Report

Background:

Solve the problems R program was used. In R, majorly “dplyr”, “tidyr”, and “reshape2” packages were used for data wrangling. And “ggplot2” and “ggbiplot” packages were used for graph visualization. For natural abundance correction package “accucor” was used for isoptop abundance correction. The usage details are given in the following sections.

library(dplyr)

library(ggplot2)

library(ggbiplot)

library(tidyr)

library(reshape2)

**Steps taken to manipulate data:**

The first step was to find the PCA for all given samples. PCA would broadly tell us if there is a difference between the samples, if so, then which samples would exhibit these differences.

Since PCA is a global approach, therefore it was wise (also suggested) to look at the changes in the metabolite levels at a gross level, that is at the pool total levels. In order to find the pool totals, the columns were