Interpreting MRS Results from LCModel + Performing the CSF correction
(please contact <u>sofia.chavez@camhpet.ca</u> for further assistance/clarification)

1. Qualitative evaluation:
- check baseline (bottom black line) : it should have no large dips or hills
- check noise/left-over after fit (top plot): it should be random and centred on 0 without any obvious structure (a few 'blips' around 3.6-3.8 is OK)
- the 3 peaks (Cho-Cr-NAA) should be apparent and more or less in order: Cho<Cr<NAA (except in cerebellum where Cr=NAA)

2. Quantitative evaluation:
- under: MISCELLANEOUS OUTPUT, accept only if: FWHM<0.1 and S/N>10
- check Cramer-Rao bounds (%SD): should be <20% (ideally, <15%)

Always check the size of your voxel along the title. It should remain the same for a given protocol.

Both Conc. (which is in institutional units (i.u.) -not absolute- scaled to the water peak, also called water-referenced) and /Cr+PCr should be used and effects on both can be studied (if no changes in Cr+PCr are expected, both should yield the same trends).

3. CSF correction

Here is a paper that uses the correction and explicitly writes the "formula" (see Eq.[2] of Jang et al, 53:708 –712, MRM 2005, DOI 10.1002/mrm.20387).

Please be aware that when I refer to concentration (conc) I don't mean absolute in mmol or anything because we have not corrected for various things (T1,T2..) to get that. We are always referring to a relative concentration but at least you can compare across subjects or time points for a given protocol if you do the following *CSF correction* to the first column of the LCmodel output (water-referenced values):

(conc in voxel)=(conc in tissue)*(fraction of tissue in voxel)

We measure (conc in voxel) but want (conc in tissue), also using the fact that:

fraction of tissue in ROI (f_t) + fraction of CSF in ROI (f_csf)=1
i.e. $f\_t+f\_csf=1$

We can write:

conc in tissue=(conc in voxel)/f_t
conc in tissue=(conc in voxel)/(1-f_csf) *** this is Eq.[2] given in the paper above ****

I don't think it is necessary to write this equation nor reference this paper in your work, just state the method you used to get f_t (what segmentation algorithm did you use) and then state that you performed a CSF correction to the water-referenced values.