Getting Started with Package `sampSurf`

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1   Introduction

The `sampSurf` package is designed to facilitate the comparison of new and existing areal sampling methods through simulation. The package is thoroughly documented in several vignettes as mentioned below. This document is meant to point you in the right direction in finding the needed information to get started using `sampSurf`.

2   Installation

`sampSurf` is installed like any other package. If you are not familiar with the routine, please check out the help for installing packages with `?install.packages`. You can install the package from within R with. . .

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```
R> install.packages('sampSurf')
```

Obviously, you can add other arguments to this command as required—see
the help page for details. Note that there are several dependencies (other
packages—see below) that will be installed if you do not have them installed
already.

Then load the package with...

```
R> library(sampSurf)
```

2.1 Dependancies

The `sampSurf` package depends on several other packages, which should be
installed automatically with the command given above. In addition, it 'sug-
gests' both the `rgl` and `rgeos` packages, which must be installed separately.
The `rgl` package allows one to visualize the sampling surface in three dimen-
sions and is not necessary for basic functionality, so installation is optional.
To look at the different graphics in `sampSurf` using `rgl`, the `rasterVis`
package is now required as well, but will be installed automatically when
installing `sampSurf`. The `rgeos`[1] package was previously only used for the
so-called "chainsaw" protocol of sampling with fixed-area plots; therefore, if
you wanted to use this protocol, you needed to install the package. However,
as of version 0.7-2 it is also required for implementing the mirage method of
boundary correction, therefore it must be installed if you want to use this
correction method in simulations.[2] The system dependencies for both `rgl`
and `rgeos` might also be more than some people want to deal with for instal-
lation, so this is another reason to make it optional, allowing the majority
of `sampSurf` functionality without these if desired.

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[1]The `gpclib` package was originally used, but `rgeos` has replaced it due to the license
restrictions on the former.

[2]`rgeos` is still a suggested method as not everyone will want to use the mirage method.

3   sampSurf Package Vignettes

Several vignettes have been written for sampSurf. Unfortunately, when vignettes are distributed pre-compiled to CRAN[3], they do not get added to the list of vignettes for the package on the web site, even though they are indeed there and they will be installed when you install the package as shown above. You can, however, view these vignettes before installing sampSurf by simply downloading the package *.tar.gz file and looking in the sampSurf/inst/doc subdirectory. Alternatively the files reside in the /doc directory of the *.zip package file. The PDF files can be readily opened from there.

The second and better option is to install the package and then use R to open the vignettes from your installation. There are two steps as follows...

1. At the R prompt, type package?sampSurf to get to the help page.[4] Scroll to the bottom of this page and find the "Index" hyperlink, and choose it. Near the top of the page you will find links to vignettes; choose the last link that says "browse directory." The vignettes will be available to read on this page.

2. The second method is easier. Just use RShowDoc (see ?RShowDoc) to look at the vignettes. You will need to know their names for this, these are listed below, or can be found via the prior step.

```
R> RShowDoc('Overview', package='sampSurf')
```

3.1   Vignette summary

Each of the vignettes can be opened as shown above. They are outlined briefly as follows...

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[3]http://www.r-project.org/, then choose the CRAN link to the left, and a nearby mirror site

[4]Note that you need to also make sure that R's internal HTML help server is the default. The easiest way to do this is to add the following to your .Rprofile file: options(list(help_type = 'html',browser='firefox')) (or whatever browser you use).

- *Overview:* This document should normally be read first, it provides an introduction to the package and provides a simple example of generating a sampling surface simulation. It also provides the relationship between the class structures that are described in the vignettes that follow.

- *StemClass:* This vignette shows how to generate individual "Stem" class objects, as well as populations or collections of such objects.

- *TractClass:* The "Tract" class provides a site for the simulated population in the form of a sample plot, or a tract.

- *ArealSamplingClass:* Each sampling method has some mechanism for choosing down logs or standing trees in a probability sampling context. This class provides a number of different subclasses that contain the necessary information on how to construct inclusion zones under the desired sampling method or protocol.

- *InclusionZoneClass:* The combination of a "Stem" object and an "ArealSampling" object provides the necessary information required to construct the inclusion zone (the former provides the log or tree attributes, the latter the sampling protocol information). This vignette details examples of the use of this class and its constructors for different sampling methods.

- *InclusionZoneGridClass:* This is an intermediate class used by the package to generate the sampling surface from the inclusion zones. The casual user need not be concerned about this class as it is generally used behind the scenes while creating the sampling surface. However, there is plenty of detail available in the vignette for those that might want to contribute new methods.

- *sampSurfClass:* This details the final product—generation of a sampling surface from simulation.

- *monte:* This set of classes was created to make it easy to do "when is n sufficiently large?" experiments. In other words, it allows repeated Monte Carlo sampling from a given "sampSurf" object at different sample sizes and gives statistics on confidence interval coverage rates. Both normal theory and bootstrap intervals can be calculated.[5]

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[5]These classes are more general than being applicable only to "sampSurf" objects, so their definitions may be moved into a separate package in the future, with only "sampSurf" support left here.

- *MonteCarloSampling:* This vignette describes the classes and methods that can be used on "Stem" subclass objects for volume estimation by Monte Carlo methods.

- *sampSurfExtensions:* If you want to know more about how to add your own sampling method to the package, this is where to look. It is advisable that you familiarize yourself with the above vignettes first before undertaking programming a new method.

4   Help Files

sampSurf has an extensive help facility. The best place to start is with

```
R> package?sampSurf
```

as mentioned above. All of the help files can be accessed from this page.

There are also help files available for each class and method, which can be accessed individually as is normal in R. For example...

```
R> class?downLog
R> ?downLog
R> methods?downLog
```

The first line will display the help for the "downLog" class in your browser. The next line will display the help for the downLog generic function[6]. Finally, the different 'constructor' methods for making "downLog" objects is displayed.

The above can be followed for any classes in sampSurf. Please do see the above vignettes for extensive examples and documentation. Finally, the full system help available in PDF format can be downloaded from the R website for the project at CRAN; e.g., http://lib.stat.cmu.edu/R/CRAN/, and then choose the sampSurf link.

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[6]This is S4 terminology, if it does not make sense right now, don't worry about it, it is not essential for using the package

5   Summary

This has just been a short primer to get you going. I hope you find `sampSurf` useful.