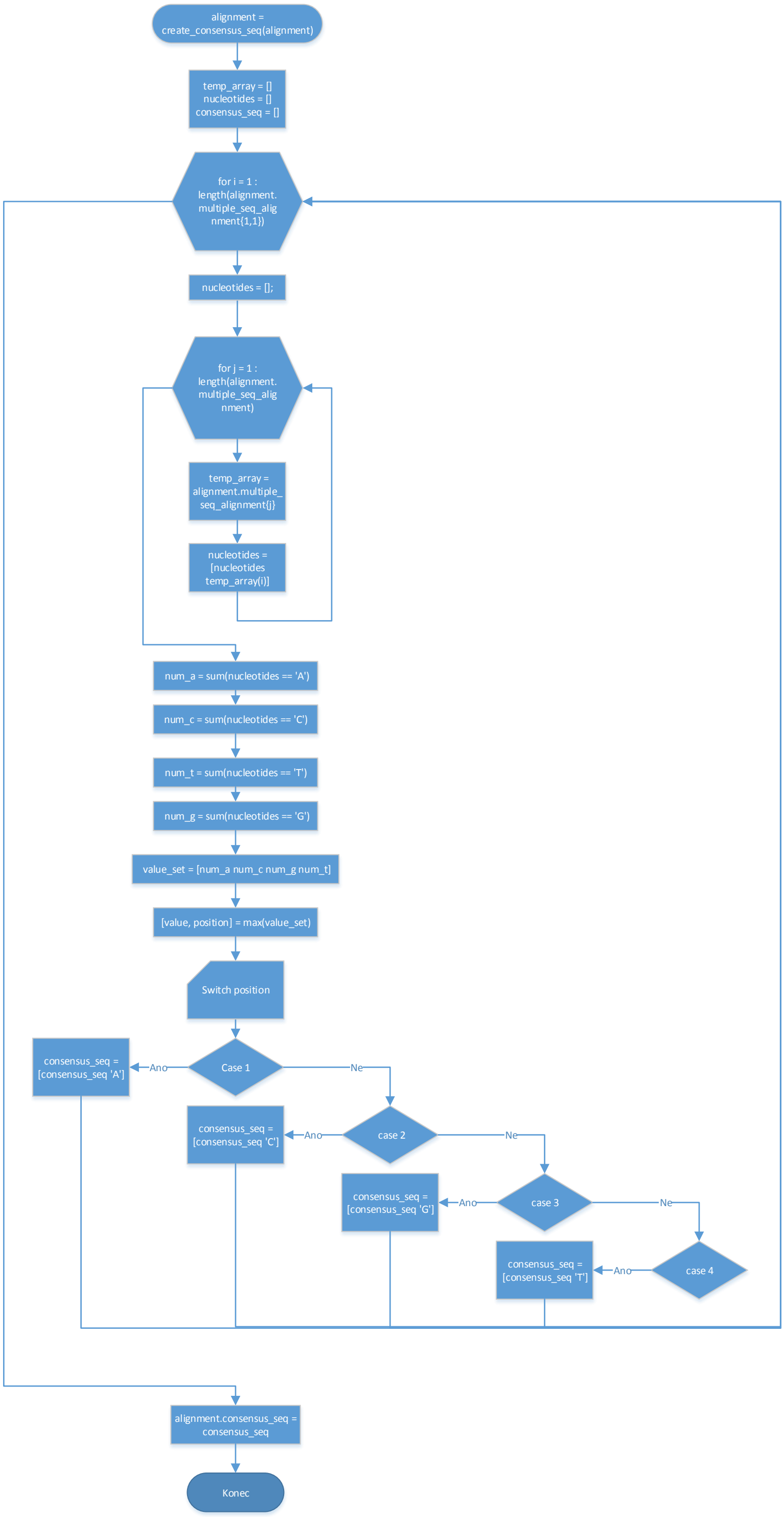
alignment = create_consensus_seq(alignment)
temp_array = []
nucleotides = []
consensus_seq = []
for i = 1 : length(alignment.multiple_seq_alignment{1,1})
nucleotides = [];
for j = 1 : length(alignment.multiple_seq_alignment)
temp_array = alignment.multiple_seq_alignment{j}
nucleotides = [nucleotides temp_array(i)]
num_a = sum(nucleotides == 'A')
num_c = sum(nucleotides == 'C')
num_t = sum(nucleotides == 'T')
num_g = sum(nucleotides == 'G')
value_set = [num_a num_c num_g num_t]
[value, position] = max(value_set)
Switch position
Case 1
Ano
consensus_seq = [consensus_seq 'A']
Ne
case 2
Ano
consensus_seq = [consensus_seq 'C']
Ne
case 3
Ano
consensus_seq = [consensus_seq 'G']
Ne
case 4
Ano
consensus_seq = [consensus_seq 'T']
alignment.consensus_seq = consensus_seq
Konec