Zero-fill User Manual (Version 1.0; Dec 12, 2014)

- Zero-fill is a program written in R for retrieving missing intensity ratio values in an metabolite-intensity data file initially generated by IsoMS. This program is part of the data processing software used for the chemical isotope labeling (CIL) LC-MS metabolomics platform.
- The zero-fill script is freely available for non-commercial use from www.mycompoundid.org.
- The instruction for using the zero-filling program is given below.
- 1) Download the zero-fill script from MyCompoundID.org.
- Assign the folder of zero-fill as the working folder of RGui by clicking: File → Change dir... (see below).

RGui (64-bit) - [R Console]	Contractory and the second second
R File Edit View Misc Packages Windows Help	
R version 3.0.1 (2013-05-16) "Good Sport" Copyright (C) 2013 The R Foundation for Statistical Computing Platform: x86_64-w64-mingw32/x64 (64-bit)	Browse For Folder
R is free software and comes with ABSOLUTELY NO WARRANTY. You are welcome to redistribute it under certain conditions. Type 'license()' or 'licence()' for distribution details.	Change working directory to: G:\Zero-filing Demo
Natural language support but running in an English locale R is a collaborative project with many contributors. Type 'contributors()' for more information and 'citation()' on how to cite R or R packages in publications. Type 'demo()' for some demos, 'help()' for on-line help, or 'help.start()' for an HTML browser interface to help. Type 'q()' to quit R. [Previously saved workspace restored]	Image: Computer Image: Solution of the second se
	Folder: Zero-filing Demo Make New Folder OK Cancel

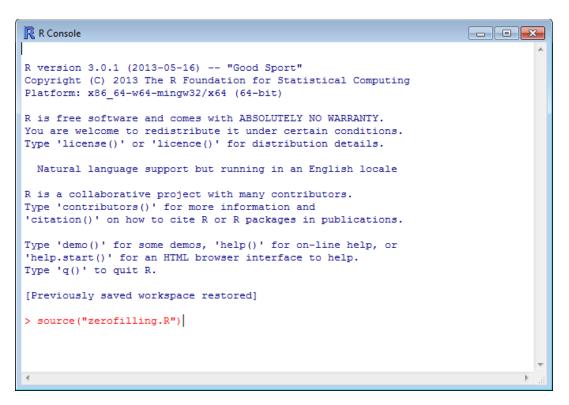
3) Open the zero-fill script (see below) and change the parameters therein (see Table 1 for the explanation of these parameters).

```
******
# This is a script to do zero filling for data file after alignment
# Tao Huan, Mar 19, 2014
# Copyright @ University of Alberta
# This is the setting part
aligned.file.path <- "G:/20140812 tumor tissues/IsoMS/IsoMS/"
raw.file.path <- "G:/20140812 tumor tissues/peak list/"
mz.tol = 5 # default 5 ppm
rt.tol = 30 # default 30 seconds
setwd(aligned.file.path)
aligned.file <- read.csv("Alignment_result.csv")
after.zerofill.file <- aligned.file
setwd(raw.file.path)
raw.file.list <- list.files(pattern = ".csv")</pre>
for (i in 1:(ncol(aligned.file) - 9)){
 print(paste("processing file", i))
```

Parameter	Function
aligned.file.path	Set the data path to the folder that contains the aligned
	dataset
raw.file.path	Set the data path to the folder that contains all the raw LC-
	MS data containing all the peak information
mz.tol	Set the mz tolerance during the zero-filling process
rt.tol	Set the retention time tolerance during the zero-filling
	process

Table 1. Zero-fill parameters that need to be changed according to the user's LC-MS instrumental conditions.

4) Save the parameter changes to the script. Type in the command code in RGui as shown in red in the following screen shot and press enter to run the script.



5) After running the script, a new csv file named "After zerofilling.csv" will be created. This csv file contains the zero-fill result.