Radiation Oncology (RadOnc) Tools

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Contents

1 Introduction

The *RadOnc* package provides a number of tools for the import and analysis of dose-volume histogram (DVH) data used routinely in Radiation Oncology clinical practice and research. Supported formats for data import currently include:

- Varian's Aria/Eclipse platform

The functionality contained herein also enables visualization of dosimetric and volumetric data, and statistical comparison among multiple DVHs. In order to use these tools, you must first load the *RadOnc* package:

```
> library(RadOnc)
```

It is assumed that the reader is already familiar with DVH analysis. If this is not the case, consult the relevant literature for a thorough treatment of the subject (Drzymala et al., 1991).

Throughout this vignette, we will be exploring actual data for 2 patients, each possessing a set of 10 structures (including organs at risk and treatment planning volumes).

2 Changes for *RadOnc* in current BioC release

- This is the first public release of the *RadOnc* package.

3 DVH file import

The `read.DVH()` function is designed to take an input text file and output a list of DVH data objects containing all relevant data. Supported file types currently include Varian's Aria/Eclipse platform (v.10 and v.11). Other treatment planning systems are not currently supported however will be included in future releases.

For Varian-specific file types, data must be exported directly from the treatment planning system and should include all DVH structures of interest. In Eclipse, this is accomplished via the "Export DVH in Tabular Format..." option, accessed by right-clicking over DVHs in Plan Evaluation mode. Exported files will adhere to the following form (an example file, 50 lines of which are shown here, is contained within this release of the *RadOnc* package):

```
Patient Name          : Doe, Jane (1111111111)
Patient ID            : 1111111111
Comment               : DVHs for one plan
Date                  : 05.24.2013  00:00:00
Type                  : Cumulative Dose Volume Histogram
Description           : The cumulative DVH displays the percentage (relative)
                        or volume (absolute) of structures that receive a dose
                        equal to or greater than a given dose.


Plan: PLAN_NAME
Prescribed dose [cGy]: 5500.0
% for dose (%): 100.0


Structure: LIVER
Approval Status: Unapproved
Plan: PLAN_NAME
Course: COURSE_1
Volume [cc]: 1635.9
Dose Cover.[%]: 100.0
Sampling Cover.[%]: 100.0
Min Dose [cGy]: 42.7
Max Dose [cGy]: 5634.2
Mean Dose [cGy]: 707.0
Modal Dose [cGy]: 99.5
Median Dose [cGy]: 276.4
STD [cGy]: 917.2
Equiv. Sphere Diam. [cm]: N/A
Conformity Index: N/A
Gradient Measure [cm]: N/A
```

Dose [cGy]	Relative dose [%]	Ratio of Total Structure Volume [%]
0	0	100
5	0.0909091	100
10	0.181818	100
15	0.272727	100
20	0.363636	100
25	0.454545	100
30	0.545455	100
35	0.636364	100
40	0.727273	100
45	0.818182	99.9247
50	0.909091	99.2638
55	1	98.1752
60	1.09091	96.8538
65	1.18182	95.3989
70	1.27273	93.8907
75	1.36364	92.3371
80	1.45455	90.7697
85	1.54545	89.2061
90	1.63636	87.6496

...
...

This DVH data may be imported using the `read.DVH()` function, with an example shown here:

```
> read.DVH(file="Jane_Doe.dvh", type="aria10", verbose=TRUE)

Reading DVH file ('/Library/Frameworks/R.framework/Versions/3.0/Resources/library/RadOn
  Patient: Doe, Jane (1111111111)
  Plan: PLAN_NAME
  Dose: 5500cGy
  ..Importing structure: LIVER  [volume: 1635.9cc, dose: 42.7 - 5634.2cGy]
  ..Importing structure: LEFT_KIDNEY  [volume: 195.7cc, dose: 75.8 - 3846.8cGy]
  ..Importing structure: STOMACH  [volume: 695.2cc, dose: 59 - 5353.2cGy]
  ..Importing structure: DUODENUM  [volume: 34.2cc, dose: 2707.8 - 5620.1cGy]
  ..Importing structure: RIGHT_KIDNEY  [volume: 223.9cc, dose: 102.4 - 4201.9cGy]
  ..Importing structure: CTV  [volume: 146.7cc, dose: 5168.6 - 5646.9cGy]
  ..Importing structure: PTV  [volume: 239.4cc, dose: 4749.8 - 5664.7cGy]
  ..Importing structure: SMALL_BOWEL  [volume: 232.2cc, dose: 59.6 - 4934.1cGy]
  ..Importing structure: CORD  [volume: 64.9cc, dose: 0 - 3442.8cGy]
  ..Importing structure: BODY  [volume: 25507.5cc, dose: 0 - 5664.7cGy]
```

4 DVH list manipulation

The `read.DVH()` function returns a DVH list that can be manipulated in multiple ways. Subsets of DVH lists can be obtained using the `[]` modifier, and any number of DVH lists can be combined using the `c()` function. Additionally, single DVH objects can be directly accessed using the `[[]]` modifier, and individual elements of a DVH list may be directly replaced with other DVH objects using the `[[<-` function.

```
> janedoe[1:4]

[1] "List containing 4 DVH objects (LIVER, LEFT_KIDNEY, STOMACH, DUODENUM)"

> c(janedoe[c("PTV")], johndoe[c("CTV", "DUODENUM")])

[1] "List containing 3 DVH objects (PTV, CTV, DUODENUM)"

> johndoe[["CTV"]]

[1] "Structure: CTV (88.4095 cc), Dose: 96.8-102.6% (5500cGy prescribed), DVH: cumulati

> janedoe[[1]] <- johndoe[["CTV"]]
> janedoe[1:4]

[1] "List containing 4 DVH objects (CTV, LEFT_KIDNEY, STOMACH, DUODENUM)"
```

Other list processing functions may be applied to DVH lists, enabling further data manipulation. The `rev()` function may be used to reverse the order of a DVH list, while the `names()` function may be used to extract (or set) the structure names for each DVH contained within the list. The `length()` function may be used to find the number of DVH objects contained within a DVH list, and the `lapply()` function can be used to perform a customizable set of operations on a DVH list and return a customizable set of values. Here are some examples employing each of these functions:

```
> names(janedoe)[1:4] <- c("A1", "B2", "C3", "D4")
> names(rev(janedoe[1:4]))

[1] "D4" "C3" "B2" "A1"

> length(johndoe)

[1] 10

> lapply(johndoe, function(DVH) { DVH[c("DMIN", "D50%", "DMAX", "V20%")] })
```

$LIVER

%	%	%	cc
0.00000000	0.07174856	92.90000000	185.28500000

$SMALL_BOWEL

%	%	%	cc
0.00000000	0.06320805	99.80000000	13.94640000

$DUODENUM

%	%	%	cc
0.00000	81.34012	102.40000	83.10130

$STOMACH

%	%	%	cc
0.00000000	0.06726741	101.30000000	31.95860000

$CTV

%	%	%	cc
96.8000	100.0081	102.6000	88.4095

$PTV

%	%	%	cc
84.10000	99.80143	102.60000	155.73500

$BODY

%	%	%	cc
0.000000e+00	6.202236e-02	1.026000e+02	1.893130e+03

$LEFT_KIDNEY

%	%	%	cc
0.00000000	0.07279133	44.40000000	18.60640000

$RIGHT_KIDNEY

%	%	%	cc
0.00000	24.25567	98.50000	85.93270

$CORD

%	%	%	cc
0.000000	4.078601	55.500000	17.496100

5   DVH data

Each DVH structure contains a variety of data related to the structure itself as well as the distribution of radiation dose within the structure volume. Detailed slot list and parameters are described in the DVH-class documentation accompanying the *RadOnc* package. Specific parameters can be extracted using the [] modifier, which can take as its argument a character string representation of the desired dose/volume parameter. For instance, the volume of duodenum receiving 20Gy or the dose to the top 2.5% (2.3286cc) of the volume can be extracted from DVH data as follows:

```
> johndoe[["DUODENUM"]]["V20Gy"]

      cc
76.5153

> johndoe[["DUODENUM"]]["D2.5%"]

       %
100.5605

> johndoe[["DUODENUM"]]["volume"] * 0.025

      cc
2.328598

> johndoe[["DUODENUM"]]["D2.3286cc"]

       %
100.5605
```

These parameters are entirely flexible and multiple parameters can be requested for a given DVH object at the same time. This functionality can also be applied to a DVH list using the $ modifier.

```
> johndoe[["DUODENUM"]][c("V5%", "V20Gy", "D2.5%", "D2.3286cc", "Dmax")]

      cc       cc        %        %        %
 90.1912   76.5153 100.5605 100.5605 102.4000

> johndoe[1:4]$"V20Gy,Dmax"

$LIVER
      cc        %
21.35734 92.90000
```

```
$SMALL_BOWEL
       cc          %
 9.370469 99.800000


$DUODENUM
      cc          %
 76.5153 102.4000


$STOMACH
       cc           %
 26.83795 101.30000
```

If an improper parameter is specified however, `NA` results will be returned for the affected parameter(s):

```
> johndoe[["DUODENUM"]][c("V5", "VGy", "volume", 2.5, "", "Dmax")]

    <NA>      <NA>        cc      <NA>      <NA>            %
      NA        NA   93.1439        NA        NA   102.4000
```

6   Plotting

Individual DVH plots can be generated by the `plot()` function, and may be altered to show dose and/or volume as relative or absolute values with DVH shown as cumulative or differential data.

```
> plot(janedoe[[3]], volume="relative", dose="absolute", type="cumulative")
```
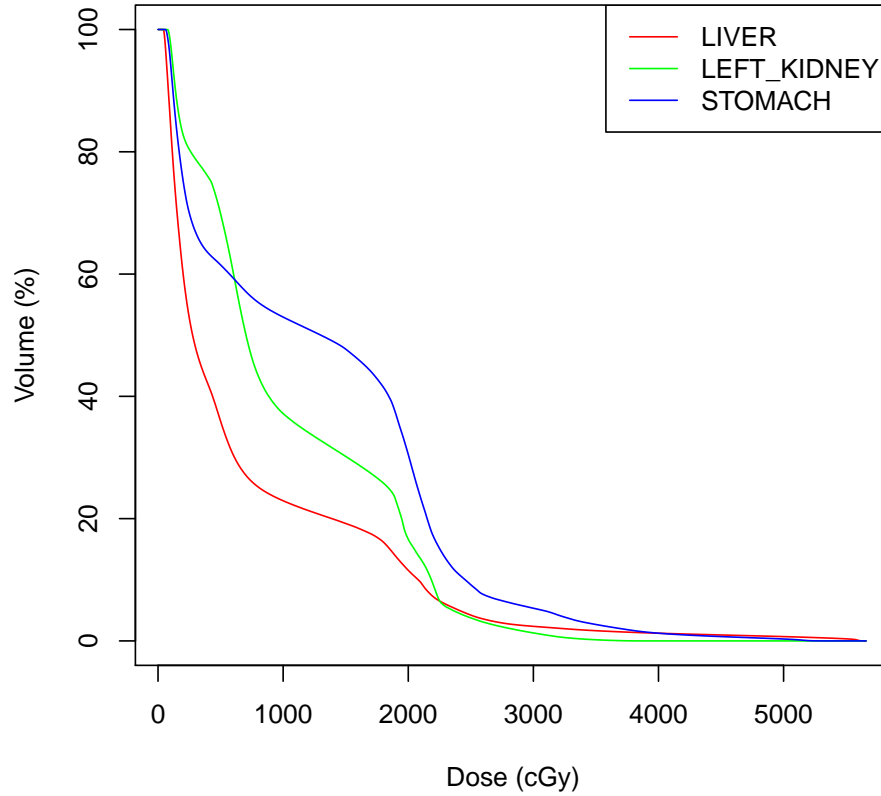

Figure 1: Standard dose-volume histogram for a single structure ("STOMACH") from patient Jane Doe. Data is shown as cumulative dose versus volume.

```
> plot(janedoe[1:3], plot.type="i", col=c("red", "green", "blue"),
+ legend="topright", legend.labels=names(janedoe[1:3]))
```

Figure 2: Standard dose-volume histogram for three structures from a single patient, Jane Doe. Data is shown as cumulative dose versus volume. Legend is displayed in the top right corner of the plot.

```
> plot(c(johndoe["STOMACH"],janedoe["STOMACH"]), #group 1
+ c(janedoe["LIVER"],johndoe["LIVER"]), #group 2
+ c(johndoe["DUODENUM"],janedoe["DUODENUM"]), #group 3
+ plot.type="g", dose="relative", col=c("blue", "red", "green"),
+ lwd=2, lty="dashed", fill.lty="solid", fill.transparency=0.3)
```
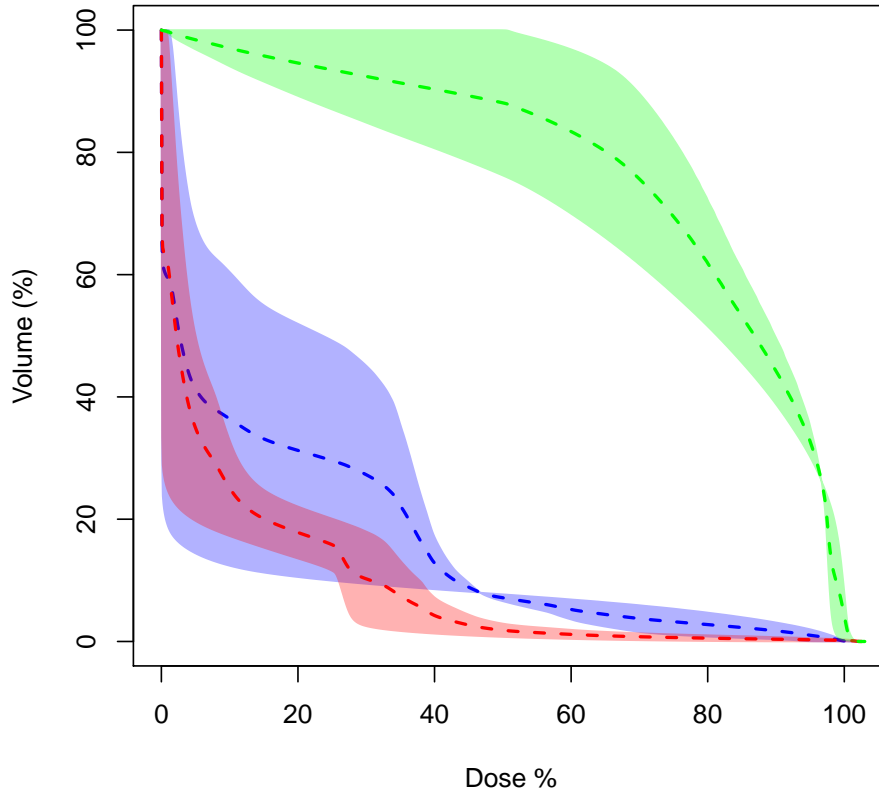

Figure 3: Mean dose-volume histograms are shown for three groups of DVHs, in this case corresponding to stomach, liver, and duodenum from two different patients (John Doe and Jane Doe). Data is shown as cumulative dose (relative) versus volume (relative). Shading represents the range of the data for each group (note that the width of the shading can be specified to represent other parameters instead of range – e.g. variance, standard deviation, interquartile range, median absolute deviation).

```
> group1 <- c("CTV", "PTV")
> group2 <- c("LIVER", "STOMACH", "SMALL_BOWEL")
> plot(c(johndoe[group1],janedoe[group1]),
+ c(janedoe[group2],johndoe[group2]),
+ plot.type="t", main="Target v. OAR t-Test", alpha=0.001,
+ col=c("red", "blue"), lty="dashed", fill.lty="solid")
```
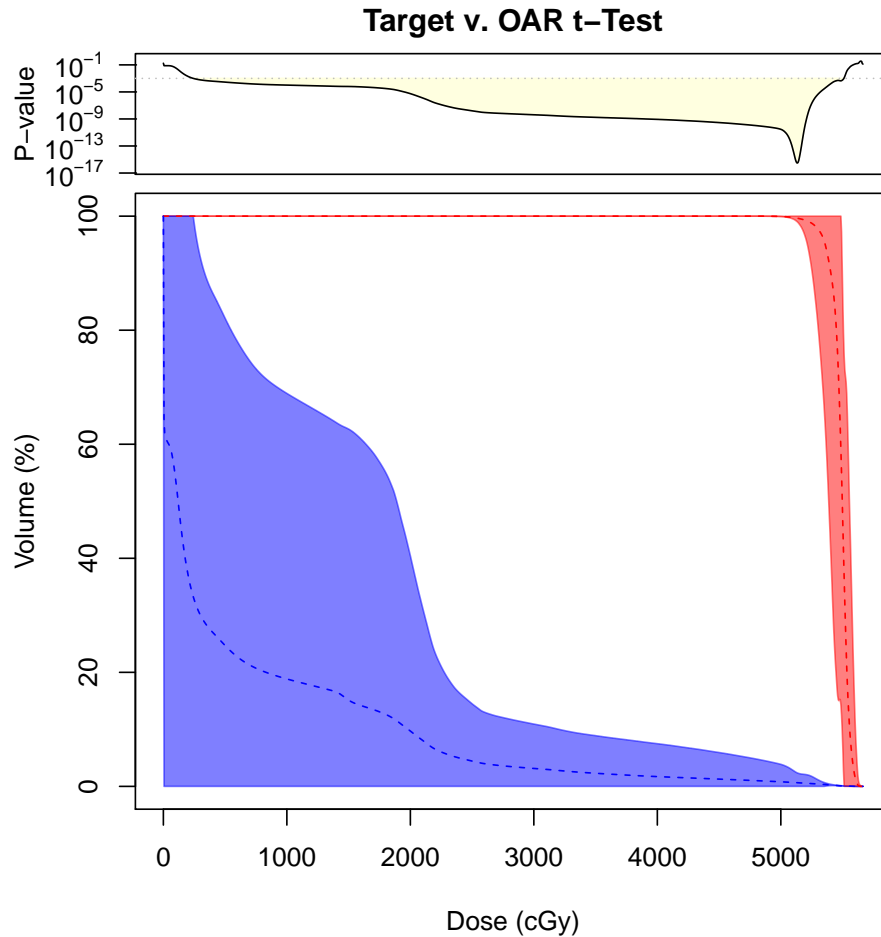
Target v. OAR t–Test

Figure 4: Mean dose-volume histograms are shown for two groups of DVHs, in this case corresponding to CTV/PTV and liver/stomach/small bowel from two different patients (John Doe and Jane Doe). Data is shown as cumulative dose (absolute) versus volume (relative). Shading represents the 99.9% confidence interval for each group (specified here by `alpha=0.001`). The corresponding p-values are shown in the upper panel, with corresponding significance threshold p<0.001.

```
> plot(janedoe[2:9], plot.type="b", volume="abs", dose="rel")
```
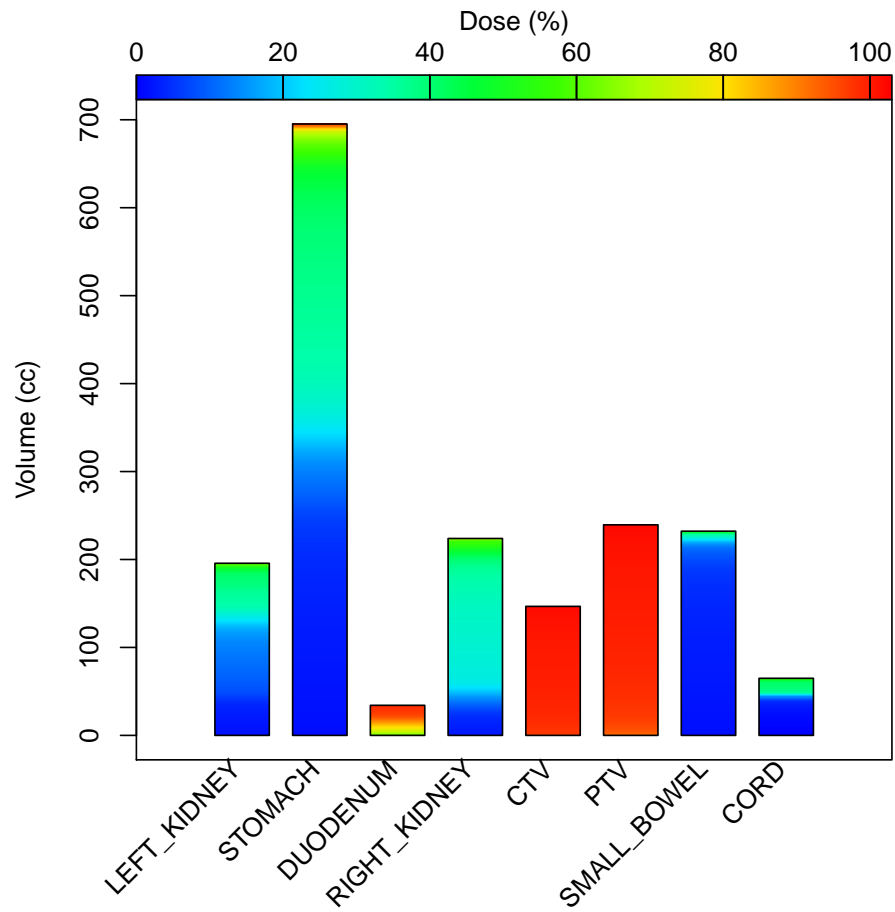

Figure 5: Bar representation of dose distributions for eight structures from a single patient (Jane Doe).

7 DVH statistics

Mean or median DVHs can be calculated using the `mean()` and `median()` functions, respectively. These functions take a DVH list as input and return a single object of class `DVH` representing the mean or median dose-volume histogram data calculated from the entire group.

```
> plot(janedoe)
> plot(median(janedoe), new=FALSE, col="red", lwd=2)
> plot(mean(janedoe), new=FALSE, col="blue", lwd=2, lty="dashed")
```
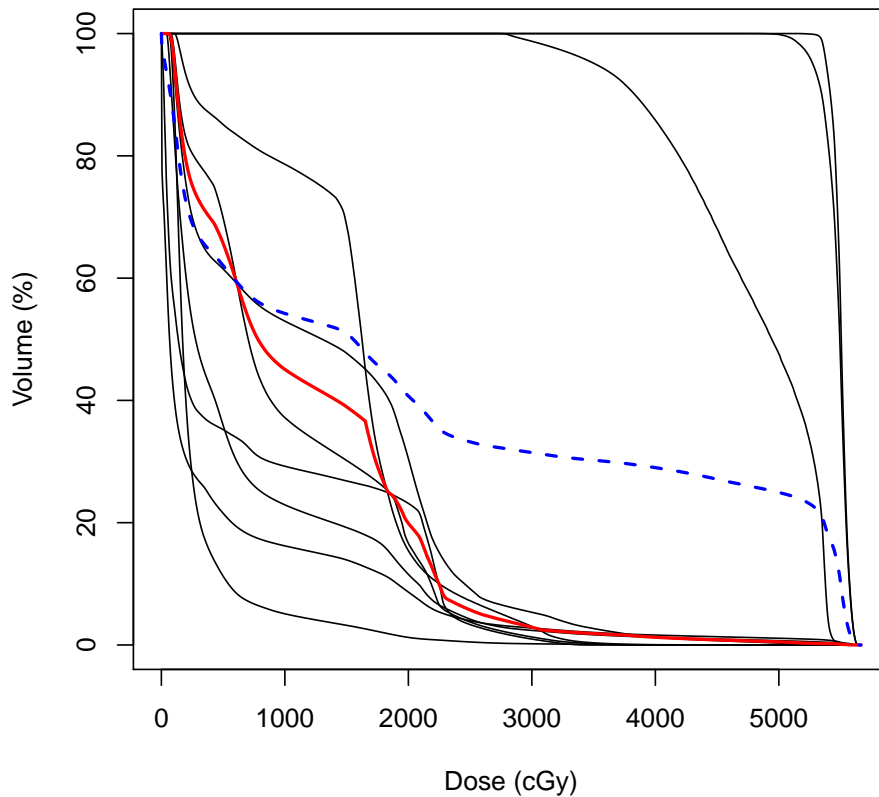

Figure 6: Mean and median DVHs are shown in blue dash and red, respectively.

In routine clinical practice and research, DVH comparisons are often performed at an individual parameter level (e.g. V20Gy from Group A compared to Group B). The *RadOnc* package enables automated comparison throughout the entire DVH. Functions such as `t.test()` and `wilcox.test()` are both enabled for DVH lists.

```
> groupA <- janedoe[c("LIVER","LEFT_KIDNEY","RIGHT_KIDNEY","CORD")]
> groupB <- janedoe[c("CTV", "PTV")]
> t.test(unlist(groupA$"V20Gy"), unlist(groupB$"V20Gy"))

        Welch Two Sample t-test

data:  unlist(groupA$V20Gy) and unlist(groupB$V20Gy)
t = -34.5156, df = 3, p-value = 5.347e-05
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -90.99543 -75.63187
sample estimates:
mean of x mean of y
 16.68635 100.00000
```

```
> AvB <- t.test(groupA, groupB)
> plot(AvB$dose, AvB$p, type="l", log="y", xlab="Dose (cGy)", ylab="p-value")
```
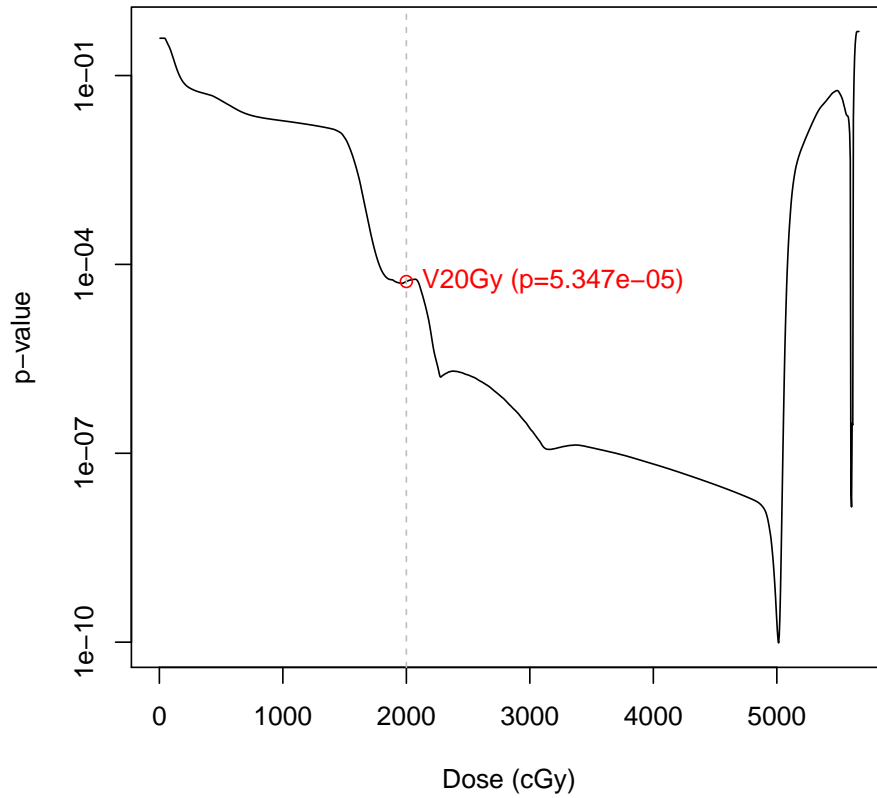

Figure 7: p-values from `t.test()` comparison as a function of dose. V20Gy is highlighted and its p-value corresponds closely to values generated from t-test of V20Gy directly.

References

R.E. Drzymala, R. Mohan, L. Brewster, J. Chu, M. Goitein, W. Harms, and M. Urie. Dose-volume histograms. *Int J Radiat Oncol Biol Phys*, 21(1):71–78, 1991.

A Previous Release Notes

- No previous releases to date.