

Opening example data

Data from the Fal estuary

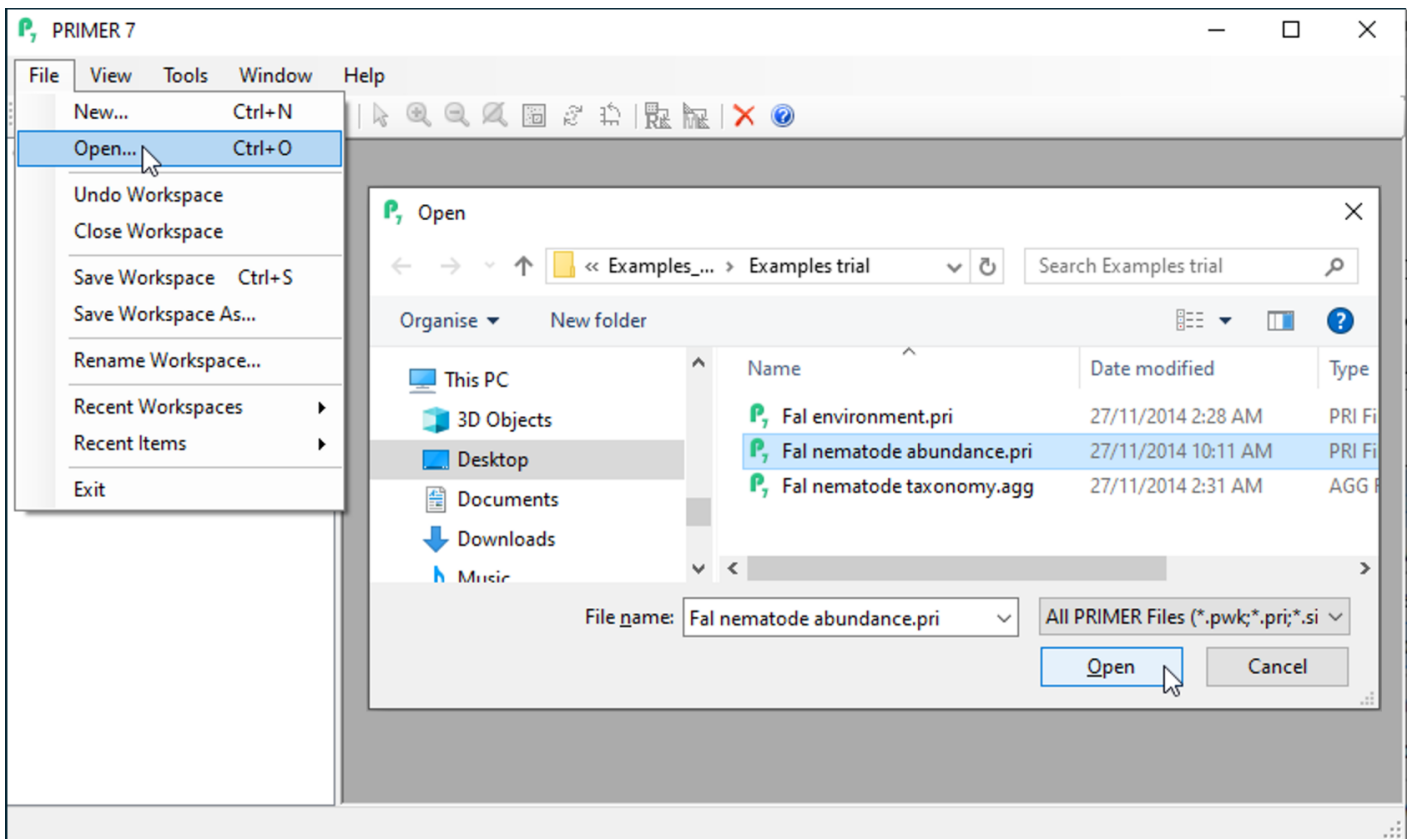
Example datasets in PRIMER can be obtained *via* the **Help** menu item. In trial mode, click **Help > Get Examples Trial...**, and you can download the following four files of example data (held in a folder called 'Examples Trial') to a location of your choice:

- **Fal environment.pri** (measured values for 12 environmental variables x 27 sites)
- **Fal environment.xls** (same as above, but in Excel format)
- **Fal nematode abundance.pri** (abundances of 62 nematode species x 27 sites)
- **Fal nematode taxonomy.agg** (taxonomic hierarchy for the 62 nematode species)

These data come from a study of benthic infaunal communities in soft sediments from 27 sites over five creeks of the Fal estuary, SW England ([Somerfield *et al.* \(1994a\)](#) , [Somerfield *et al.* \(1994b\)](#)). Sediments at these sites were contaminated to varying degrees by heavy metals, from historic mining activities. Both faunal counts (nematodes) and environmental measures were obtained from the same set of sites. (Note: the extension ***.pri** indicates a file containing a data matrix that has been saved in PRIMER 7's own internal (binary) format, unreadable by other software or earlier versions of PRIMER. Similarly, the ***.agg** extension indicates an aggregation-type file for PRIMER.)

Open the Fal data in PRIMER

To open the species-by-samples data matrix, launch PRIMER, then click **File > Open** from the main menu, navigate to the 'Examples trial' directory in the location you have specified, and select '**Fal nematode abundance.pri**'. Click **Open** to display the species matrix.



Alternatively, because this is a PRIMER file type (*.pri), you can instead use Windows Explorer to navigate to your specified folder and just double-click on the file name. This will launch a PRIMER session, with the data matrix open in the PRIMER desktop.

The screenshot shows the PRIMER 7 application window with the 'Fal nematode abundance' data matrix loaded. The table displays the abundance of various nematode species across seven samples (R1 to R7).

Fal estuary nematodes		Samples						
Abundance		R1	R2	R3	R4	R5	R6	R7
Anoplostoma vivip		0	0	0	0	0	0	0
Halalaimus gradis		0	0	0	0	0	0	0
Halalaimus longica		0	0	0	0	0	0	0
Oxystomina elongat		0	0	0	0	0	0	0
Viscosia viscosa		0	0	0	0	0	0	0
Tripyloides gradis		149	181	385	289	170	614	
Atrochromadora mi		0	0	0	0	0	0	0
Chromadora macro		0	4	29	63	263	123	
Chromadora nudica		0	0	0	0	0	0	7
Chromadorella ?du		0	0	0	0	0	0	0
Chromadorita nana		0	0	0	0	0	0	0
Chromadorita tenta		0	0	0	0	0	0	0
Dichromadora geop		5	0	0	0	0	0	7
Hypodontolaimus h		40	44	25	18	5	14	

Properties of the data

Click on **Edit > Properties** and you will see that PRIMER-format *.pri sheets carry other information about the data matrix as well, including:

- Title,
- Data type,
- Array size (number of columns and rows),
- Orientation (whether samples are found in columns or rows),
- a Description, and
- a History of what pre-treatments (such as a transformation) have been applied to them.

Sample Data Properties

Title:
Fal estuary nematodes

Data type:
☒ Abundance
☐ Biomass
☐ Environmental
☐ Unknown/other

History:

Samples as:
☒ Columns
☐ Rows

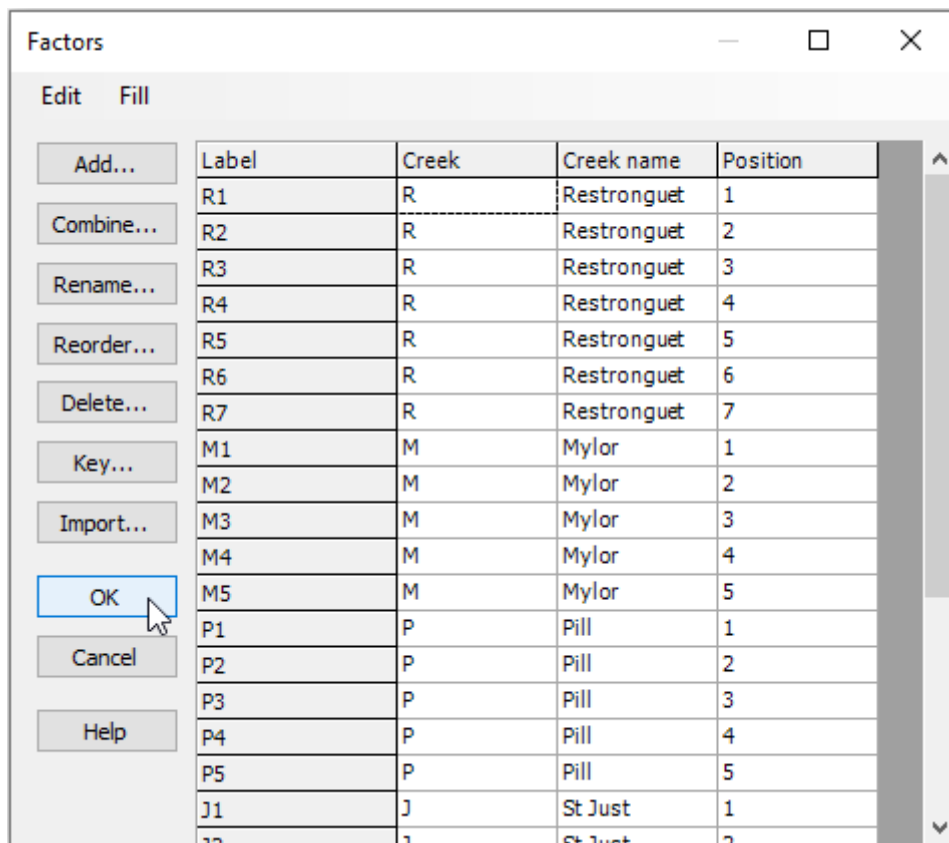
Number of columns: 27
Number of rows: 62

Description:
Abundance of nematodes (counts from identifications in a random sub-sample multiplied up by total nematode count for each sample, so has the statistical properties of density rather than pure count).
Data from meiofauna cores of the sediments of 27 sites over 5 creeks of the Fal estuary, Cornwall, UK.

OK Cancel Help

Factors associated with the data

Click on **Edit > Factors**, and you can see that a subsidiary sheet of three factors is also linked to this worksheet: 'Creek', a single-letter abbreviation for the creeks, the full 'Creek name' and a numeric 'Position' factor identifying the location of each sampling site down each creek.



Note that additional factors could be added here by clicking **Add**, and also combinations of levels of existing factors can be created by clicking on **Combine**.

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