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REGISTERED REPORT

The eLife research article

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REPRODUCIBILITY PROJECT CANCER BIOLOGY

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**, $^{\text{superscript}}$, $_{\text{subscript}}$ or SMALL CAPS. MathML is also allowed: $_{m}p^{=0}$.

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.

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Competing interest: See page 14

Funding: See page 13

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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, 2012*** and ***Morgan, 2016***. Approximately half of the articles that are selected for peer review go on to be published (***Brettar et al., 2014b***). 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 et al., 2004***; ***Wolski et al., 2008***; ***Walker, 1995***; ***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., 2014a***).

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., 2014b***).

Full submission (level 3 heading)

For manuscripts that are invited for in-depth peer review, see ***Coyne et al., 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*** 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.

I. Genus: Plasmodium; following species are known to infect humans
    i. *P. falciparum*
    ii. *P. vivax*
    iii. *P. ovale*
    iv. *P. malariae*
    v. *P. knowlesi*
II. Genus: Leishmania. There are 3 subgenus of Leishmania:
    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

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 $P(f|\mu,\sigma)$, 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. 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 $P(f|{\sim}c)$, 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:

   $$P(c|f) = \frac{P(f|c)P(c)}{P(f)} \tag{2}$$

   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 $P(f|c)P(c)+P(f|{\sim}c)(1-P(c))$, the above equation can be rewritten as Equation 3:

   $$P(c|f) = \frac{1}{1+\frac{7P(f|\sim c)}{P(f|c)}} \tag{3}$$

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 ($\Delta\mu$) 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 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 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.

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

Math

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 σ_c^2 and variance μ_c over the mean of a (Gaussian) distribution of reward options R (with variance σ_c^2). When R is observed, a posterior expectation about the context is obtained by application of Bayes rule (***The Shigella* Genome Sequencing Consortium, 2015b**):

$$\mu_{C|R} = \mu_C + \frac{\sigma_C^2}{\sigma_C^2 + \sigma_R^2}(R - \mu_C) \tag{1}$$

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"
```

Table 1. 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_{lox}	0.37% ± 0.29% a	—	a_{TPS}	— a	—	2.13% ± 0.85%	0.96% ± 0.42%	1.68% ± 0.98%	—
TPS10	7	7	2.37% ± 1.55%	2.84% ± 0.63%	a_{lox}	18.97% ± 6.03% b	0.94% ± 0.53%	a_{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_{lox}	— a	0.15% ± 0.15%	b_{TPS}	— 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%	b_{lox}	7.39% ± 2.56% b	2.08% ± 0.84%	b_{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.

DOI: https://doi.org/10.7554/eLife.00666.002

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

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 ***Zhong et al., 2013***; ***World Health Organization, 2016***).

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

Videos

Video 1 shows the editorial process.

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.

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, 2012***
Vam3p	2×10^3	11×10^4	22×10^4	***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***
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.

DOI: https://doi.org/10.7554/eLife.00666.002

Table 3.

Data collection	
Space group	$P6_2$
Cell dimensions (Å)	a = b = 78.33, c = 62.32
	α = β = 90°, γ = 120°
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

DOI: https://doi.org/10.7554/eLife.00666.002

The following source data available for 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.

DOI: https://doi.org/10.7554/eLife.00666.002

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.
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

DOI: https://doi.org/10.7554/eLife.00666.002

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

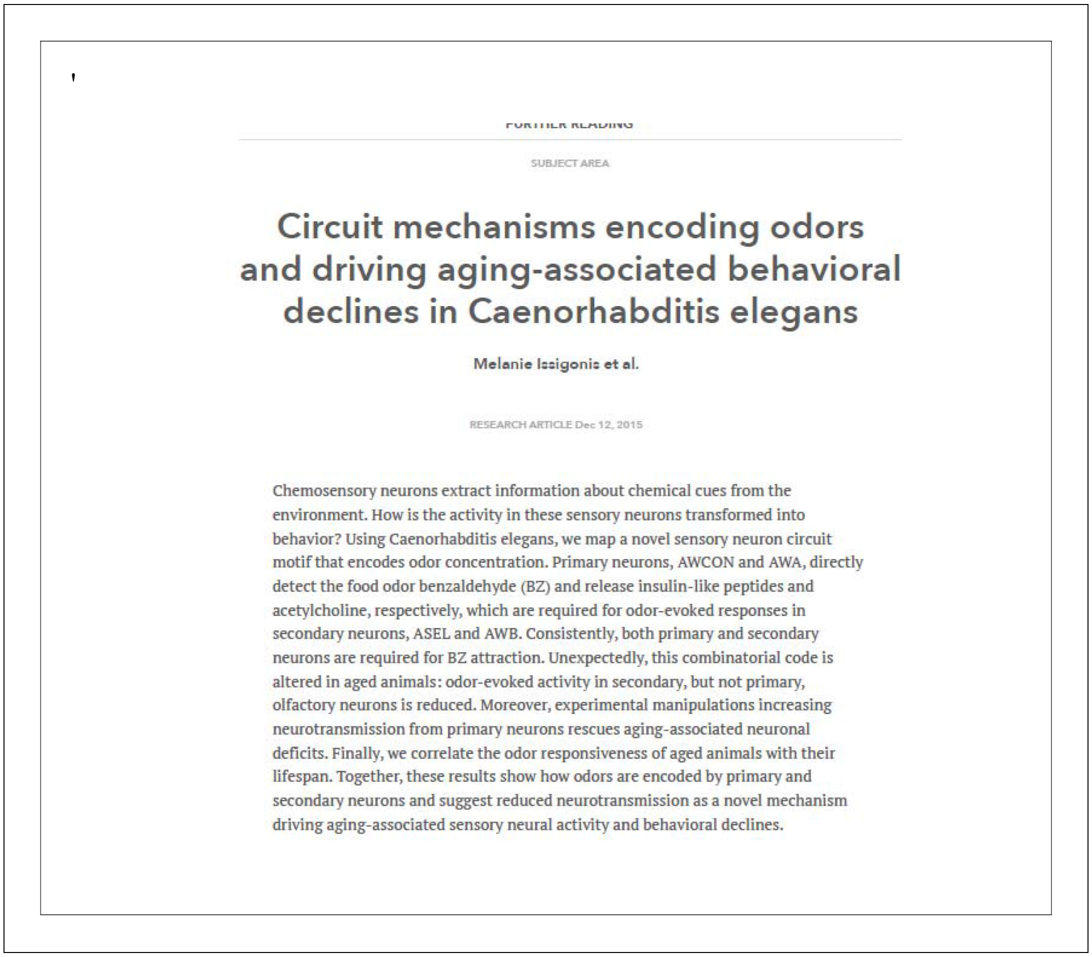
All files attached to an article must be cited in the main text as well. So, ***Supplementary file 1*** and ***Source data 1*** have to be cited in the text.

References

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


FURTHER READING

SUBJECT AREA

Circuit mechanisms encoding odors and driving aging-associated behavioral declines in Caenorhabditis elegans

Melanie Issigonis et al.

RESEARCH ARTICLE Dec 12, 2015

Chemosensory neurons extract information about chemical cues from the environment. How is the activity in these sensory neurons transformed into behavior? Using Caenorhabditis elegans, we map a novel sensory neuron circuit motif that encodes odor concentration. Primary neurons, AWCON and AWA, directly detect the food odor benzaldehyde (BZ) and release insulin-like peptides and acetylcholine, respectively, which are required for odor-evoked responses in secondary neurons, ASEL and AWB. Consistently, both primary and secondary neurons are required for BZ attraction. Unexpectedly, this combinatorial code is altered in aged animals: odor-evoked activity in secondary, but not primary, olfactory neurons is reduced. Moreover, experimental manipulations increasing neurotransmission from primary neurons rescues aging-associated neuronal deficits. Finally, we correlate the odor responsiveness of aged animals with their lifespan. Together, these results show how odors are encoded by primary and secondary neurons and suggest reduced neurotransmission as a novel mechanism driving aging-associated sensory neural activity and behavioral declines.

Figure 2. Figure with figure supplements. In the PDF this asset box will take full column width. This is the basic infomration provided about an article. ***Figure 1*** shows an expanded view (***Kok et al., 2015***; ***National Institute of Mental Health, 1990***).

DOI: https://doi.org/10.7554/eLife.00666.002

The following figure supplements are available for figure 2:

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

DOI: https://doi.org/10.7554/eLife.00666.002

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

DOI: https://doi.org/10.7554/eLife.00666.002

Video 1. A descirption of the eLife editorial process.

DOI: https://doi.org/10.7554/eLife.00666.002

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

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

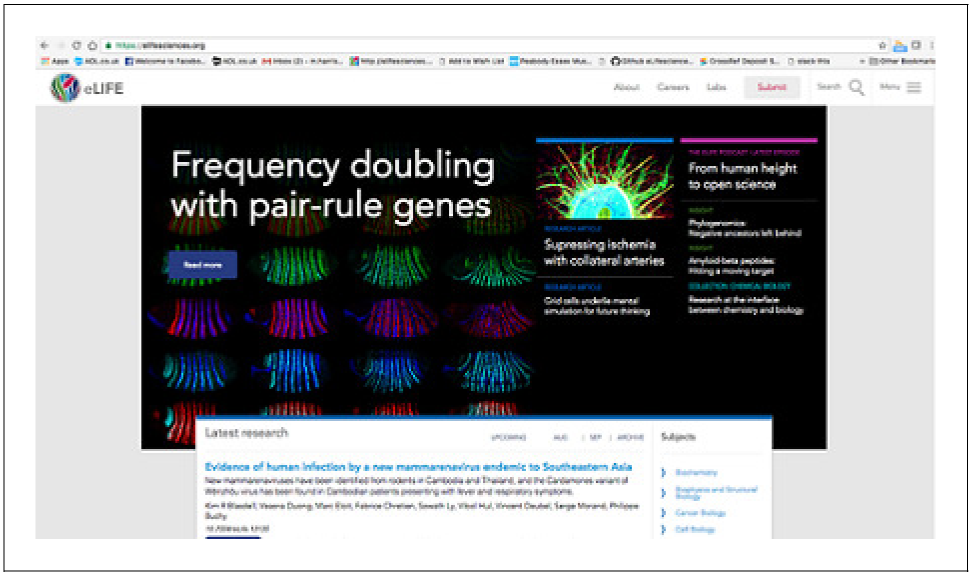


Figure 3. Figure with figure supplements and figure supplement with source data and a video (see ***Koch, 1959***) .
DOI: https://doi.org/10.7554/eLife.00666.002
The following source data and figure supplements are available for figure 3:

Figure supplement 1. Title of the figure supplement
DOI: https://doi.org/10.7554/eLife.00666.002
Figure supplement 1—Source data 1. Title of the figure supplement source data.
DOI: https://doi.org/10.7554/eLife.00666.002
Figure 3—Video 1. A description of the eLife editorial process.
DOI: https://doi.org/10.7554/eLife.00666.002

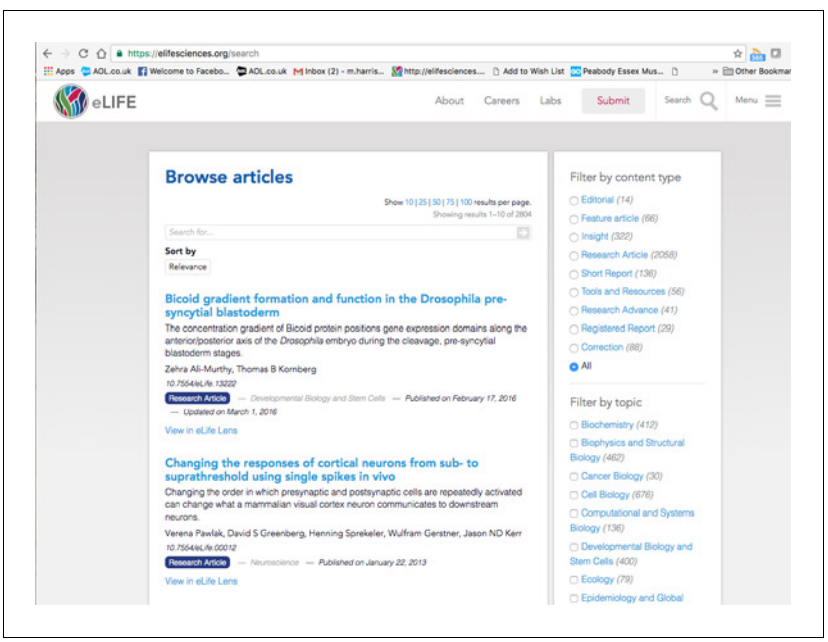


Figure 4. Single figure with source code.
DOI: https://doi.org/10.7554/eLife.00666.002
The following source code is available for figure 4:

Source code 1. Title of the source code.
DOI: https://doi.org/10.7554/eLife.00666.002

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***) Vestibulum ultrices vehicula nibh, a ullamcorper dui semper suscipit. Etiam in sem augue.

DOI: https://doi.org/10.7554/eLife.00666.002

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.

$P_{NRE+AP-1}$: `5′– CTTCGTGACTAGTCTTGAC TCAGA –3′`

P_{RAM}: `5′– CTAGAAGTTTGTTCGTGACTCAGA –3′`

`E1: 5′– CTAGAAGTTTGTTGACTCACCCGA –3′`

`E2: 5′– CTAGAAGTTTGTTGACTCATTAGA –3′`

`E3: 5′– CTAGAAGTTTGTGTATGACTCAGA –3′`

`CME: 5′– CTAGAAATTTGTACGTGCCACAGA –3′`

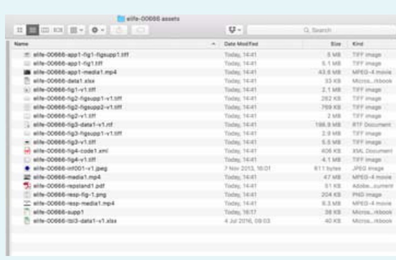
Acknowledgements

Main thanks

We thank JATS4R, ExeterPremedia and PMC for their contributions.

Box 2. Example of a large box

This box contains a ***Box 2–figure 1***. 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

DOI:

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.

DOI: https://doi.org/10.7554/eLife.00666.002

Sub-thanks
We need to allow authors to have sections in their acknowledgements

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Competing interests

Melissa Harrison: Chair of JATS4R. eLife Technology Group: Graham Nott is not an eLife employee. The other authors declare that no competing interests exist.

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Author contributions

Melissa Harrison, Completed the XML mapping exercise and wrote this XML example; James F Gilbert, Contributed to the XML mapping exercise and quality checked all the tagging and content; eLife Technology Group, Reviewed the PDF product; eLife Editorial Production Group, 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

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Ethics

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.

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Decision letter and Author response

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Additional files

Supplementary files

• Supplementary file 1. This is the title of the supplementary file 1. A file containing underlying data.
DOI:

• 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.
DOI:

• 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.
DOI:

• Reporting Standard 1. CONSORT flow diagram.
DOI:

Major datasets

The following dataset was generated:

Author(s)	Year	Dataset title	Dataset URL	Database, license, and accessibility information
M Harrison	2016	xml-mapping	https://github.com/elifesciences/XML-mapping/blob/master/elife-00666.xml	Publicly available on GitHub

The following previously published datasets were used:

Author(s)	Year	Dataset title	Dataset URL	Database, license, and accessibility information
M Harrison	2012	elife-vendor-workflow-config	https://github.com/elifesciences/elife-vendor-workflow-config/blob/master/elife-kitchen-sink.xml	Publicly available on GitHub
K KokA AyL LiDN Arnosti	2015	Data from: Genome-wide errant targeting by Hairy	Dryad Digital Repositoryhttps://doi.org/10.5061/dryad.cv323	

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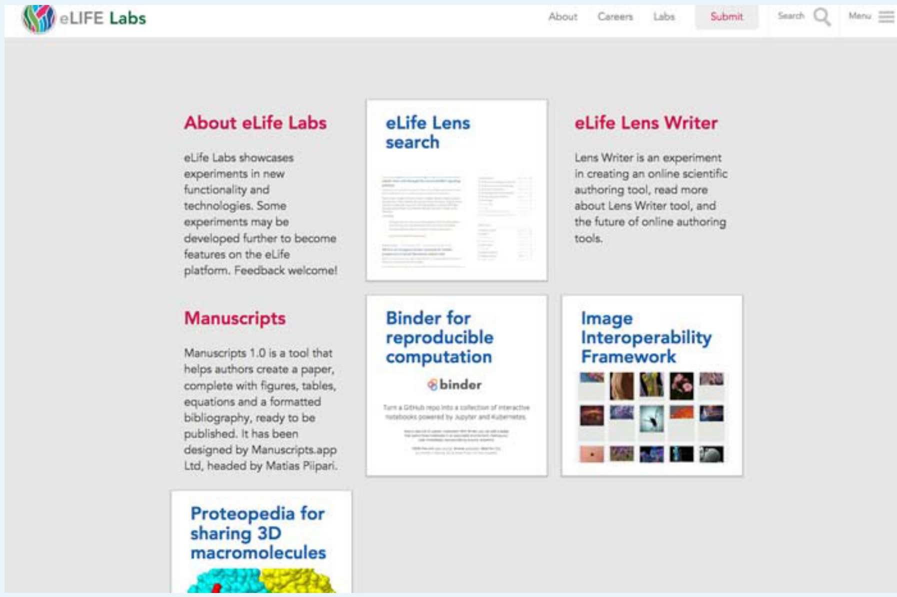
Appendix 1

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, 1589***).



Appendix 1—Figure 1. Appendix figure title. If there is a caption to accompany the title it would display here (***Koch, 1589***).

DOI:

The following figure supplement is available for figure app11:

Appendix 1—Figure 1 supplement 1. Appendix figure supplement title.

DOI:

Sub heading 1

This is the text of the content of subheading 1 within appendix 2.

Sub heading 2

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

Appendix 1—Table 1. This is the title.
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_{lox}	0.37% ± 0.29% a	—	a_{TPS}	— a	—	2.13% ± 0.85%	0.96% ± 0.42%	1.68% ± 0.98%	—
TPS10	7	7	2.37% ± 1.55%	2.84% ± 0.63%		18.97% ± 6.03% b	0.94% ± 0.53%		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%		— a	0.15% ± 0.15%	b_{TPS}	— 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%	b_{lox}	7.39% ± 2.56% b	2.08% ± 0.84%		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.

DOI:

Appendix 2—Table 1. Appendix table.

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