

HOWTO generate biocViews HTML

VJC

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Suppose the following vector of package names lists packages whose DESCRIPTION file include a biocViews tag.

```
> plist
```

```
[1] "AnnBuilder"      "DNACopy"         "GeneTS"          "GlobalAncova"    "KEGGSOAP"
[6] "MCRestimate"     "MLInterfaces"    "RBGL"            "ROC"             "RSNPper"
[11] "Rdbi"            "Resourcerer"     "Rgraphviz"       "SAGElyzer"       "affxparser"
[16] "affy"            "affyPLM"         "affyQCReport"    "affylmGUI"       "altcdfenvs"
[21] "arrayMagic"      "biocViews"       "biomaRt"         "bridge"          "clusterStab"
[26] "ecolitz"         "edd"             "fdrame"          "genArise"        "genefilter"
[31] "geneplotter"     "globaltest"      "graph"           "gtkWidgets"      "hexbin"
[36] "ideogram"        "limmaGUI"        "maDB"            "macat"           "made4"
[41] "marray"          "matchprobes"     "nnNorm"          "pdmclass"        "pgUtils"
[46] "prada"           "rama"            "reb"             "sagenhaft"       "siggenes"
[51] "splicegear"      "timecourse"      "tkWidgets"       "twilight"        "vsn"
[56] "widgetInvoke"    "widgetTools"     "xcms"            "G0stats"         "goCluster"
[61] "multtest"
```

Then the following generates a list of CTV structures based on a vocabulary graph sep05:

```
> library(biocViews)
> data(sep05)
> vv <- getBcViews(plist, sep05)
> cc <- getCTVs(vv, sep05)
> cc[[1]]
```

CRAN Task View

Name: Annotation
Topic: Annotation
Maintainer: None

Packages: altcdfenvs, AnnBuilder, ecolitz, GlobalAncova, globaltest, G0stats,
matchprobes, Resourcerer, RSNPper

An important part of the view presentation is the linkage to the repository being documented. We need a complete specification of the path to the html file that documents the package availability.

```
> purl <- "http://www.bioconductor.org/packages/bioc/devel/src/contrib/html/"
```

Now we iterate over the list of CTV structures and emit HTML that knows about the repository location. We use `bcv2html`, a minor modification to `ctv2html`, to propagate the DESCRIPTION Title field.

```
> jnk <- sapply(cc, bcv2html, packageURL = purl, reposname = "Bioconductor")
```

Here are the created files:

```
> dir(patt = "html")
```

```
[1] "Annotation.html"
[2] "CellBasedAssays.html"
[3] "Classification.html"
[4] "Clustering.html"
[5] "DataImport.html"
[6] "DifferentialExpression.html"
[7] "DNACopyNumber.html"
[8] "FactorialDesign.html"
[9] "GeneralInfrastructure.html"
[10] "Genetics.html"
[11] "GO.html"
[12] "GraphInfrastructure.html"
[13] "GraphsAndNetworks.html"
[14] "Infrastructure.html"
[15] "LinearModels.html"
[16] "MassSpectrometry.html"
[17] "Microarray.html"
[18] "MultipleComparisons.html"
[19] "OneChannel.html"
[20] "Pathways.html"
[21] "Preprocessing.html"
[22] "ProprietaryPlatforms.html"
[23] "QualityControl.html"
[24] "SAGE.html"
[25] "SNPsAndGeneticVariability.html"
[26] "StatisticalModelingForHighThroughputBiology.html"
[27] "Statistics.html"
[28] "Technology.html"
```

```
[29] "TimeCourse.html"
[30] "Transcription.html"
[31] "TwoChannel.html"
[32] "Visualization.html"
```

There is no index.html. We need to create one that knows about the top level vocabulary. The `topwrap` function helps. There is also some fragmentary HTML that starts out the index.html content.

```
> els <- topwrap(sep05)
> toptop <- readLines(system.file("htmlfrags/topfrag.html", package = "biocViews"))
> cat(toptop, els, "</ul>\n", file = "index.html")
> readLines("index.html")

[1] "<html> <head>    <title>Bioconductor Task View: top level views</title>    <link re
[2] " <ul><li> subviews: <a href=OneChannel.html>OneChannel</a>, <a href=TwoChannel.ht
[3] " <li><a href=Visualization.html>Visualization</a>"
[4] " <li><a href=Statistics.html>Statistics</a>"
[5] " <ul><li> subviews: <a href=DifferentialExpression.html>DifferentialExpression</a>
[6] " <li><a href=GraphsAndNetworks.html>GraphsAndNetworks</a>"
[7] " <li><a href=Technology.html>Technology</a>"
[8] " <ul><li> subviews: <a href=Microarray.html>Microarray</a>, <a href=Proteomics.ht
[9] " <li><a href=Annotation.html>Annotation</a>"
[10] " <ul><li> subviews: <a href=GO.html>GO</a>, <a href=Pathways.html>Pathways</a>, <
[11] " <li><a href=Infrastructure.html>Infrastructure</a>"
[12] " </ul>"
```