MS04-P03 | Efficient Real-Space Refinement For Cryo-Em And Crystallography

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Recent progress in cryoEM made it possible to refine atomic models against cryoEM maps, ρ_{exp}, at resolutions ~2.5–3Å. Usually such real-space refinement calculates a map ρ_{model} from an atomic model and matches it with ρ_{exp}, e.g. by calculating their correlation value *CCmaps*. An accurate but computationally expensive way to calculate ρ_{model} is by obtaining the model Fourier coefficients, truncating them up to the resolution of ρ_{exp} and calculating the respective Fourier series. Alternatively, ρ_{model} can be calculated as a sum of contributions of individual atoms where each contribution reflects the resolution of ρ_{exp}. In both cases, the calculation time of the refinement target grows at least as a product of the number of atoms by a cube of the value inverse to the grid step of the map.

We have developed a new refinement procedure *phenix.real_space_refine* [1] that does not require calculating ρ_{model} at all thus saving both the computational time and memory. We showed that *CCmaps* can be approximated by a sum of the ρ_{exp} values in the positions of atomic centers for any resolution and not only at a very low resolution as suggested earlier [2]. This leads to the refinement algorithm with a very low computational cost independent of the grid size. In turn, this allowed to automate a number of refinement stages, e.g. the weight optimization between the data and restraints terms.

[1] Afonine_et_al.,2018,*ActaCryst.,*D**74**,531
[2] Rossmann,2000,*ActaCryst*.,D**56**,1341