

# OPTIC: orthologous and paralogous transcripts in clades

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## ABSTRACT

The genome sequences of a large number of metazoan species are now known. As multiple closely related genomes are sequenced, comparative studies that previously focussed on only pairs of genomes can now be extended over whole clades. The orthologous and paralogous transcripts in clades (OPTIC) database currently provides sets of gene predictions and orthology assignments for three clades: (i) amniotes, including human, dog, mouse, opossum, platypus and chicken (17 443 orthologous groups); (ii) a *Drosophila* clade of 12 species (12 889 orthologous groups) and (iii) a nematode clade of four species (13 626 orthologous groups). Gene predictions, multiple alignments and phylogenetic trees are freely available to browse and download from <http://genserv.anat.ox.ac.uk/clades>. Further genomes and clades will be added in the future.

## INTRODUCTION

New technologies and reduced costs are driving a marked increase in the numbers of genomes that are being sequenced. This steep rise in data presents opportunities for predicting evolutionary relationships of genes not between pairs of genomes, as previously, but instead among genomes from a clade of closely related species. Computational tools for gene prediction, orthology assignment and multiple alignment are now needing to be developed using phylogenetic approaches. To meet this challenge, we have developed a pipeline for gene prediction and orthology assignment for any clade of genomes (Heger and Ponting, in press). The current release of the orthologous and paralogous transcripts in clades (OPTIC) database contains three clades: 12 species from the genus *Drosophila*, an amniotic clade of five mammals with chicken as outgroup, and four *Caenorhabditis* nematodes (Table 1).

The pipeline predicts orthology for both orthologous groups and simple 1:1 ortholog sets. Here, orthologous groups contain orthologs and in-paralogs but exclude out-paralogs (1), those duplicated genes that were each present in the last common ancestor of a clade. Simple 1:1 ortholog sets are derived from orthologous groups by examining the gene tree and extracting sub-trees that contain exactly one gene per species. To enable inferences of gene duplication or loss, or positive selection on individual codons, we supply amino acid or nucleotide multiple sequence alignments, and phylogenetic trees, for each orthologous group. All data may be searched or downloaded freely from <http://genserv.anat.ox.ac.uk/download/clades>.

## Database construction

The pipeline requires a set of genome sequences and ENSEMBL (2) gene sets for each genome. If a gene set for a genome is unavailable, we predict transcripts by homology from a reference transcript set and thereafter automatically derive a gene set from them (Heger and Ponting, in press). A quality control step removes partial predictions and marks those predictions as pseudogenes that contain in-frame stop-codons and frameshift insertions and deletions. Both genes and pseudogenes comprise a predicted gene set. ENSEMBL and predicted gene sets are then submitted to an orthology assignment process. A full description of the pipeline, including parameter settings, is provided on the web site. Briefly, the pipeline implements the following steps:

- (i) Gene prediction by homology from a transcript set using Exonerate (3).
- (ii) Pairwise orthology assignment between all pairs of genomes using:
  - (a) BlastP (4) all-against-all alignments of all translated transcripts and
  - (b) PhyOP (5) tree-based orthology assignment of genes.

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**Table 1.** Gene sets and orthology assignments in three clades

Species	Genes	Genes with orthologs (%)	Orphaned genes (%)
<i>D. melanogaster</i> *	13 836	13 563 (98)	273 (2)
<i>D. simulans</i>	13 203	12 318 (93)	885 (7)
<i>D. sechellia</i>	15 467	14 356 (93)	1111 (7)
<i>D. erecta</i>	14 199	13 471 (95)	728 (5)
<i>D. yakuba</i>	14 971	14 218 (95)	753 (5)
<i>D. ananassae</i>	14 337	13 205 (92)	1132 (8)
<i>D. pseudoobscura</i>	12 304	11 609 (94)	695 (6)
<i>D. persimilis</i>	12 973	11 876 (92)	1097 (8)
<i>D. willistoni</i>	13 144	11 360 (86)	1784 (14)
<i>D. virilis</i>	12 017	11 096 (92)	921 (8)
<i>D. mojavensis</i>	11 717	10 883 (93)	834 (7)
<i>D. grimshawi</i>	11 800	11 011 (93)	789 (7)
<i>C. elegans</i> *	20 093	14 037 (70)	6056 (30)
<i>C. remanei</i>	18 137	14 961 (82)	3176 (18)
<i>C.PB2801</i>	21 931	17 759 (81)	4172 (19)
<i>C. briggsae</i>	18 388	13 460 (73)	4928 (27)
<i>H. sapiens</i> *	22 611	19 339 (86)	3272 (14)
<i>M. musculus</i> *	24 442	20 758 (85)	3684 (15)
<i>C. familiaris</i> *	19 314	18 066 (94)	1248 (6)
<i>M. domestica</i> *	19 597	18 123 (92)	1474 (8)
<i>O. anatinus</i> *	18 596	15 312 (82)	3284 (18)
<i>G. gallus</i> *	16 715	13 893 (83)	2822 (17)

Gene sets marked with an asterisk (\*) were obtained from ENSEMBL, whereas all others have been predicted by the pipeline. Orphans represent genes that have no ortholog in any of the other genomes in the clade. These will represent results of heuristic failures in our ortholog prediction pipeline or in gene predictions, as well as true gene losses.

- (iii) Graph-based grouping of genes from all species into clusters.
- (iv) Multiple alignment of translated exons using MUSCLE (6).
- (v) Estimation of phylogenetic tree topology using NJTree (7).
- (vi) Decomposition of clusters into orthologous groups.
- (vii) Branch length estimation using codeml from the PAML package (8).
- (viii) Computation of simple 1:1 ortholog sets.

Data are stored in a relational database and gene predictions are displayed within a GMOD genome browser (<http://www.gmod.org>). Software is open source and available without charge on request to the authors.

### Database contents

For the current release, we have applied our pipeline to three metazoan clades (Table 1) each containing between 4 and 12 species. Genes were predicted for *Drosophila* and *Caenorhabditis* species' genome assemblies using *D. melanogaster* (9) and *C. elegans* (10) protein-coding transcripts as templates. Mammalian and chicken gene sets were from ENSEMBL release 42 (2). The web server provides an up-to-date list of genome assemblies for the current release.

We find 12 889 orthologous groups in the *Drosophila* clade, 17 443 groups in the amniotic clade and 13 626 groups in the four *Caenorhabditis* species. Of these, 10 563 orthologous groups in the *Drosophila* clade, 9675 groups

in the amniotic clade and 6545 groups in the *Caenorhabditis* clade contain the full species complements. The numbers of simple 1:1 ortholog sets are smaller (5241, 7587, and 5987 for the three clades, respectively) owing to gene duplications and absences from incomplete assemblies.

For each orthologous group, we provide:

**Transcript predictions:** Predicted transcripts are available as exonic genomic coordinates, and as peptide and coding sequences.

**Orthologs:** Orthologous groups and simple 1:1 ortholog sets.

**Multiple alignments:** Multiple alignments of transcripts and genes within an orthologous group are provided both as aligned nucleic acid sequences and as aligned peptide sequences. Frameshift insertions or deletions in pseudo-genes have been removed, and stop-codons have been masked in order to facilitate downstream analyses. Genes have been aligned by concatenating exons of all transcripts while maintaining frame.

**Phylogenetic trees:** For each orthologous group, we provide a phylogenetic tree. The topology of the tree has been calculated from NJTree, while branch lengths (nucleotide substitutions per site) have been assigned using PAML.

### Database access and web service

The web service permits interactive data querying and browsing of orthologous groups and simple 1:1 ortholog sets for each clade (Figure 1). Species distributions of orthologous groups are denoted by phylogenetic profiles denoting the presence ('+') or absence ('0') of one or more genes in a group. For example, a search for orthologous groups in the amniotic clade with the phylogenetic profile '+++000' lists 542 orthologous groups that contain genes in human, mouse and dog, but have no orthologs in opossum, platypus and chicken.

In queries for simple 1:1 ortholog sets, '1' indicates that exactly one copy of this gene is present and '-' indicates that this particular species should not be considered. Thus, the profile '111—' applied to simple 1:1 ortholog sets yields 13 788 simple 1:1 ortholog sets that contain exactly one gene in human, dog and mouse, and any number of homologs in opossum, platypus or chicken.

For each orthologous group and simple 1:1 ortholog set, multiple alignments and a phylogenetic tree may be displayed. A synteny viewer also allows an assessment of whether orthologs occur in regions of conserved synteny. Genes of particular interest can be located either by identifier or by genomic location. Computational biologists interested in performing large-scale analyses can download complete datasets from the download area.

### OUTLOOK

OPTIC is designed to provide precalculated phylogenetic datasets that are of benefit to clade genomic analyses.

**Simple 1:1 orthologs for 111111**

Simple 1:1 ortholog sets for phylogenetic pattern 111111.

The species currently selected are:

Nr.	Species
1	<i>H. sapiens</i>
2	<i>M. musculus</i>
3	<i>C. familiaris</i>
4	<i>M. domestica</i>
5	<i>O. anatinus</i>
6	<i>G. gallus</i>

A simple 1:1 ortholog set includes exactly one gene as indicated

Set	Pattern	Species
57	111111	6
114	111111	6
171	111111	6
228	111111	6
285	111111	6

**Amniota**

Gene search: Species *H. sapiens* Gene Id

Simple set search: Identifier  Pattern 111111 Species *H. sapiens* Gene

Group search: Identifier  Pattern  Species *H. sapiens* Gene

Interpro search: Identifier  Description

**Simple 1:1 ortholog set 114**

This strict 1:1 ortholog set was derived from orthologous cluster 2.

**Summary**

Species	Species	Genes
<i>C. familiaris</i>	1	
<i>G. gallus</i>	1	
<i>H. sapiens</i>	1	
<i>M. domestica</i>	1	
<i>M. musculus</i>	1	
<i>O. anatinus</i>	1	

**Members**

Schema	Gene
<i>C. familiaris</i>	ENSCAFG00000015145
<i>G. gallus</i>	ENSGALG00000005894
<i>H. sapiens</i>	ENSG00000138592
<i>M. domestica</i>	ENSMODG00000002220
<i>M. musculus</i>	ENSMUSG000000027363
<i>O. anatinus</i>	14870

Schema

Species	Gene
<i>C. familiaris</i>	ENSCAFG00000015145
<i>G. gallus</i>	ENSGALG00000005894
<i>H. sapiens</i>	ENSG00000138592
<i>M. domestica</i>	ENSMODG00000002220
<i>M. musculus</i>	ENSMUSG000000027363
<i>O. anatinus</i>	14870

Sequence alignment (partial):

```

C. familiaris  ENSCAG00000015145  YNLIKRRPDFKQDDYFHSILGLANIKKATIEEAERLSKLRVEAEVRKKLEEDRQEEQLQKQKQ
G. gallus      ENSGALG00000005894  YNFIKKRPDFKQDDYFHSILGPTNLKKAIEEAERLSKLRVEAEVRKKLEEDRQEEAOLQKQKQ
H. sapiens     ENSG00000138592  YNLIKRRPDFKQDDYFHSILGPTNLKKAIEEAERLSKLRVEAEVRKKLEEDRQEEAOLQKQKQ
M. domestica   ENSMODG00000002220  YNLIKRRPDFKQDDYFHSILGPTNLKKAIEEAERLSKLRVEAEVRKKLEEDRQEEAOLQKQKQ
M. musculus    ENSMUSG000000027363  YNLIKRRPDFKQDDYFHSILGPTNLKKAIEEAERLSKLRVEAEVRKKLEEDRQEEAOLQKQKQ
O. anatinus    14870             YNLIKRRPDFKQDDYFHSILGPTNLKKAIEEAERLSKLRVEAEVRKKLEEDRQEEAOLQKQKQ
  
```

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**Figure 1.** Browsing the orthology database. A sample session starts with a query for all simple 1:1 ortholog sets (bottom left). It continues with a list of all simple 1:1 ortholog sets containing all six species from the amniotic clade, then by a selection of one particular ortholog set (number 114), and finally with a viewing of the gene-based multiple sequence alignment.

Our approach complements other existing projects (2,7,11,12) in four respects: (i) we apply the pipeline to diverse, and not just experimental model, organisms; (ii) we define clades with respect to phylogenetic distances that are amenable to evolutionary rate analysis (roughly, where the number of synonymous substitutions per synonymous site is  $<2.0$  (5)); (iii) our orthology relationships are inferred by considering all species equally, in a phylogenetic approach and (4) we use all exons across all alternative transcripts as opposed to the longest transcripts only. A particularly useful feature of OPTIC is its provision of multiple alignments either for genes as concatenated exons, or for alternative transcripts.

We plan to update gene predictions and orthology assignments and add more genomes and clades when they become available.

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*Conflict of interest statement.* None declared.

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