CHOYCE: a web server for constrained homology modelling with cryoEM maps

Reda Rawi, Lee Whitmore and Maya Topf

Abstract: CHOYCE is a web server for homology modelling of protein components and the fitting of those components into cryo electron microscopy (cryoEM) maps of their assemblies. It provides an interactive approach to improving the selection of models based on the quality of their fit into the EM map.

Methods

1. CHOYCE input

- The server requires a density map and its parameters including the origin (in respect to the Cartesian coordinates) and the resolution (Å). The density map format can be either CCP4/MRC or XPLOR and its size must be smaller than 2 GB. It provides two input options: (i) an aligned pair of a target sequence and a template structure and (ii) an unaligned pair. In both cases, the template has to be pre-fitted into the density map, or at least placed in an approximated position.

2. Homology modelling

- In the first step, CHOYCE generates homology models for the target sequence using the automodel class of the MODELLER-9v7 python interface (Eswar et al., 2008; Sali and Bhundel, 1993). If the first input option is selected, CHOYCE uses the given target-template alignment to calculate n models, as requested by the user. If the second input option is selected, it generates l different alignments (as requested by the user) using the align method (align or align2d) in MODELLER-9v7 (Madhusudan et al., 2009), including one optimal alignment, and l–1 suboptimal alignments (Saqi and Sali, 1991). Ten models are then built per alignment (n = 10 × l) and each of them is assessed by the statistical potential score DOPE (normalized_dope method in MODELLER-9v7) (Shen and Sali, 2006).

3. Density fitting and model assessment

- In the next step, CHOYCE selects the model with the lowest DOPE score, and starting from the initial position for the template fitted into the input density map, it fits the model locally within the map. The local fitting is performed using the Scanning Monte Carlo (SMC) optimization option of Mod-EM (density.grid_search in MODELLER-9v7; Topf et al., 2005), with the “SPECIFIC” and “GAUSS” options for the starting position and the atomic density function, respectively. Next, all the remaining models are superposed onto the fitted template structure. Each of the models is then scored in the map based on their CCF with the MAP (Topf et al., 2005).

- A typical CHOYCE job of modelling and fitting 50 models of 200 amino acids is completed in ~10 min (independent of the size of the map). The computational cost scales linearly with the size of the protein and the number of models generated.

1 Institute of Structural and Molecular Biology, Crystallography, Department of Biological Sciences, Birkbeck College, University of London, London, UK and 2 Department of Bioinformatics, Center for Medical Biotechnology, University of Duisburg-Essen, Universitaetsstr. 1-5, 45141, Essen, Germany

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CHOYCE results appear in a web-based table, which may be accessed via a hyperlink automatically e-mailed to the user when the job is completed. The table consists of the names of n homology models built for the input target sequence and fitted in the EM map, sorted based on their CCF score (the highest score at the top). For each model both the CEF score and the normalized-DOPE score are reported. The coordinates of each model can be downloaded in a PDB format.

3 CASE STUDIES

As test cases, we used CHOYCE to generate two comparative models, one constrained by a simulated density map and the other by an experimental cryoEM map. In both cases, to measure the accuracy of the models, we calculated Cα RMSDs from the known native structures using least-square minimizations (model.superpose in MODELLER-9v7).

The first model is of subunit III of bovine heart cytochrome c oxidase, based on the structure of E.coli ubiquinol oxidase (PDB id: 1FFT, chain C, 22% sequence identity). The density map was generated from the native structure of cytochrome c oxidase (PDB id: 1OCC, chain C, residues 74–261) using the molmap command in Chimera (Petterson et al., 2004). We then used CHOYCE option 2align2d to generate 50 models based on five alignments to 1FFT, and scored them applying the local fit first.

The second model is of the S.cerevisiae receptor of activated protein kinase C 1 (RACK1) (PDB id: 3FRX, chain A, residues 5–317), based on the structure of its homolog from Arabidopsis thaliana (PDB id: 3MDO, chain A, 49% sequence identity). For fitting, we used the 8.9 Å resolution cryoEM density map (EMDB ID: 1344, >85% sequence identity to S.cerevisiae). Because the density associated with RACK1 was identified on the small subunit (40S) where it is bound near the mRNA exit, we used only the density of the small subunit, which was previously segmented from the entire 80S density (Taylor et al., 2009). We then fitted 3MDO into the associated density and used CHOYCE option 2align to generate and score 100 models based on 10 alignments to 3MDO, and scored them in the position of the fitted template.

In both test cases, the best-fitted model is the most accurate model (ranked first among 50 and 100 models, respectively). For 1OCC, the best model has Cα RMSD of 3.00 Å from the native structure. It is 18.5% more accurate than the best model based on the normalized-DOPE score (Cα RMSD = 3.68 Å, ranked last, Fig. 1). For RACK1, since the range of accuracy of the models was quite small (Cα RMSD between 2.84 and 3.07 Å), the best-fitted model is only slightly more accurate than the best normalized-DOPE model (2.84 Å versus 2.94 Å), although ranked much higher (1 versus 40) (Supplementary Fig. 1).

4 CONCLUSION

The CHOYCE web server provides a platform for homology modelling and fitting into cryoEM maps. The server aids in selecting one of the most accurate models from an ensemble of models based on the goodness-of-fit to the EM map. Future improvements will include modelling based on multiple template structures, as well as iterative alignment, fitting and refinement using a combination of CCF and statistical potential scores (Topf et al., 2005, 2006).

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