

```

Raw data load("Week 2 - Principal Component Analysis/drug_use.RData")MvB :
Not that you give the correct folder of the project. Preferably use Git repository
Inspect raw data, by means of simple
-princomp(drug_use, cor = TRUE)summary(res.raw)screepplot(res.raw, ylabs = '
Eigenvalue')biplot(res.raw, asp = 1, xlabs = rep("", nrow(drug_use)))screepplot(res.raw)
Compute proportion of drug use proportionally per individual (divide by row
sums) drug_use$share <- -drug_use/matrix(rowSums(drug_use), nrow = nrow(drug_use), ncol =
ncol(drug_use))res.share <- -princomp(drug_use$share, cor = T)summary(res.share)
screepplot(res.share) dev.print(png, "C:
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Week 2 - Principal Component Analysis
Screepplot_drug_use_raw.png", width = 400, height = 350)directly save to disk biplot(res.share, asp =
1, xlabs = rep("", nrow(drug_use)))dev.print(png, "C :
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Biplot_drug_use_raw.png", width = 400, height = 350)directly save to disk
Do a bootstrap on eigenvalues to see how stable the eigenvalues are. li-
brary("boot") Use the boot package boot.pca.fn j- function(data, index) Make
a function that returns the res j- princomp(drug_use$share[index, ], cor = TRUE)pcasingularvalues for data selected
by the vector index res.boot j- boot(drug_use$share, boot.pca.fn, R = 1000)Run 1000 bootstraps print(res.boot, digi-
3)Print bootstrap results plot(res.boot, index = 1)Histogram of 1st singular value of the bootstraps dev.print(png,
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Bootstrap_drug_use_first_singular_value.png", width = 400, height = 350)directly save to disk plot(res.boot, index =
2)Histogram of 2nd singular value of the bootstraps dev.print(png, "C :
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Bootstrap_drug_use_second_singular_value.png", width = 400, height = 350)directly save to disk boot.ci(res.boot, in-
1, type = "perc")[4]Show show 95

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