

Elsevier L^AT_EX template[☆]

Elsevier¹

Radarweg 29, Amsterdam

Elsevier Inc^{a,b}, Global Customer Service^{b,}*

^a1600 John F Kennedy Boulevard, Philadelphia

^b360 Park Avenue South, New York

Abstract

This template helps you to create a properly formatted L^AT_EX manuscript.

Keywords: `elsarticle.cls`, L^AT_EX, Elsevier, template

2010 MSC: 00-01, 99-00

1. The Elsevier article class

Installation. If the document class *elsarticle* is not available on your computer, you can download and install the system package *texlive-publishers* (Linux) or install the L^AT_EX package *elsarticle* using the package manager of your T_EX
5 installation, which is typically T_EX Live or MikT_EX.

Usage. Once the package is properly installed, you can use the document class *elsarticle* to create a manuscript. Please make sure that your manuscript follows the guidelines in the Guide for Authors of the relevant journal. It is not necessary to typeset your manuscript in exactly the same way as an article, unless
10 you are submitting to a camera-ready copy (CRC) journal.

[☆]Fully documented templates are available in the *elsarticle* package on CTAN.

^{*}Corresponding author

Email address: support@elsevier.com (Global Customer Service)

URL: www.elsevier.com (Elsevier Inc)

¹Since 1880.

Functionality. The Elsevier article class is based on the standard article class and supports almost all of the functionality of that class. In addition, it features commands and options to format the

- document style
- 15 • baselineskip
- front matter
- keywords and MSC codes
- theorems, definitions and proofs
- lables of enumerations
- 20 • citation style and labeling.

2. Front matter

The author names and affiliations could be formatted in two ways:

- (1) Group the authors per affiliation.
- (2) Use footnotes to indicate the affiliations.

25 See the front matter of this document for examples. You are recommended to conform your choice to the journal you are submitting to.

3. Test import

4. HWU Use Case

A gene is a hereditary unit consisting of a sequence of DNA that occupies a
30 specific location on a chromosome and determines a particular characteristic in an organism. A gene is considered *active* if it is transcribed resulting in one or more RNA products and, following translation, one or more protein products. This phenomenon of transcription and translation is additionally known as gene expression.

35 Diseases such as cancer, and abnormal features like cleft lips are potentially
caused by a change in the genes expressed in an anatomical structure. In order
to investigate such conditions, it is necessary to start by understanding the
gene expression in the so-called *normal* (healthy) structures. EMAGE [2] is one
resource that provides such information to biomedical researchers. EMAGE,
40 and its developmental mouse *in situ* hybridisation gene expression data was the
focus of the HWU use case.

EMAGE’s gene expression information is obtained by experimenting on a
series of mouse embryos. Each embryo corresponds to a point in time of the
developmental mouse: the mouse from conception until birth. The time window
45 is split into 26 distinct periods called Theiler Stages (TS). Each stage has its
own anatomy, and corresponding anatomy ontology, called EMAP [1].

The initial version of EMAP documented the anatomy as a tree with each
structure being *partOf* another, e.g., the digit is *partOf* the paw. Subsequent
extensions have resulted in a directed acyclic graph (DAG), yet *partOf* remains
50 the dominant relationship.

The result of an *in situ* hybridization (ISH) experiment is recorded as an
image displaying an area of a mouse (from a particular TS) in which some
subsections of the mouse are highly coloured, as depicted in Figure 1. Areas of
colour indicate that a gene is expressed in that location. Furthermore, the image
55 provides some indication of the level (strength) of expression: the more intense
the colour, the stronger the expression. Results are analysed manually under
a microscope. A human expert determines in which anatomical structures the
gene is expressed, and at what level of expression. Strength (level) information
is described using natural language terms: strong, moderate, weak, possible,
60 detected or not detected. Some of the strength labels are ordered: possible
< weak < moderate < strong. However, ‘detected’ implies any one of weak,
moderate or strong. ‘Not detected’ does not mean the gene is absent, instead
it implies the experiment was not sensitive enough to detect the gene. When a
gene is detected, weak, moderate or strong then it is deemed active or *expressed*.
65 Not detected genes are treated as inactive or *not expressed*. Genes that have an

assignment of ‘possible’ have an unknown level of expression.

Ultimately, when analysing an ISH experiment result (like Figure 1) the biologist produces a series of *textual annotations*. Each annotation links a gene, level of expression and anatomical structure at a particular TS. For example,
70 the gene *Bmp4* is strongly expressed in the future brain from TS15. The relationships encoded within the textual annotations are what the biomedical researchers are interested in, with common queries including:

- where is gene G expressed and which other genes are expressed there?
- which genes are expressed in anatomical structure S ?



Figure 1: **Probably no room for this image?** A sample image of an experimental result from EMAGE (accession ID EMAGE:672). This image shows a mouse from TS17. The areas of colour show where the gene *Sox10* is expressed.

75 Another salient feature of the EMAGE repository is the lack of numerical data. In addition to the textual annotations there is just provenance information: who did what, when and how. Further distinguishing this use case from

those that traditionally deploy BI, is the unhelpfulness of top k queries. For example, find the top 5 most expressed genes in the heart? This query will
80 return the strongly expressed genes that have the most experimental data (i.e., greatest number of experiments indicating that they are strongly expressed in the heart). However, this merely implies that these genes are very popular. It is likely that the typical EMAGE user will already know that these genes are active in the heart. Instead (s)he wishes to discover something new; which are
85 the less renowned genes expressed in the heart?

[1] Baldock, R. and Davidson, D. *Anatomy for ontologies for bioinformatics: principles and practise* chapter: The Edinburgh Mouse Atlas 2008: Springer

[2] <http://nar.oxfordjournals.org/content/early/2013/11/20/nar.gkt1155>

5. Bibliography styles

90 There are various bibliography styles available. You can select the style of your choice in the preamble of this document. These styles are Elsevier styles based on standard styles like Harvard and Vancouver. Please use BibTeX to generate your bibliography and include DOIs whenever available.

Here are two sample references: [? ?].

95 References