pathRender: KEGG and Biocarta pathway visualization

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1 Introduction

Pathways are useful for organizing knowledge about molecular biological processes. Several major catalogs of pathways are available, and this package addresses the visualization of pathways from KEGG and Biocarta. Ultimately we want to be able to link statistical data to pathway representations to aid interpretation. This package addresses only the graph structures, annotation, and rendering of pathway diagrams. Much work remains to be done to harvest in a scalable and customizable way the information provided on pathways.

2 Quick illustrations

As of 9/15/2007 it is not clear why some of the symbols are not translated to molecule or interaction terms.

```
> library(pathRender)
> plot(G1 <- graphcMAP("p53pathway"))
> G1
> nodes(G1)[1:5]
```
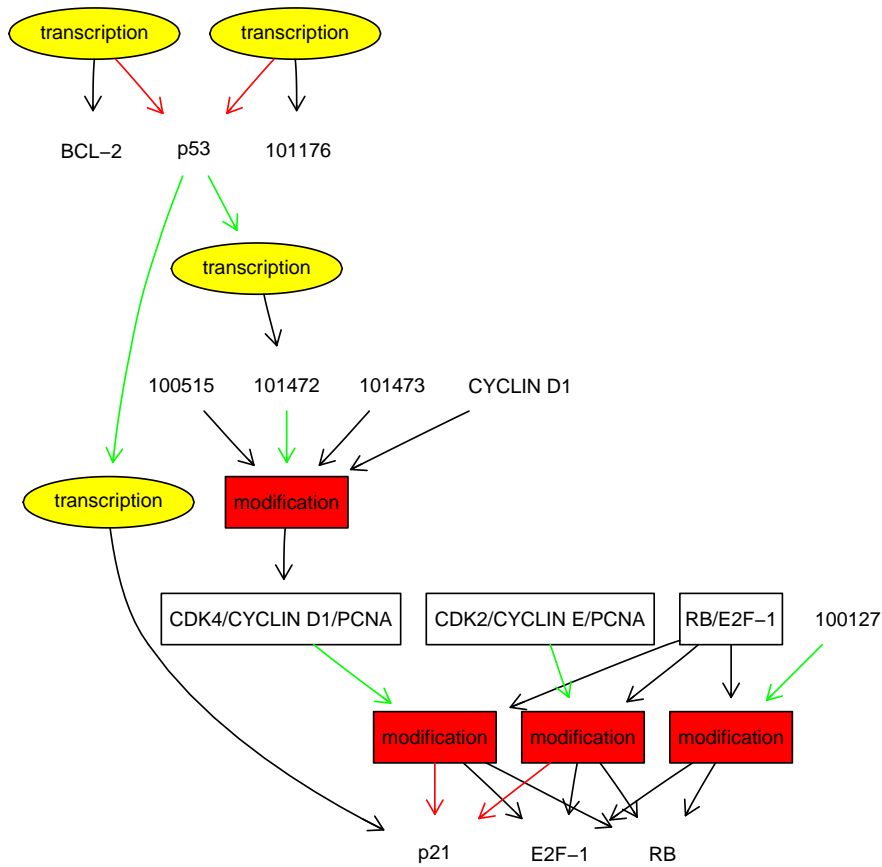

Figure 1: A rendering of the p53 pathway according to Biocarta.

```
> plot(G2 <- graphcMAP("raspathway"))
```
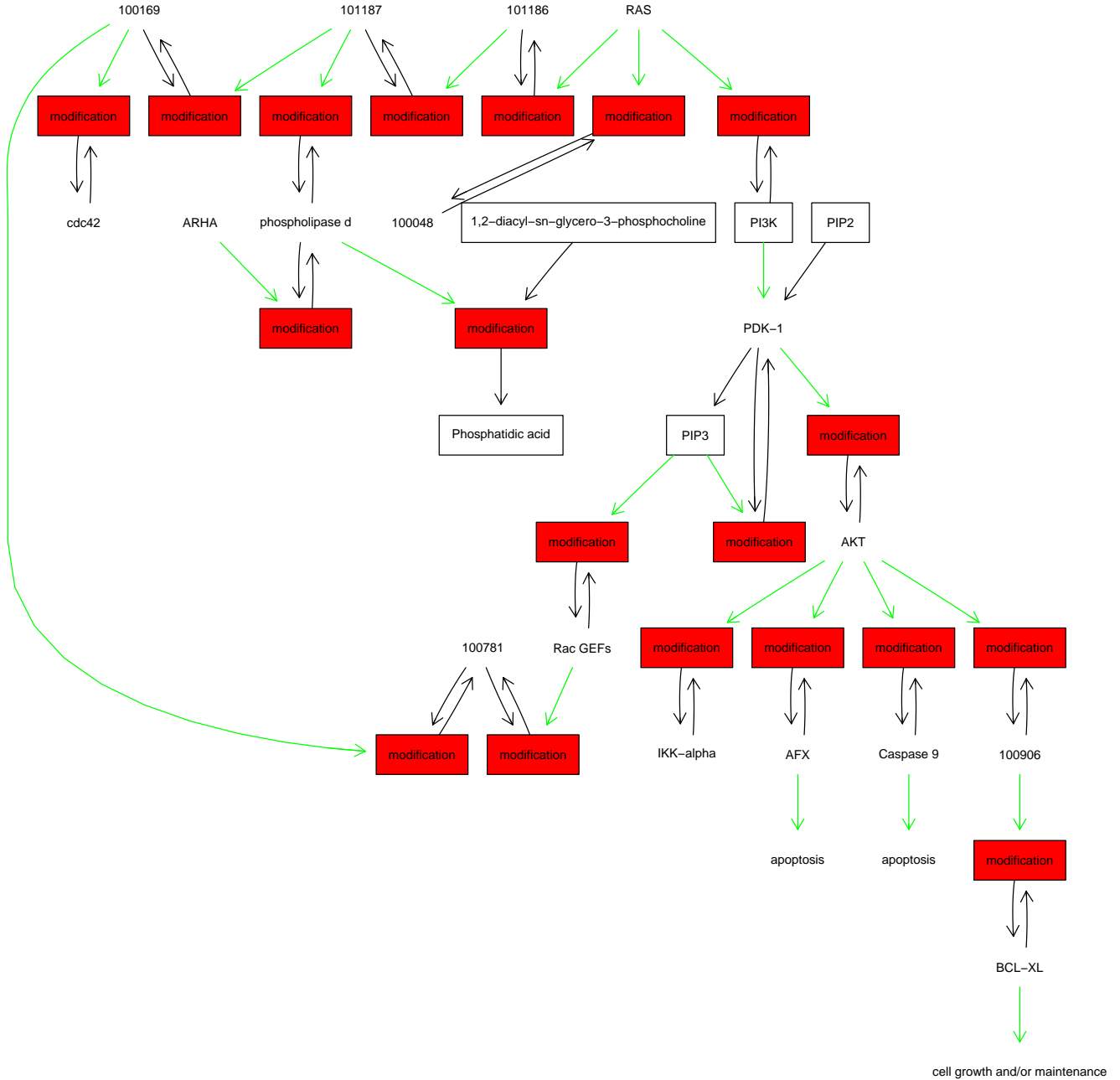

Figure 2: A rendering of the Ras pathway according to Biocarta. The height and width of the plotting surface are set to 12in each.