**Approach**

The simplest approach starts with the realization that the longest common substring can not be longer than the shortest string we're looking at. It should also be obvious that if we start with the longest possible candidate and only examine shorter candidates after eliminating longer ones, then we can stop as soon as we find a common substring.

So, we begin by sorting the DNA strings by length and removing the shortest to a privileged position. This can be either outside the list, or at position zero of the list, whichever you prefer, but we'll call that one [Holmes](http://en.wikipedia.org/wiki/Jon_Holmes), and we'll refer to the length of Holmes as l.

Once we've identified our Holmes string, the obvious procedure is to test its substrings, beginning with the single substring of length l, and then the two substrings of length l-1, and so forth, until a match is found and we return it.