De novo assembly exercise

Todos Santos Genomics Workshop 2019

Your job in this exercise is to de novo assemble the 'genome' from which the 'reads' below derive.

Rules/info:
(*) Like real sequencing data, these reads contain errors. The error rate is ~2%
(*) These are single-end 11-base reads
(*) The average coverage is ~6x
(*) You're not allowed to google the answer
(*) You can use your computers (i.e. word processors or text editors) or paper and whatever strategy you want to do the assembly...

```
_gew_kjinns
n_outdjinn_
djinns_that
_are_djinns
will_get_dd
en_if_they_
_if_they_ar
_will_get_d
hat_can_out
will_get_dj
_djinns_tha
_if_they_ar
get_djinns_
_can_outdji
_j_will_get
_outdjinn_t
djinns_i_wi
re_djinns_i
e_djinns_i_
ven_if_they
t_can_outdj
_ehat_can_o
_djinns_tha
t_djinns_th
l_get_djinn
en_if_they_
en_if_they_
y_are_djinn
an_outdjinn
ns_i_willpg
t_can_outdj
an_outdjinn
inns_i_will
jinns_i_wil
that_gan_ou
```

This exercise was inspired by and created using C. Titus Brown's Assembly Exercise:
http://ivory.idyll.org/blog/the-assembly-exercise.html