My goal here is to automatically produce a multiple sequence alignment between any number of given sequences, and a given HHOMP cluster.

Input: Any number of z-aligned PDB files, the name of a cluster, the name of a matrix, and the time for the matrix (if relevant)

Output: A multiple sequence alignment.

Core function:

Input: a filename containing sequences, and a filename of a matrix.

Output: a multiple sequence alignment.

Cluster-retriever:

Input: a cluster name.

Output: a multiple sequence alignment object

Sequence-retriever:

input: filenames of pdb files

output: seqrecord objects

Combinator:

input: a multiple sequence alignment and some sequences

make a list containing every *real* sequence in the MSA, and the given sequences

create a file containing all the sequences in FASTA format, using Bio.SeqIO

output: nothing

Matrix-retriever:

input: a description of a matrix.

may have to create the files for the matrix  
output: filename of a matrix file readable by clustal