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:

1. Research article
2. Short Report
3. Tools and Resources
4. Research Advance
5. Registered Report
6. 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

1. article-commentary (used for Insights)
2. correction
3. discussion (used for Feature 1 and Feature 2)
4. editorial
5. 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

1. (a) *P. falciparum*
   (b) *P. vivax*
   (c) *P. ovale*
   (d) *P. malariae*
   (e) *P. knowlesi*

   Genus: Leishmania. There are 3 subgenus of Leishmania:
2. (a) Leishmania
   (b) Sauroleishmania
   (c) Viannia
   (d) 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 , and f value. Any given value in the matrix indicates P(f ,), that is, the probability of a given frequency given a particular and . The columns (all f values for a given and combination; Figure 2—figure supplement 1, upper-right) thus constitute the forward model (by which stimuli are generated), and the planes (all combinations of and 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(fc) 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:

$$P\left(c|f\right) = \frac{P\left(f|c\right)P\left(c\right)}{P\left(f\right)}$$

Here, P(cf) 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(fc)P(c)+P(f~c)(1-P(c)), the above equation can be rewritten as Equation 3:

$$P\left(c|f\right) = \frac{1}{1 + \frac{7P(f|\sim c)}{P(f|c)}}$$

6. For each segment, the above calculation of P(cf) 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(cf), 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 ( ) and precision (1/variance). Changes to predictions ($\Delta\mu$) were calculated as the absolute change (in octaves) in 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).

10.7554/eLife.00666.003

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 (p
Genotype	**Day n**	**Night n**	**Day**
WT	8	8	0.99%
TPS10	7	7	2.37%
lox2/3	7	8	0.13%
lox2/3*x*TPS10	7	7	0.07%

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.

10.7554/eLife.00666.004

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	Reference
Vam7p	2×10^3	30×10^4	6.5×10^4
Vam3p	2×10^3	11×10^4	22×10^4
Vti1p	2×10^3	10×10^4	13×10^4
Nyv1p	2×10^3	4.3×10^4	8.1×10^4

Protein	Molar ratio of lipid:protein in RPL reactions*	Molar ratio of lipid:protein on vacuoles	Reference
Ypt7p	4×10^3	1.9×10^4	1.8×10^4
Sec17p	7×10^3	41×10^4	13×10^4
Sec18p	1×10^3	10×10^4	13×10^4
Vps33p	6×10^3	17×10^4	31×10^4

*

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.

10.7554/eLife.00666.005

Table 3.

10.7554/eLife.00666.006 Table 3—source data 1. Representative curves of steady-state kinetic analyses for each IGF1R protein characterized. Each data point was performed in duplicate and is shown separately.

Data collection	
Space group	$P6_2$
Cell dimensions (Å)	a = b = 78.33, c = 62.32
= = 90°, = 120°	
Wavelength (Å)	0.9794
R_{sym} or R_{merge} (%)	8.4
Resolution (Å)	`50-2.05 (2.09-2.05)`
I/ I	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 (M)
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

	pY	Experiment	Concentration (M)
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):

$$\mu_{C|R} = \mu_C + \frac{\sigma_C^2}{\sigma_C^2 + \sigma_R^2}(R - \mu_C)$$

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_c
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.

10.7554/eLife.00666.007

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.

image

2016

eLife

For the purpose having a example of how to tag a separate license for an item, we have indicated in the XML and display this is a copyrighted figure; however it is not.

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

10.7554/eLife.00666.008

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).

image

10.7554/eLife.00666.009

Figure 2—figure supplement 1.

The representation of the Major Subject Areas, Research Organisms and author keywords on the eLife HTML page

image

10.7554/eLife.00666.010

Figure 2—figure supplement 2.

Representation of figure with figure supplements on the HTML view.

image

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).

10.7554/eLife.00666.011

Figure 3.

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

image

10.7554/eLife.00666.012

Figure 3—figure supplement 1.

Title of the figure supplement

10.7554/eLife.00666.013 Figure 3—figure supplement 1—source data 1. Title of the figure supplement source data. Legend of the figure supplement source data.

image

10.7554/eLife.00666.035

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).

10.7554/eLife.00666.014

Figure 4.

Single figure with source code.

image

10.7554/eLife.00666.015 Figure 4—source code 1. Title of the source code. Legend of the source code.

Videos

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

10.7554/eLife.00666.016

Video 1.

A description of the eLife editorial process.

10.7554/eLife.00666.037 Video 1—source data 1. Title of the source code. Legend of the source code.

10.7554/eLife.00666.038

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.

10.7554/eLife.00666.017

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.

© Some author

1998

Some Author

Boxes are also allowed license statements, as they can contain text that is repeated or adapted from previously published content.

10.7554/eLife.00666.018

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.

10.7554/eLife.00666.036

Box 2—Figure 1.

Box figure

image

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 image.

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

All references have to be cited in the main text. They are listed in the reference list in alphabetical order, however, in the text the citations do not have to be in the same order as they are listed according to when the author of the article cites them. This article is littered with citations to ensure all the references are cited at some point. They have no relevance to the content Aivazian et al., 2006.

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

Key resources table

	Designation	Source or reference
gene (*Drosophila melanogaster*)	nito	NA
gene (*D. melanogaste*r)	Sxl	NA
genetic reagent (D. melanogaster)	MTD-Gal4	Bloomington Drosophila Stock
genetic reagent (*D. melanogaster*)	ap-Gal4	Bloomington Drosophila Stock
genetic reagent (*D. melanogaster*)	nub-Gal4	PMID:20798049
genetic reagent (*D. melanogaste*r)	dome-Gal4	PMID:12403714

	Designation	Source or reference
genetic reagent (*D. melanogaster*)	UAS-2xEYFP	PMID:12324968
genetic reagent (*D. melanogaster*)	nito[HP25329]	Bloomington Drosophila Stock
genetic reagent (*D. melanogaster*)	nito[1]	this paper
genetic reagent (*D. melanogaster*)	nito shRNA (HMJ02081)	Bloomington Drosophila Stock
genetic reagent (*D. melanogaster*)	nito dsRNA (VDRC 20942)	Vienna Drosophila RNAi Cent
genetic reagent (*D. melanogaster*)	FRT[G13]	Bloomington Drosophila Stock
genetic reagent (*D. melanogaster*)	"y w hsflp; ubiGFP FRT[G13]"	PMID:18160348
cell line (*D. melanogaste*r)	S2	other
antibody	anti-Nito	this paper
antibody	anti-alpha-Spectrin (mouse monoclonal)	Developmental Studies Hybrid
antibody	anti-Vasa (rabbit polyclonal)	Santa Cruz Biotechnology
antibody	anti-Sxl (mouse monoclonal)	Developmental Studies Hybrid
antibody	anti-GFP (rabbit polyclonal)	Molecular Probes
antibody	anti-GFP (mouse monoclonal)	Molecular Probes
antibody	anti-HA (rat monoclonal)	Roche
antibody	Alexa 488- or 555- secondaries	Molecular Probes
other	DAPI stain	Molecular Probes
recombinant DNA reagent	pAGW (Gateway vector)	Drosophila Genomics Resource
recombinant DNA reagent	pAHW (Gateway vector)	Drosophila Genomics Resource
recombinant DNA reagent	GH11110 (cDNA)	Drosophila Genomics Resource
recombinant DNA reagent	GFP-Nito (plasmid)	this paper
recombinant DNA reagent	HA-Sxl (plasmid)	PMID:16207758
recombinant DNA reagent	GFP-Sxl (plasmid)	PMID:16207758

eLife is tagged up as XML using the NISO standard JATS DTD. We conform to the JATS4R recommendations where possible and also deliver our content to PMC. We also convert our JATS XML to PubMed and CrossRef DTDs when we deposit our content with them. eLife content is delivered to more repositories and it can be scraped from the eLife site (Gall et al., 2012; Horne and Page, 2008; McQuilton et al., 2012; Staab et al., 2013).

The following is an example of monotype text within the body of an eLife article.

```
PNRE+AP-1: 5’- CTTCGTGACTAGTCTTGACTCAGA -3’

PRAM: 5’- CTAGAAGTTTGTTCGTGACTCAGA -3’

E1: 5’- CTAGAAGTTTGTTGACTCACCCGA -3’

E2: 5’- CTAGAAGTTTGTTGACTCATTAGA -3’

E3: 5’- CTAGAAGTTTGTGTATGACTCAGA -3’

CME: 5’- CTAGAAATTTGTACGTGCCACAGA -3’
```

In some cases, authors will include extremely long gene sequences or other letter strings that need to be enclosed withing a particular style tagging in order

that they can be wrapped on the final HTML display. If this tagging is not included, the strings will likely spill across the edge of the text column, which can look very messy, not to mention rather silly: TAATAAGGAAGAACT-
GCTTATTCTTAATTATTTCTACCTACTAAACTAACTAATTATCAA-
CAAATATCATCTATTTAATAGTATATCATCACATGCGGTGTAAGAGGATGACATAAAGATTGAGAAA
Sequences like this should be tagged during pre-editing. This tagging will also increase discoverability of gene sequences in eLife articles.

Additional information

Chair of JATS4R

No competing interests declared

Graham Nott is not an eLife employee

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

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

Animal subjects: If there were animal subjects involved in the study the approval number for the research along with protocol approval would be listed here.

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.

Additional files

10.7554/eLife.00666.019

Supplementary file 1.

This is the title of the supplementary file 1.

A file containing underlying data.

10.7554/eLife.00666.020

Source data 1.

This is the title of the source data that is not attached to a specific figure, but to the article as a whole.

10.7554/eLife.00666.021

Source code 1.

This is the title of the source code that is not attached to a specific figure, but to the article as a whole.

10.7554/eLife.00666.034

Consort checklist and flow diagram.

10.7554/eLife.00666.022

Transparent reporting form.

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 10.5061/dryad.kj1f3v4

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 GSE48760

Garcia Miguel A 2018 Shear Manuscript Open Science Framework kvu5j

Main thanks

We thank JATS4R, ExeterPremedia and PMC for their contributions.

Sub-thanks

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

Preparation

10.7554/eLife.00666.023

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).

10.7554/eLife.00666.024

Appendix 1—Figure 1.

Appendix figure title.

If there is a caption to accompany the title it would display here (Koch, 1959).

image

10.7554/eLife.00666.025

Appendix 1—Figure 1—Figure Supplement 1.

Appendix figure supplement title.

If there is a caption to accompany the title it would display here.

image

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.

10.7554/eLife.00666.039

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 (p
Genotype	**Day n**	**Night n**	**Day**
WT	8	8	0.99%
TPS10	7	7	2.37%
lox2/3	7	8	0.13%
lox2/3*x*TPS10	7	7	0.07%

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

WT, wild type.

Negotaition

10.7554/eLife.00666.026

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.

10.7554/eLife.00666.027

Appendix 2—Video 1.

A descirption of the eLife editorial process.

10.7554/eLife.00666.028

Apendix 2—Table 1.

Appendix table.

Name	Units	Value
E_{AMPA}	mV	0
$_{\mathrm{AMPA}}$	ms	1

Name	Units	Value
E_{NMDA}	mV	0
$_{\mathrm{NMDA}}$	ms	100

10.7554/eLife.00666.034

This is an example of an appendix with no sections.

10.7554/eLife.00666.029

Decision letter

Collings

Andrew

Reviewing Editor

eLife Sciences

United Kingdom

Darian-Smith

Corinna

Reviewer

Stanford University

United States

Smith

Alison M.

Reviewer

John Innes Centre

United Kingdom

In the interests of transparency, eLife includes the editorial decision letter and accompanying author responses. A lightly edited version of the letter sent to the authors after peer review is shown, indicating the most substantive concerns; minor comments are not usually included.

Thank you for submitting your article "The eLife research article" for consideration by *eLife*. Your article has been reviewed by three peer reviewers, one of whom, Joe Bloggs, is a member of our editorial board and also oversaw the process as Senior editor. John Doe (peer reviewer) has agreed to reveal his identity.

The reviewers have discussed the reviews with one another and the Reviewing Editor has drafted this decision to help you prepare a revised submission.

You need to make sure the XML structure you creates works on the display of the PMC platform and also that there is enough information contained within the tagging to generate a typeset PDF from the XML with no additional information provided.

10.7554/eLife.00666.030

Author response

> The reviewers have discussed the reviews with one another and the Reviewing Editor has drafted this decision to help you prepare a revised submission.
>
> You need to make sure the XML structure you creates works on the display of the PMC platform and also that there is enough information contained within the tagging to generate a typeset PDF from the XML with no additional information provided.

In response to this comment, we validated the XML against the DTD (JATS 1) each time we made an update. We also regularly used the PMC validator to check our decisions against display on the PMC site, see Author response image 1., Author response video 1 and Author response table 1.

10.7554/eLife.00666.031

Author response image 1.

Single figure: The header of an eLife article example on the HTML page.

image

10.7554/eLife.00666.032

Author response Table 1.

Author response table

Sample	Same	Difference more than 10%
DKO1.cell.1	77.00%	6.90%
DKO1.cell.2	78.80%	7.20%
DKO1.cell.3	79.10%	6.70%
DKO1.exo.1	78.90%	6.50%
DKO1.exo.2	80.00%	5.80%
DKO1.exo.3	86.80%	2.30%
DKS8.cell.1	77.30%	7.80%
DKS8.cell.2	79.70%	6.70%

10.7554/eLife.00666.033

Author response video 1.

Caption and/or a title is required for all author response assets

However, some decisions required some communication with PMC to discuss whether any of our updates could be accomodated by them - during this review we aimed to reduce the complexity of the XML structure and remove all formatting and bioler plate text required for a PDF display format. We also produced buisness rules {Insert table} in order to produce rules for the production systems and the website to follow. These buisness rules also informed the basis for a set of Schematron rules for our references.{Insert table}

If an author referes to a reference in the response letter it is cross linked to the reference in the reference list (Coyne and Orr, 1989), however, if it is a new reference only cited in the decision letter or author response it is not added to the main reference link and is just listed as free text, for example, Butcher et al, 2006. If the author provides the reference it can be added as free text to the end of the letter, however, this is not a requirement .

Adding some MathML to the sub-article.$_m\, p_m = 0$