```python
#!/usr/bin/env python
# -*- coding: utf-8 -*-

# fasta_reorder-join_v1.py
# version: 1.0
# By: Eric Normandeau
# Last revision: 2010-11-11

"""Reorder sequences from a fasta file and join them.
"""

### WARNINGS!
# This program has the following known limitations:
# - Output fasta sequences are not wrapped
# - No documentation/help
# - Prints useless information to standard output
# - Memory intensive for very large fasta files
# - Not thoroughly tested


## Import modules
import sys
import re
from Bio import SeqIO

# Parse program options
fasta_file = sys.argv[1]  # Input fasta file
order_file = sys.argv[2]  # Input wanted file, one name per line
output_file = sys.argv[3] # Output fasta file

# Build list of sequence order from file
order = list()
with open(order_file) as f:
    for line in f:
        line = line.strip()
        if line != "":
            order.append(line)
print order

# Input sequences and prepare variables
fasta_sequences = SeqIO.parse(open(fasta_file),'fasta')
fasta_dict = {}
final_sequence = ""

# Create dictionary of sequences (name: sequence)
for s in fasta_sequences:
    fasta_dict[s.id] = s.seq.tostring()
print fasta_dict

# Open output file, join sequences, print to file
with open(output_file, "w") as f:
    for s in order:
        print s, fasta_dict[s]
        final_sequence += fasta_dict[s]
    f.write(">final_sequence\n")
    f.write(final_sequence)

print "Total sequence:"  # Remove from final program
print final_sequence  # Remove from final program
```