Using MLModern in R Markdown

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Sample text

For example, suppose we treat each gene as a *term* and say each sample is a *document.* In that case, we can use word embedding methods in NLP like `word2vec` or `GloVe` to learn low-dimensional vector representations for genes, given the gene expression count data for a collection of samples.

$$\mathrm{E}\left[(T\left(F_n\right) \; T(F))^r\right] = \mathrm{E}\left[\left(\sum_{j=1}^{k} T_{j,n}/j!\right)^r\right] + o\left(n^{(r+k1)/2}\right)$$

Traditional methods might assume two genes are similar if they have highly correlated expression profiles or overlaps in labels. In contrast, we assume that two genes are only similar if their **expression context** is similar, i.e., the groups of genes that frequently express together with them are similar.

Sample code block

```r
#' Classify any file into text or binary
is_text_file <- function(path, n = file.info(path)$size) {
  bytecode <- readBin(path, what = "raw", n = n)

  if (length(bytecode) == 0L) return(FALSE)

  allow <- as.raw(c(9, 10, 13, 32:255))
  block <- as.raw(c(0:6, 14:31))
  cond1 <- any(bytecode %in% allow)
  cond2 <- !any(bytecode %in% block)

  cond1 && cond2
}
```