```
    seqfile = seqfile.txt   * sequence data filename
    outfile = results.txt    * main result file name


      noisy = 9        * 0,1,2,3,9: how much rubbish on the screen
    verbose = 1        * 1:detailed output
    runmode = -2       * -2:pairwise


    seqtype = 1        * 1:codons
  CodonFreq = 0        * 0:equal, 1:F1X4, 2:F3X4, 3:F61 [CHANGE THIS]
      model = 0        *
    NSsites = 0        *
      icode = 0        * 0:universal code


  fix_kappa = 1        * 1:kappa fixed, 0:kappa to be estimated [CHANGE THIS]
      kappa = 1        * fixed or initial value


  fix_omega = 0        * 1:omega fixed, 0:omega to be estimated
      omega = 0.5      * initial omega value
```

Further details for about the assumptions tested in Excercise 2

Assumption set 1:   **Codon bias = none;**   **Ts/Tv bias = none**
Control file..   CodonFreq=0;   kappa=1; fix_kappa=1

Assumption set 2:   **Codon bias = none;**   **Ts/Tv bias = Yes**
Control file..   CodonFreq=0;   kappa=1; fix_kappa=0

Assumption set 3:   **Codon bias = yes [F3x4];**   **Ts/Tv bias = none**
Control file..   CodonFreq=2;   kappa=1; fix_kappa=1

Assumption set 4:   **Codon bias = yes [F3x4];**   **Ts/Tv bias = Yes**
Control file..   CodonFreq=2;   kappa=1; fix_kappa=0

Assumption set 5:   **Codon bias = yes [F61];**   **Ts/Tv bias = none**
Control file..   CodonFreq=3;   kappa=1; fix_kappa=1

Assumption set 6:   **Codon bias = yes [F61];**   **Ts/Tv bias = Yes**
Control file..   CodonFreq=3;   kappa=1; fix_kappa=0

Overview of the three different ways to model codon frequencies that are evaluated in Exercise 2.

Example: A → C

AAA → **C**AA

A**A**A → A**C**A

AA**A** → **AAC**

	Target codon (nucleotide)			
	CAA	**ACA**	**AAC**	**NP**
Fequal	1/61	1/61	1/61	0
F3×4 (GY)	$\pi_C^1\pi_A^2\pi_A^3$	$\pi_A^1\pi_C^2\pi_A^3$	$\pi_A^1\pi_A^2\pi_C^3$	9
F61 (GY)	π_{CAA}	π_{ACA}	π_{AAC}	61

NOTE: There are **even more ways** to model frequencies; but these are the only one we will deal with in this lab.