Plot a life cycle diagram from a matrix model

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The exercise plots a life cycle with the stages and transitions of a give matrix chosen from the `comadre` database. It will use the R function `plotLifeCycle` from the COMADRE/COMPADRE GitHub repository. This function works well with matrices of relatively low dimensionality ($\sim< 7$), and where not many transitions are depicted. The function uses the `DiagrammeR` package, so this needs to be called first:

```r
library(DiagrammeR)
```

```
> Warning: package 'DiagrammeR' was built under R version 3.2.2
```

Let's plot the lifecycle described by the `A` matrix for a species containing the word "lion" in the common name used by the author(s) in the original source publiction.

First load the data:

```r
load("COMADRE_v.1.0.0.RData")
```

To find the species with the word `lion` in their common name, we use the function `grep`.

```r
lions <- grep("lion",comadre$metadata$CommonName)
unique(comadre$metadata$CommonName[lions])
```

```
> [1] "Northern sea lion; Steller sea lion"
> [2] "New Zealand sea lion"
> [3] "California sea lion"
```

Unfortunately, no actual lion (*Panthera leo*) has been included in this version of COMADRE, but there are plenty of other "lions" in it. We will plot the life cycle of the red lionfish (*Pterois volitans*):

```r
matNum <- which(comadre$metadata$CommonName == "Red Lionfish")
matNum
```

```
> [1] 143
```

```r
sp <- gsub("_"," ",comadre$metadata$SpeciesAccepted[matNum])
sp
```

```
> [1] "Pterois volitans"
```

The matrix 'A' and the stages of this study are:

```r
matA <- comadre$mat[[matNum]]$matA
matA
```

```
>          A1    A2      A3
> [1,] 0e+00 0.000 35.315
> [2,] 3e-05 0.777  0.000
> [3,] 0e+00 0.071  0.949
```

```
stages <- comadre$matrixClass[[matNum]]$MatrixClassAuthor
stages
```

```
> [1] "Larvae"                    "Juvenile (20 - 174 mm)"
> [3] "Adult (> 174 mm)"
```

To plot its lifecycle, use `source_url` to obtain the function `plotLifeCycle.R` from the CO-MADRE/COMPADRE GitHub. This function is available in the `devtools` package.

```
require(devtools)
```

```
> Loading required package: devtools
```

```
> Warning: package 'devtools' was built under R version 3.2.2
```

```
> WARNING: Rtools is required to build R packages, but is not currently installed.
>
> Please download and install Rtools 3.1 from http://cran.r-project.org/bin/windows/Rtools/ and then
```

```
source_url("https://raw.githubusercontent.com/jonesor/compadreDB/master/Functions/plotLifeCycle.R")
```

```
> SHA-1 hash of file is 9c8b033012c5de1418bf653804811179fb7cda5b
```

```
plotLifeCycle(matA, title = "Red Lionfish")
```