

4.2.4 more than 2 components

```
library(ggplot2)
library(tidyverse)
```

```
## Warning: package 'dplyr' was built under R version 4.2.3
```

```
## Warning: package 'stringr' was built under R version 4.2.3
```

```
## -- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
```

```
## v dplyr      1.1.4      v readr      2.1.4
```

```
## v forcats    1.0.0      v stringr    1.5.1
```

```
## v lubridate  1.9.3      v tibble     3.2.1
```

```
## v purrr      1.0.2      v tidyr      1.3.0
```

```
## -- Conflicts ----- tidyverse_conflicts() --
```

```
## x dplyr::filter() masks stats::filter()
```

```
## x dplyr::lag()     masks stats::lag()
```

```
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

beyond $n = 2$, $n = 4$ (4 nucleotides)

```
masses = c( A = 331, C = 307, G = 347, T = 322 )
```

```
probs  = c( A = 0.12, C = 0.38, G = 0.36, T = 0.14 )
```

```
n      = 7000 # 7000 nucleotides
```

```
sd      = 3
```

```
nuclt   = sample( length(probs), n, replace = TRUE, prob = probs)
```

```
quadwts = rnorm( length(nuclt),
                 mean = masses[nuclt],
                 sd    = sd )
```

```
ggplot(tibble(quadwts = quadwts), aes(x = quadwts)) +
  geom_histogram(bins = 100, fill = "purple")
```

