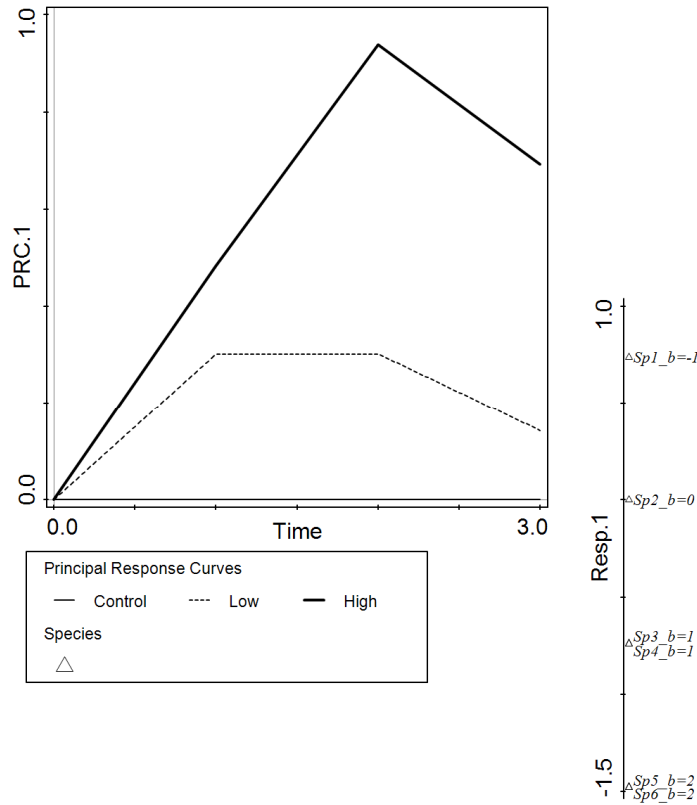


which is the intended level. If you select any level different from the base one, the *Set Base Level* button becomes enabled, allowing you to choose a new base level. Note that after such change, an existing PRC analysis should not be re-executed. Instead, click the *Modify* button and go through the settings with the Analysis Setup Wizard to reinitialize the information present there. Changing the base level replaces the corresponding response curve with a straight line and reshapes the curves for other treatment levels accordingly.

The following graph shows *Graph1* in the *PRC* analysis notebook and we will use it to describe the PRC diagram.



The three curves in the main area of the diagram show, for each combination of treatment and time levels, the PRC score, calculated using this formula:

$$(6.1) \quad \text{PRC1} = \text{RegrE.1} * \text{TAU} / \text{SDE}$$

where *RegrE.1* and *SDE* are, respectively, the canonical coefficient (on the first ordination axis) and the standard deviation of the particular component of the interaction term between the temporal and treatment factor. Both values can be found in the *ExplVars* page of the analysis notebook, while *TAU* is the total standard deviation of the species data, which can be found by clicking the *Details* button on the *Summary* page of the analysis notebook. The additional vertical plot at the right side of the diagram (which has its zero value aligned with the zero value of the PRC scores in the main plot) shows the response variable (species) scores for the first ordination axis (that is, *Resp.1* on the *RespVars* page in the non-brief mode, see section 6.1.1).

On the logarithmic scale, the inferred changes of species abundance with respect to the control are calculated as the PRC (treatment) score * species score. The log-change of