Errata to "DiffFit: Visually-Guided Differentiable Fitting of Molecule Structures to a Cryo-EM Map" by Deng Luo, Zainab Alsuwaykit, Dawar Khan, Ondřej Strnad, Tobias Isenberg, Ivan Viola (Digital Object Identifier no. 10.1109/TVCG.2024.3456404)

The authors would like to make the following errata after correcting the initialization related bugs in the associated program.

On page 1, the last two sentences of Fig. 1's caption should be "Right: the final composited structure overlaid on the original target volume (RMSD: 0.138). The involved computation takes 10 seconds in total, and the human-in-the-loop interaction takes ≈3 minutes." On page 5, "10-element array" should be "3-element array." On page 10, in the ACKNOWLEDGMENTS section, the authors add: "The authors also thank Alexandra Irger for her narration in the submission video." The authors also make changes to Fig. 3 (c−f), Fig. 4, Table 1−3, which are attached below, and an updated attachment "ExpRes.xlsx" in the supplementary materials.

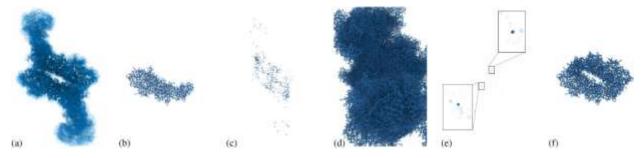


Fig. 3: Clustering and filtering: (a) target volume, (b) atom coordinates of the source structure, (c) positions of 1000 fit results (the dots are clustered, hiding the number of results), (d) 1000 instances of the structure, (e) positions of 1000 fit results with a transparency level set based on an exponential scaling of the sum of sampled density metric (two clusters stand out, as in the zoom-in insets), and (f) instances of the structure at those two clusters.

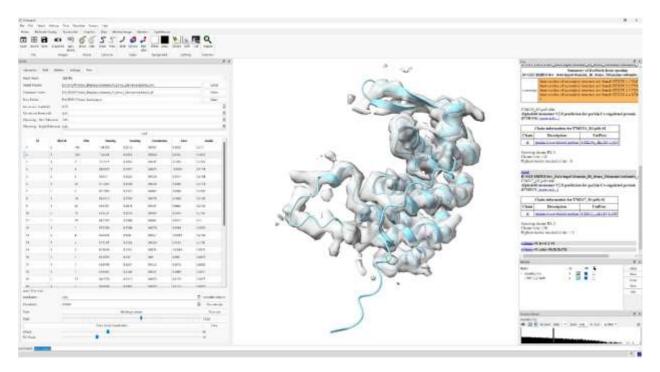


Fig. 4: Visual browser based on ChimeraX. The target volume on the middle is overlaid with a fitted molecule corresponding to the selected fit result in the table on the left (clustered fits, each row is the representative placement with the highest correlation from that cluster). After inspection, users can save the placement and then select "Simulate volume" and "Zero density" to zero out the corresponding voxels from the target volume.

Table 1

PDB	Res	Hit rate			Comp	outing	time	RMSD (Å)					
		C	D	G	C	D	G	M	c	D	DC		
6WTI	2.38	0.0	136.8	n/a	150.3	3.8	39.7	1.310	n/a	0.942	0.037		
7D8X	2.60	0.0	202.0	n/a	196.0	5.2	37.6	1.960	n/a	0.984	0.014		
7SP8	2.70	4.6	188	40.9	130.6	2.6	50.5	1.290	0.996	0.969	0.025		
7STE	2.73	14.0	110.4	7.9	806.1	12.1	66.6	1.740	0.062	0.662	2 0.015		
7JP0	3.20	5.4	191.8	35.5	250.7	6.7	37.2	2.540	0.017	0.922			
7PM0	3,60	44.0	195.4	4.4	352.4	4.1	86.7	1.640	0.030	0.907			
6M5U	3.80	0.0	105.0	n/a	162.2	4.1	39.2	2.360	n/a	0.912	0.018		
6MEO	3.90	7.4	116.0	15.7	128.2	3.2	40.1	1.940	0.489	0.786	0.488		
7MGE	3.94	4.8	123.6	25.8	337.6	4.3	78.1	1.870	0.017	0.819	0.017		
High-avg		8.9	152.1	21.7	279.3	5.1	52.8	1.850	0.268	0.878	0.077		
5NL2	6.60	1.8	163.2	90.7	94.6	2.0	48.0	2.440	0.093	1.124	0.056		
7K2V	6.60	49.0	165.6	3.4	240.6	4.1	58.2	25,290	0.338	1.323	0.338		
7CA5	7.60	55.8	72.4	1.3	322.6	2.9	110.0	3.290	2.042	1.207	2.042		
5VH9	7.70	68.6	158.0	2.3	1147.8	14.1	81.3	0.960	0.085	0.991	0.085		
6AR6	9.00	78.0	182.6	2.3	74.9	1.5	49.3	2.200	0.123	2.617	0.117		
311Z	13.00	138.6	172,2	1.2	64.4	2.0	33.0	32,330	0.396	2.612	0.388		
Med-avg		65.3	152.3	16.9	324.1	4,4	63.3	11.085	0.513	1.646	0.504		
All-avg		31.5	152.2	19.8	297.3	4.9	57.0	5.544	0.366	1.185	0.248		

Table 2

Structure	C Hit	D Hit	Gain		
17MLV6_D3	108	254	2.4×		
I7M317_D1	127	240	1.9×		

Table 3

PDB	EMDB	#S	#A	Res	s Vs	L	Hit rate			Computing time			RMSD (Å)			
		тэ	m/A	into.			C	D	G	C	D	G	M	C	D	DC
6WTI	21897	4	9,980	2.38	1.08	0.7660	0.0	136.8	n/a	150.3	3.8	39.7	1.310	n/a	0.942	0.037
7D8X	30614	4	10,928	2.60	1.08	0.0229	0.0	202.0	n/a	196.0	5.2	37.6	1.960	n/a	0.984	0.014
7SP8	25368	3	6,090	2.70	1.08	5.5755	4.6	188	40.9	130.6	2.6	50.5	1.290	0.996	0.969	0.025
7STE	25426	5	14,249	2.73	0.83	0.0963	14.0	110.4	7.9	806.1	12.1	66.6	1.740	0.062	0.662	0.058
7JPO	22417	5	16,087	3.20	1.07	0.0240	5.4	191.8	35.5	250.7	6.7	37.2	2.540	0.017	0.922	0.015
7PM0	13508	3	10,169	3.60	1.10	0.0068	44.0	195.4	4.4	352.4	4.1	86.7	1.640	0.030	0.907	0.024
6M5U	30093	3	10,549	3.80	1.06	0.0350	0.0	105.0	n/a	162.2	4.1	39.2	2.360	n/a	0.912	0.018
6MEO	9108	3	7,465	3.90	1.06	0.0500	7.4	116.0	15.7	128.2	3.2	40.1	1.940	0.489	0.786	0.488
7MGE	23827	4	9,010	3,94	0.94	0.2550	4.8	123.6	25.8	337.6	4.3	78.1	1.870	0.017	0.819	0.017
High-	avg	3.78	10,503	3.21	1,03	n/a	8.9	152.1	21.7	279.3	5.1	52.8	1.850	0.268	0.878	0.077
5NL2	3658	2	4,312	6.60	1.35	0.0297	1.8	163.2	90.7	94.6	2.0	48.0	2,440	0.093	1.124	0.056
7K2V	22647	2	5.717	6.60	1.05	0.0050	49.0	165.6	3.4	240.6	4.1	58.2	25.290	0.338	1.323	0.338
7CA5	30324	2	6,484	7.60	1.06	0.0100	55.8	72.4	1.3	322.6	2.9	110.0	3.290	2.042	1.207	2.042
5VH9	8673	2	22,042	7.70	1.20	0.0074	68.6	158.0	2.3	1147.8	14.1	81.3	0.960	0.085	0.991	0.085
6AR6	8898	2	2,395	9.00	3.00	0.0739	78.0	182.6	2.3	74.9	1.5	49.3	2.200	0.123	2.617	0.117
3J1Z	5450	2	4,586	13.00	2.74	3.8989	138.6	172,2	1.2	64.4	2.0	33.0	32.330	0.396	2.612	0.388
Med-avg		2.00	7,589	8.42	1.73	n/a	65.3	152.3	16.9	324.1	4.4	63.3	11.085	0.513	1.646	0.504
All-av	g	3.01	9,337	5.29	1.31	n/a	31.5	152.2	19.8	297.3	4.9	57.0	5.544	0.366	1.185	0.248