	2	A good attempt.

^a This is an example of a footnote in a table. Lowercase, superscript italic letters (a, b, c, etc.) are used by default. You can also use *, **, and *** to indicate conventional levels of statistical significance, explained below the table.