The eLife research article

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# Deceased (not really!!)
¶ This footnote text must work in isolation as nothing is processed on the html view to make it "work"

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Abstract

This is the abstract. This article will describe the eLife article and the process. An abstract can contain any formatting, such as *italics*, **bold**, ^{superscript}, $_{subscript}$ or small caps. MathML is also allowed: m p m = 0 .

eLife does not structure abstracts into sub headings expect in a clinical trial article, but the abstract can have multiple paragarahs. The sub DOI is always .001 as it is the first asset in any article. I have added an unmatched > bracket as this has been an issue for PubMed deposits in the past.

If this was a clinical trial the clinical trial details would be listed at the end of the abstract:

Clinical trial Registration: EudraCT2004-000446-20.

Abstract

eLife digest

eLife digest are now optional and not every research article will contain one. These are layman abstracts, designed for non-specialists in this field to be able to understand this article, as well as the general public.

Here is paragraph 2 of the digest.

Introduction (Level 1 heading)

This article is a guide to the tagging and display of eLife articles and will encompass all the elements that can possibly be contained in an eLife article. It will also include information from the author guide. For this reason, it is colloquially known as the eLife 'kitchen sink'.

The eLife editorial process (level 2 heading)

eLife publishes the most highly influential research across the life sciences and biomedicine. Before you submit your work, please note that eLife is a very selective journal that aims to publish work of the highest scientific standards and importance. Leading academic researchers evaluate new submissions and approximately two-thirds are returned to the authors without further peer review. See DeLano (2002) and Department of Education and Morgan (2016). Approximately half of the articles that are selected for peer review go on to be published (Brettar et al., 2004a). If other researchers publish similar findings after submission, this will not be a reason for rejection. The eLife editorial process broadly occurs in three phases (Turlings and Wäckers, 2004a; Turlings and Wäckers, 2004b; Wolski et al., 2008; Walker, 1994; Tanaka et al., 2016). If you are interested in submitting your work to eLife, please review the guidelines relating to initial submissions. If you have received an encouraging response to your initial submission, please review the guidelines relating to full submissions. If your full submission has been peer reviewed and you have been asked to make revisions, please review our guidelines for revised submissions (Brettar et al., 2004b).

Initial submission (level 3 heading)

eLife publishes research of the very highest (Bricogne et al., 2011) standard and significance, so many manuscripts are returned to the authors without in-depth peer review. During the initial submission phase, members of eLife's senior editorial team rapidly assess new submissions, often in consultation with members of the Board of Reviewing Editors or with external guest editors where necessary, to identify the ones that are appropriate for in-depth peer review (Cardé and Millar, 2004; Cartwright, 2016; Chmeil, 2008). To simplify the submission process, authors should submit their full manuscript as a single PDF. Limited additional information is collected via the submission screen questions to complete the submission (Brettar et al., 2004b).

Full submission (level 3 heading)

For manuscripts that are invited for in-depth peer review, see Coyne and Orr (1989) and Du et al. (2014), we request detailed information about the work to support the peer review process, to ensure that the work meets appropriate standards for the reporting of new findings, and, if accepted, to assist in rapid publication and further dissemination of the work in relevant indexes and repositories. Authors are asked to agree to publish their work under the terms of the Creative Commons Attribution license (PDF of the agreement), or the Creative Commons CC0 public domain dedication (PDF of the agreement) if one or more authors are US-government employees (Hubbard and Thornton, 1993; GlaxoSmithKline UK, 2016; Jain et al., 2010).

Revised submission (level 3 heading)

We will require a response to the essential revision requirements outlined in the decision letter. A response to minor comments is optional. In the event of acceptance, the substantive revision requests and the authors' response will be published, under the terms of the Creative Commons Attribution license. In preparation for submission, authors should ensure they have all the materials and information necessary to expedite the submission and assessment of their work (Eisen, 2016; Ferry et al., 2014; Gavrilov et al., 2014; Goodstadt, 2010; Hoang et al., 2015).

The eLife production process (level 2 heading)

Immediate publication (accepted manuscript) (level 3 heading)

On acceptance an eLife article can be published in accepted manuscript form immediately. The mean time from acceptance to publication at this stage is 1 day. Using SQl, basic metadata is exported from the submission system to an AWS bucket as CSV files. The author files are exported to another AWS bucket and an eLife process generates a package of this information and the author files to deliver to the online platform, Continuum.

Publication of the full version (version of record) (level 3 heading)

The production process includes an author proofing cycle, the output of which is the final full text version of the article online, as well as a typeset PDF.

Publication of versions (level 3 heading)

eLife allows the publication of updates to an article after the full version has been produced. These are treated as new versions of the article. All previous versions of the article will continue to exist online and will be accessible from the latest live version.

level 4 heading

eLife allows up to four levels of headings and no more. This is a demonstration of a level 4 heading.

Results

This section will be used to demostrate the majority of eLife XML tagging and editorial policies. However, the Introduction section was used to demostrate heading levels. See Appendix 1.1 and 2.

eLife controlled lists

eLife has no strict requirements for the display of lists. Below we will show examples of how to present lists. See Figure 2—figure supplement 1 for the representation of the Major Subject Areas, Research Organisms and author keywords on the eLife HTML page (The *Shigella* Genome Sequencing Consortium, 2015a).

Article types

This is an example of a list where the prefix character is a lowercase roman numeral. eLife Article Types are taken from a controlled list:

i. Research article
ii. Short Report
iii. Tools and Resources
iv. Research Advance
v. Registered Report
vi. Replication Study

Article types (XML only, not display) (level 4 heading)

This is an example of a list where the prefix character is a uppercase roman numeral. This is a controlled list from the JATS DTD

I. article-commentary (used for Insights)
II. correction
III. discussion (used for Feature 1 and Feature 2)
IV. editorial
V. research-article (all reseasrch content)

Nested lists are allowed and these are very common in Registered Peports. Below is an example of a nested list to 3 levels.

Genus: Plasmodium; following species are known to infect humans

I.
    i. *P. falciparum*
    ii. *P. vivax*
    iii. *P. ovale*
    iv. *P. malariae*
    v. *P. knowlesi*

    Genus: Leishmania. There are 3 subgenus of Leishmania:

II.
    i. Leishmania
    ii. Sauroleishmania
    iii. Viannia
    iv. Within Viannia subgenus, there are 11 species:
        - *L. braziliensis*
        - *L. colombiensis*
        - *L. equatorensis*
        - *L. guyanensis*
        - *L. lainsoni*
        - *L. naiffi*
        - *L. panamensis*
        - *L. peruviana*
        - *L. pifanoi*
        - *L. shawi*
        - *L. utingensis*

Major Subject Areas

This is an example of a bulleted list. eLife Major subject areas are taken from a controlled list:

- Biochemistry
- Biophysics and Structural Biology
- Cell Biology
- Computational and Systems Biology
- Developmental Biology and Stem Cells
- Ecology
- Epidemiology and Global Health
- Genes and Chromosomes
- Genomics and Evolutionary Biology
- Human Biology and Medicine
- Immunology
- Microbiology and Infectious Disease
- Neuroscience
- Plant Biology

Multi-lists

1. Here is an example of a list with multiple paragraphs and equations.

   A discrete three-dimensional model space was generated (represented as a three-dimensional matrix; Figure 2—figure supplement 1A, left), with dimensions corresponding to population μ, population σ, and f value. Any given value in the matrix indicates P(f|μ,σ), that is, the probability of a given frequency given a particular μ and σ. The columns (all f values for a given μ and σ combination; Figure 2—figure supplement 1, upper-right) thus constitute the forward model (by which stimuli are generated), and the planes (all combinations of μ and σ for a given f value; Figure 2—figure supplement 1, lower-middle) constitute the inverse model (by which hidden parameters can be estimated from observed f values).

2. 2) For each segment, the model was inverted for its particular f value, yielding a two-dimensional probability distribution for the hidden parameters (Figure 2—figure supplement 1, lower-

middle). Steps 3-6 were then worked through for each stimulus segment in order, starting at the beginning of the stimulus.

3. These probability distributions, for each segment subsequent to the most recent estimated population change (as defined later), were multiplied together, and scaled to a sum of 1. The resulting probability distribution (Figure 2—figure supplement 1, lower-right) thus reflects parameter probabilities taking into account all relevant f values

4. This combined parameter probability distribution was then scalar multiplied with the full model space, in order to weight each of the forward model columns (each corresponding to a particular parameter combination) by the probability of that parameter combination being in effect. The resulting weighted model space was then averaged across parameter dimensions, to yield a one-dimensional (forward) probability distribution, constituting an optimal prediction about the f value of the next stimulus segment, provided a population change did not occur before then. A probability distribution applicable if a population change were to occur was calculated the same way, but without weighting the forward model columns (so as to encompass every possible parameter combination).

5. It was assumed that a population change occurred immediately prior to the first stimulus segment. To infer subsequent population changes, for each segment the probability of observing the present f value was compared for the two probability distributions (the distribution assuming a population change, and the distribution assuming no change), that is, P(f|c) and P(f|~c), respectively, with c denoting a population change. The probabilities were compared, in conjunction with the known prior probability of a population change (1/8), using Bayes' rule, as stated in Equation 2: (1) P (c | f) = P (f | c) P (c) P (f)

   Here, P(c|f) is the chance that a population change occurred at that particular time. Given that P(c) is known to be 1/8, and P(f), the total probability of the observed f value, can be rewritten P(f|c)P(c)+P(f|~c)(1-P(c)), the above equation can be rewritten as Equation 3: (2) P (c | f) = 1 1 + 7 P (f | ~ c) P (f | c)

6. For each segment, the above calculation of P(c|f) was made not only with respect to the immediately preceding segment, but also a number of segments preceding that, up to a maximum of 4. Therefore, for segment t, it was possible to conclude that a population change had occurred immediately prior to t, t-1, t-2, t-3, or none of the above. A population change was judged to have occurred at the time point with the highest value of P(c|f), provided this value was greater than 0.5. Using more than 4 lags did not appreciably alter the estimates obtained by model inversion. Importantly, any retrospective inference of population changes did not retrospectively alter any prior predictions generated by the model (e.g. at time t, if a population change were inferred to have occurred at time t-3 then the priors for t-2, t-1 and t were not affected, but only the priors for t+1 onwards).

7. Once the above steps were worked through for each stimulus segment in order, the optimal prior predictions were used to calculate the perceptual inference variables of interest. Predictions themselves were summarised by their mean (μ) and precision (1/variance). Changes to predictions (Δμ) were calculated as the absolute change (in octaves) in μ from one prediction to the next. Surprise (S) was calculated as the negative log probability of the observed f value given the prior prediction, and prediction error (irrespective of prediction precision) was calculated as the absolute difference (in octaves) between the observed f value and the mean of the prior prediction. Mathematically, surprise is directly proportional to prediction precision multiplied by prediction error. Finally, Δf was calculated as the absolute difference between the current and preceding value of f.

Research Organisms

This is an example of an ordered list, the "system" will default to numbers. eLife Research organsims are taken from a controlled list from the submission system:

1. *Arabidopsis*
2. *B. subtilis*
3. *C. elegans*
4. *C. intestinalis*
5. Chicken
6. *D. melanogaster*
7. *Dictyostelium*
8. *E. coli*
9. Frog
10. Human
11. *M. mulatta*
12. Maize
13. Mouse
14. *M. thermophila*
15. *M. crassa*
16. *Neurospora*
17. None
18. Other
19. *O. fasciatus*
20. *P. falciparum*
21. *P. dumerilii*
22. Rat
23. *S. cerevisiae*
24. *S. pombe*
25. *S. enterica*serovar Typhi
26. *S. pyogenes*
27. Virus
28. *Volvox*
29. *Xenopus*
30. *P. cynocephalus*
31. Zebrafish

However, additional research organisms can be added during the production process so this is not a controlled list once it is output from the editorial system. The research organism "Other" is hidden from display on the eLife website.

Tables

This section is an example of different tables, there are four in total (Tables 1 to 3 and an unnamed inline table).

Table 1.:
This is the title.
This is the caption: A table containing interesting formating that is large enough to require landscape orientation in the PDF.

			GLVs (percent IS plant^{-1})			TPS10 products (percent IS plant^{-1})				Non-target volatiles (percent IS plant^{-1})			
			(*Z*)-Hexen-3-ol			TAB			TBF	α-Duprezianene		Germacrene A	
Genotype	**Day n**	**Night n**	**Day**	**Night**		**Day**	**Night**		**Day**	**Night**	**Day**	**Night**	**Day**	**Night**
WT	8	8	0.99% ± 0.99%	7.96% ± 4.25%	} **a**	0.37% ± 0.29%	**a** —	**a**	—	**a** —	2.13% ± 0.85%	0.96% ± 0.42%	1.68% ± 0.98%	—
TPS10	7	7	2.37% ± 1.55%	2.84% ± 0.63%	} **lox**	18.97% ± 6.03%	**b** 0.94% ± 0.53%	} **TPS**	9.34% ± 3.44%	**b** 0.20% ± 0.20%	9.47% ± 5.26%	0.94% ± 0.26%	2.78% ± 1.52%	—
lox2/3	7	8	0.13% ± 0.13%	1.06% ± 0.64%	} **b**	—	**a** 0.15% ± 0.15%	} **b**	—	**a** —	2.75% ± 1.12%	0.60% ± 0.19%	1.68% ± 1.49%	—
lox2/3xTPS10	7	7	0.07% ± 0.07%	1.24% ± 0.84%		**lox** 7.39% ± 2.56%	**b** 2.08% ± 0.84%		**TPS** 4.47% ± 1.70%	**b** 0.40% ± 0.40%	3.02% ± 1.42%	0.73% ± 0.31%	0.66% ± 0.37%	—

Footnotes not linked to content within the table text are usually to define abbreviations. For example:

WT, wild type.

Table 2 is an example of a standard table that will be the width of the text column in the PDF. It does not contain any unusual styling. It does have footnotes linked to content in the table using the prescribed symbols.

Table 2.: This table contains references and footnotes and is sized to the text column width in the PDF.

Protein	Molar ratio of lipid:protein in RPL reactions*	Molar ratio of lipid:protein on vacuoles		References†
		BJ3505	DKY6218	
Vam7p	2×10^3	30×10^4	6.5×10^4	DeLano, 2002
Vam3p	2×10^3	11×10^4	22×10^4	Department of Education and Morgan, 2016
Vti1p	2×10^3	10×10^4	13×10^4	Zhong et al., 2013
Nyv1p	2×10^3	4.3×10^4	8.1×10^4	Ferry et al., 2014
Protein	**Molar ratio of lipid:protein in RPL reactions***	**Molar ratio of lipid:protein on vacuoles**		**References†**
Ypt7p	4×10^3	1.9×10^4	1.8×10^4	Zhong et al., 2013
Sec17p	7×10^3	41×10^4	13×10^4	Wolski et al., 2008
Sec18p	1×10^3	10×10^4	13×10^4	This article (Figure 1)
Vps33p	6×10^3	17×10^4	31×10^4	Zhong et al., 2013

* Footnotes can be used to highlight properties of data reported in a table such as statistical significance. They are separate from the table caption and appear afterwards. They are hyperlinked to allow easy navigation. Footnotes in tables use the same standard set of symbols used for authors footnotes.
† Authors are fully allowed to cite references and figures in tables. There is no difference in citation style between the main text and tables.

Order: Designated footnotes (e.g. *, †, ‡, §, #, ¶, **, and so on), p value footnotes (*p, **p, ***p), undesignated footnotes and abbreviations.

Table 3 is an example of a narrow table that will appear at half the text column width in the PDF. It also has source data.

Table 3.:

Representative curves of steady-state kinetic analyses for each IGF1R protein characterized.

Each data point was performed in duplicate and is shown separately.

DOI: 10.7554/eLife.00666.006
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Data collection	
Space group	$P6_2$
Cell dimensions (Å)	a = b = 78.33, c = 62.32
	$\alpha = \beta = 90^o$, $\gamma = 120^o$
Wavelength (Å)	0.9794
R_{sym} or R_{merge} (%)	8.4
Resolution (Å)	50–2.05 (2.09–2.05)
I/σI	19.19 (3.23)
Completeness (%)	99.8 (97.3)
Redundancy	6.2 (5.4)
Refinement	
No. reflections	12,206
Resolution (Å)	39.17–2.06 (2.14–2.06)
R_{work}/R_{free}	0.17/0.21 (0.16/0.19)
No. atoms	
Protein	1608
Ligand/ion	3
Water	61
R.m.s. deviations	
Bond lengths (Å)	0.0077
Bond angles (°)	0.932

The following unnamed table is an example of an inline table that has no heading.

	pY	Experiment	Concentration (μM)
IGF1R-fl + IGF1	+	K_m ATP	500, 400, 300, 250, 125, 62.5, 31.3, 15.6, 7.8
IGF1R-fl + IGF1	+	K_m Peptide	600, 300, 150, 75, 37.5, 18.8, 9.4
IGF1R-fl + IGF1	–	K_m ATP	2000, 1000, 500, 250, 125, 62.5, 31.3, 15.6, 7.8
IGF1R-fl + IGF1	–	K_m Peptide	500, 250, 125, 62.5, 31.3, 15.6, 7.8, 3.9
IGF1R-fl	+	K_m ATP	500, 400, 300, 250, 125, 62.5, 31.3, 15.6, 7.8
IGF1R-fl	+	K_m Peptide	500, 400, 250, 125, 62.5, 31.3, 15.6, 7.8
IGF1R-fl	–	K_m ATP	1000, 500, 250, 125, 62.5, 31.3, 15.6, 7.8
IGF1R-fl	–	K_m Peptide	1000, 500, 250, 125, 62.5, 31.3, 15.6
IGF1R-icd	+	K_m ATP	500, 250, 125, 62.5, 31.3, 15.6, 7.8, 3.9
IGF1R-icd	+	K_m Peptide	1000, 500, 250, 125, 62.5, 31.3, 15.6, 7.8
IGF1R-icd	–	K_m ATP	1000, 500, 250, 125, 62.5, 31.3
IGF1R-icd	–	K_m Peptide	1000, 500, 250, 125, 62.5, 31.3
IGF1R-kin	–	K_m Peptide	1250, 625, 312.5, 156.3, 78.1, 39.1

This is an unmarked footnote for an anchored/inline table

Maths

Content can contain inline formulae or display formulae. Below is an example of a mixture of inline and display formula. MathMl is used in all instances.

We propose a Bayesian scheme for BCV (see equation 1) that accommodates the influence of context on incentive value. BCV focuses on scenarios (i) where incentive value depends on contextual information (either represented by cues or by previous rewards) provided before options or rewards are presented, and (ii) where reward is defined by a single attribute (e.g., reward amount). To describe the basic principles of BCV, we adopt the formalism of Bayesian graphs (The *Shigella* Genome Sequencing Consortium, 2015c) where a generative model is described by nodes or circles, representing random variables (shaded and white circles refer to observed and non-observed variables respectively), and arrows, representing causal relationships among variables. A simple generative model hypothesized by BCV is shown in Figure 1A of another article (not linked here), where C represents prior beliefs about the average reward expected in a given context. Formally, this corresponds to a (Gaussian) prior belief (with mean μ c and variance σ c 2 over the mean of a (Gaussian) distribution of reward options R (with variance σ R 2). When R is observed, a posterior expectation about the context is obtained by application of Bayes rule (The *Shigella* Genome Sequencing Consortium, 2015b): (3) μ C | R = μ C + σ C 2 σ C 2 + σ R 2 (R − μ C) where text following on from this equation but still within the same paragraph should not be indented in the PDF. This is usually used by authors wanting to explain the terms used in the maths.

Additional to maths, eLife articles can also contain code blocks for the display of computer code snipets. For example:

```
<MotifGraft name="motif_grafting"
context_structure="%%context%%"
motif_structure="truncatedBH3.pdb"
RMSD_tolerance="3.0"
NC_points_RMSD_tolerance="2.0"
clash_score_cutoff="0"
clash_test_residue="ALA"
hotspots="9:12:13:14:16:17"
combinatory_fragment_size_delta="0:0"
max_fragment_replacement_size_delta="0:0"
full_motif_bb_alignment="1"
allow_independent_alignment_per_fragment="0"
graft_only_hotspots_by_replacement="0"
only_allow_if_N_point_match_aa_identity="0"
only_allow_if_C_point_match_aa_identity="0"
revert_graft_to_native_sequence="1"
allow_repeat_same_graft_output="1"/>
```

Figures

This section of the article shows how figures should be presented and will include examples of single figures and figures arranged with a variety of additional assets.

Figure 1 is an example of a single figure.

Figure 1.: Single figure: The header of an eLife article example on the HTML page. In the PDf this is represented as a single column.

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Figure 2 is an example of a figure with figure supplements, Figure 2—figure supplement 1 and Figure 2—figure supplement 2.

Figure 2.: Figure with figure supplements. In the PDF this asset box will take full column width.

This is the basic information provided about an article. Figure 1 shows an expanded view (Kok et al., 2015; National Institute of Mental Health, 1990).
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DOI: 10.7554/eLife.00666.008

Figure 2—figure supplement 1.: The representation of the Major Subject Areas, Research Organisms and author keywords on the eLife HTML page

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DOI: 10.7554/eLife.00666.009

Figure 2—figure supplement 2.: Representation of figure with figure supplements on the HTML view.

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Figure 3 is an example of a figure with a figure supplement (Figure 3—figure supplement 1) with two sub-assets, Figure 3—figure supplement 1—source data 1 and Figure 3—video 1 (see Zhang et al., 2010, Zhong et al., 2013; World Health Organization, 2016).

Figure 3.: Figure with figure supplements and figure supplement with source data and a video (see Koch, 1959) .

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Figure 3—figure supplement 1.: Title of the figure supplement

Title of the figure supplement source data.

Legend of the figure supplement source data.

DOI: 10.7554/eLife.00666.013
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Figure 3—video 1.

A description of the eLife editorial process.

Figure 4 is an example of a figure with source code (Figure 4—source code 1).

Figure 4.: Single figure with source code.

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Title of the source code.

Legend of the source code.

DOI: 10.7554/eLife.00666.015
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Videos

Video 1 shows the editorial process and Animation 1 shows how we represent animated gif files.

Video 1.

A description of the eLife editorial process.

Title of the source code.

Legend of the source code.

DOI: 10.7554/eLife.00666.037
Download
Animation 1.

A demonstration of how to tag an animated gif file to ensure it is autolooped when on the eLife website.

Other stuff

Boxes

It is rare for eLife research articles to contain boxes; however they are common in Feature content. Box 1 is a simple box that contains very little text and Box 2 is larger.

Box 1.
Example of a small box

Donec rhoncus in odio non vulputate. Donec vitae enim at erat tincidunt tincidunt in nec arcu. Pellentesque habitant morbi tristique senectus et netus et malesuada fames ac turpis egestas. Aliquam id nunc id arcu maximus rutrum. Praesent bibendum nisl orci, ac sollicitudin purus aliquam in. Duis eu fermentum arcu. Fusce eget dolor augue. Nulla facilisi. Suspendisse eu nisl vitae neque ullamcorper imperdiet (see Nellåker, 2014; Pages et al., 2014; and Palmer et al., 2007). Boxes, like main text, can contain hyperlinks at any point. Etiam in sem augue.

Box 2.

Example of a large box

This box contains a figure. Lorem ipsum dolor sit amet, consectetur adipiscing elit. Quisque vel rhoncus lorem. Suspendisse posuere non enim vel tempor. Fusce quis sem sed nulla tincidunt faucibus. Vivamus dictum magna in ante porttitor faucibus. Aenean lobortis, sem in viverra dignissim, odio purus vestibulum libero, in eleifend lacus metus id tortor. Phasellus tincidunt ipsum ut ornare hendrerit. Praesent lobortis consectetur egestas. Curabitur viverra lectus eu venenatis sagittis. Aliquam lobortis metus mauris, in tincidunt diam ullamcorper ac. Phasellus sagittis, leo eget lacinia commodo, eros justo mattis eros, quis dapibus ipsum ex sit amet sapien. Quisque consequat arcu ut efficitur tincidunt. Ut convallis, ex maximus aliquam tempor, lorem elit fermentum ipsum, nec volutpat velit sem a lectus. Morbi sed mauris vel purus interdum consectetur dapibus vel velit. Nam pellentesque, ipsum vel euismod mattis, turpis augue mattis nunc, ac aliquam dolor massa non mi. Vestibulum sit amet elit a augue semper facilisis interdum quis nibh. Mauris consectetur nisi aliquam urna lobortis, eu efficitur nisl lobortis; Bates et al., 2016 and Patterson et al., 2011.

Box 2—Figure 1.: Box figure

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DOI: 10.7554/eLife.00666.036

Donec rhoncus in odio non vulputate. Donec vitae enim at erat tincidunt tincidunt in nec arcu. Pellentesque habitant morbi tristique senectus et netus et malesuada fames ac turpis egestas. Aliquam id nunc id arcu maximus rutrum. Praesent bibendum nisl orci, ac sollicitudin purus aliquam in. Duis eu fermentum arcu. Fusce eget dolor augue. Nulla facilisi. Suspendisse eu nisl vitae neque ullamcorper imperdiet. Vestibulum ultrices vehicula nibh, a ullamcorper dui semper suscipit. Etiam in sem augue.

RRIDs

If an author mentions an RRID in their content, it is required that we link it, for example, RRID:IMSR_JAX:004435.

Coloured text

Here is an example of making text display in different colours: Blue text: #366BFB; Purple text: #9C27B0; and Red text: #D50000.

Inline graphics

Here is an example of pulling in an inline graphic .

Additional files

All files attached to an article must be cited in the main text as well. So, Supplementary file 1 and Source data 1 have to be cited in the text.

References

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Discussion

The function of the Discussion is to interpret your results in light of what was already known about the subject of the investigation, and to explain our new understanding of the problem after taking your results into consideration. The Discussion will always connect to the Introduction by way of the question(s) or hypotheses you posed and the literature you cited, but it does not simply repeat or rearrange the Introduction. Instead, it tells how your study has moved us forward from the place you left us at the end of the Introduction (Schneider, 2006; Schwartz, 1993).

Materials and methods

Reagent type (species) or resource	Designation	Source or reference	Identifiers	Additional information
gene (*Drosophila melanogaster*)	nito	NA	FLYB:FBgn0027548	
gene (*D. melanogaster*)	Sxl	NA	FLYB:FBgn0264270	
genetic reagent (D. melanogaster)	MTD-Gal4	Bloomington Drosophila Stock Center	BDSC:31777; FLYB:FBtp0001612; RRID:BDSC_31777	FlyBase symbol: P{GAL4-nos.NGT}
genetic reagent (*D. melanogaster*)	ap-Gal4	Bloomington Drosophila Stock Center	BDSC:3041; FLYB:FBti0002785; RRID:BDSC_3041	FlyBase symbol: P{GawB}ap[md544]
genetic reagent (*D. melanogaster*)	nub-Gal4	PMID:20798049	FLYB:FBti0016825	FlyBase symbol: P{GawB}nubbin-AC-62
genetic reagent (*D. melanogaster*)	dome-Gal4	PMID:12403714	FLYB:FBti0022298	FlyBase symbol: P{GawB}dome[PG14]
genetic reagent (*D. melanogaster*)	UAS-2xEYFP	PMID:12324968	FLYB:FBtp0016537	FlyBase symbol: P{UAS-2xEYFP}
genetic reagent (*D. melanogaster*)	nito[HP25329]	Bloomington Drosophila Stock Center	BDSC:22092; FLYB:FBal0238892; RRID:BDSC_22092	Genotype: w[1118]; P{w[+mC]=EPg}nito[HP25329]/CyO
genetic reagent (*D. melanogaster*)	nito[1]	this paper		Progenitor = nito[HP25329]; imprecise excision; lethal
genetic reagent (*D. melanogaster*)	nito shRNA (HMJ02081)	Bloomington Drosophila Stock Center	TRiP:HMJ02081; BDSC:56852; RRID:BDSC_56852	FlyBase symbol: P{TRiP.HMJ02081}attP40
genetic reagent (*D. melanogaster*)	nito dsRNA (VDRC 20942)	Vienna Drosophila RNAi Center	VDRC:20942	
genetic reagent (*D. melanogaster*)	FRT[G13]	Bloomington Drosophila Stock Center	BDSC:1956; FLYB:FBti0001247	FlyBase symbol: P{FRT(whs)}G13
genetic reagent (*D. melanogaster*)	"y w hsflp; ubiGFP FRT[G13]"	PMID:18160348		
cell line (*D. melanogaster*)	S2	other	FLYB:FBtc0000181; RRID:CVCL_Z992	Cell line maintained in N. Perrimon lab; FlyBase symbol: S2-DRSC.
antibody	anti-Nito	this paper		Rabbit polyclonal; against aa 479-500; used YZ3137 (1:500)
antibody	anti-alpha-Spectrin (mouse monoclonal)	Developmental Studies Hybridoma Bank	DSHB:3A9; RRID:AB_528473	(1:10)
antibody	anti-Vasa (rabbit polyclonal)	Santa Cruz Biotechnology	Santa Cruz:sc-30210; RRID:AB_793874	(1:250)
antibody	anti-Sxl (mouse monoclonal)	Developmental Studies Hybridoma Bank	DSHB:M18; RRID:AB_528464	(1:10)
antibody	anti-GFP (rabbit polyclonal)	Molecular Probes	Molecular Probes:A-6455; RRID:AB_221570	(1:1000)
antibody	anti-GFP (mouse monoclonal)	Molecular Probes	Molecular Probes:A-11120; RRID:AB_221568	(1:200)
antibody	anti-HA (rat monoclonal)	Roche	Roche:3F10; RRID:AB_2314622	
antibody	Alexa 488- or 555- secondaries	Molecular Probes		(1:1000)
other	DAPI stain	Molecular Probes		(1:1000)
recombinant DNA reagent	pAGW (Gateway vector)	Drosophila Genomics Resource Center	DGRC:1071	
recombinant DNA reagent	pAHW (Gateway vector)	Drosophila Genomics Resource Center	DGRC:1095	
recombinant DNA reagent	GH11110 (cDNA)	Drosophila Genomics Resource Center	DGRC:5666	
recombinant DNA reagent	GFP-Nito (plasmid)	this paper		Progenitors: GH11110 (cDNA); Gateway vector pAGW
recombinant DNA reagent	HA-Sxl (plasmid)	PMID:16207758		Progentiors: PCR, UAS-Sxl flies; Gateway vector pAHW
recombinant DNA reagent	GFP-Sxl (plasmid)	PMID:16207758		Progentiors: PCR, UAS-Sxl flies; Gateway vector pAGW

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P_{RAM}: 5’– CTAGAAGTTTGTTCGTGACTCAGA –3’

E1: 5’– CTAGAAGTTTGTTGACTCACCCGA –3’

E2: 5’– CTAGAAGTTTGTTGACTCATTAGA –3’

E3: 5’– CTAGAAGTTTGTGTATGACTCAGA –3’

CME: 5’– CTAGAAATTTGTACGTGCCACAGA –3’

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Additional information

Competing interests

Chair of JATS4R

No competing interests declared

Graham Nott is not an eLife employee

Author contributions

Completed the XML mapping exercise and wrote this XML example

Contributed to the XML mapping exercise and quality checked all the tagging and content

Reviewed the PDF product

Chris Wilkinson, Performed the XML mapping exercise and generated the JSON Schema

Graham Nott, Wrote the JATSscraper

Luke Skibinski, Identified missing components from the JATSscraper

Ethics

Human subjects: If Research Ethics Committee and Institutional Review Board approval was required for this article the details would be listed here.

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If this article was part of a clinical trial the Clinical trial registry and ID would be listed here, for example:

Clinical trial Registry: EudraCT.

Registration ID: EudraCT2004-000446-20.

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The funders had no role in study design; collection, analysis, and interpretation of data; writing the article; and or the decision to submit to the journal.

Additional files

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A file containing underlying data.

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Consort checklist and flow diagram.

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Data availability

A data availability statement will generally describe how the authors have provided the source data for their work. This can list the source data files accompanying their figures, supplementary files, and/or external dataasets. Hyperlinks can be included here, for example: https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE102999

The following dataset was generated:

Düsterwald KM , Currin CB , Burman RJ , Akerman CJ , Kay AR , Raimondo JV . 2018. *Data from: Biophysical models reveal the relative importance of transporter proteins and impermeant anions in chloride homeostasis*. Dryad Digital Repository. data

The following previously published datasets were used:

Rau CD , Wang J , Wang Y , Lusis AJ . 2013. *Transcriptomes of the hybrid mouse diversity panel subjected to Isoproterenol challenge*. NCBI Gene Expression Omnibus. data

Garcia Miguel A . 2018. *Shear Manuscript*. Open Science Framework. data

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We need to allow authors to have sections in their acknowledgements.

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Appendix 1

Preparation

In order to prepare for this Kitchen sink we reviewed our archive and found common errors or miscommunication from the archive, tagging of Appendix 1—Figure 1 is a classic example and here the tagging is updated. Appendices figures can also have figure supplements, for example Appendix 1—Figure 1—Figure Supplement 1 (Koch, 1959).

Appendix 1—Figure 1.: Appendix figure title.

If there is a caption to accompany the title it would display here (Koch, 1959).
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Appendix 1—Figure 1—Figure Supplement 1.: Appendix figure supplement title.

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1.1 Sub heading

This is the text of the content of subheading 1 within appendix 2. In some cases, authors will use 1.1, 1.2, 1.2.1, 1.2.2, 1.3 etc as prefixes to their headings. We retain this in the appendix sections only and allow them to cite these as Appendix 1.1, Appendix 1.2 etc in the main text. This is entirely optional on the part of the authors and articles may or may not include this style of heading/citation. This style of heading/citation is not allowed for main text headings.

1.2 Sub heading

This is the text of the content of subheading 2 within appendix 2.

Apendix 1—Table 1.:
This is the title.
This is the caption: A table containing interesting formating that is large enough to require landscape orientation in the PDF.

			GLVs (percent IS plant^{-1})		TPS10 products (percent IS plant^{-1})				Non-target volatiles (percent IS plant^{-1})			
			(*Z*)-Hexen-3-ol		TAB		TBF		α-Duprezianene		Germacrene A	
Genotype	Day n	Night n	Day	Night	Day	Night	Day	Night	Day	Night	Day	Night

			GLVs (percent IS plant^{-1})			TPS10 products (percent IS plant^{-1})					Non-target volatiles (percent IS plant^{-1})		
			(*Z*)-Hexen-3-ol			TAB			TBF		α-Duprezianene	Germacrene A	
WT	8	8	0.99% ± 0.99%	7.96% ± 4.25%	**a**	0.37% ± 0.29%	**a** —	**a**	—	**a** —	2.13% ± 0.85%	0.96% ± 0.42%	1.68% ± 0.98% —
TPS10	7	7	2.37% ± 1.55%	2.84% ± 0.63%	**lox**	18.97% ± 6.03%	**b** 0.94% ± 0.53%	**TPS**	9.34% ± 3.44%	**b** 0.20% ± 0.20%	9.47% ± 5.26%	0.94% ± 0.26%	2.78% ± 1.52% —
lox2/3	7	8	0.13% ± 0.13%	1.06% ± 0.64%	**b**	—	**a** 0.15% ± 0.15%	**b**	—	**a** —	2.75% ± 1.12%	0.60% ± 0.19%	1.68% ± 1.49% —
lox2/3xTPS10	7	7	0.07% ± 0.07%	1.24% ± 0.84%	**lox**	7.39% ± 2.56%	**b** 2.08% ± 0.84%	**TPS**	4.47% ± 1.70%	**b** 0.40% ± 0.40%	3.02% ± 1.42%	0.73% ± 0.31%	0.66% ± 0.37% —

Footnotes not linked to content within the table text are usually to define abbreviations. For example:

WT, wild type.

Appendix 2

Negotaition

Generating the new rules involved negotation with varous vendors and downsteam hosts to ensure display would work for all instances. See Appendix 2—Video 1 and Apendix 2—Table 1.

Appendix 2—Video 1.

A descirption of the eLife editorial process.

Apendix 2—Table 1.: Appendix table.

Name	Units	Value
E_{AMPA}	mV	0
τ_{AMPA}	ms	1
E_{NMDA}	mV	0
τ_{NMDA}	ms	100

Appendix 3

This is an example of an appendix with no sections.