Tutorial

MoProSuite : Crystallographic software

for charge density refinement

http://crm2.univ-lorraine.fr/lab/software/mopro/download-mopro/

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MoProSuite working under Windows, linux & mac.

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Step 1 Lauch MoProGUI

MoPro Graphical User Interface

Colored → MoProSuite 1407 →	MoProGUI - D:\Users\Ch	nristian\Desktop\jelsch_pavia\	alamet_tutorial			
	<u>File Edit M</u> oPro <u>V</u> MoP	Pro MoProV <u>i</u> ewer Molly <u>n</u> x	<u>H</u> elp			
퉲 bin-linux32	MoPro Input File 🗙					
鷆 bin-linux64	∃ mopro.inp Files	Files				
퉬 bin-mac		Molecular structure		Browse	Edit	< previous
퉬 bin-win32			II			next >
퉬 Doc						
퉬 examples		Reflections hkl		Browse		
퉬 LibMoPro						
퉬 MoProGUI		Bulk solvent Fhkl		Browse		
퉬 MoProViewer-linux32						
퉬 MoProViewer-linux64		Atomic Table	D:\MoProSuite\LibMoPi	Browse	Edit	
퉬 MoProViewer-mac		Ways Expetience	DuMaBraQuital ibMaBr	Drawaa	Edit	
퉬 MoProViewer-win32		Vvave Functions	D.MoProSulle/LIDMOPI	Browse	Eall	
) Publications		Anomalous asf Kissel	D:\MoProSuite\LibMoPr	Browse		
install.sh]			
MoProGUI_1407.jar	Comment/Activate	Constraints		Browse	Edit	
moproviewer.log	Remove		,I			
RunMoProGUI	Run MoPro	Restraints		Browse	Edit	
	Run morro					

Requires JAVA, which can be downloaded at: https://www.java.com/fr/download/

Step 2 initial steps : follow the GUIDE



Step 3 Display molecule with MoProViewer



Step 4 Select reflections file

MoPro Guide
Set working directory
Import molecular file
Set molecular file
Display molecule
Set hkl file
Refine scale factor
Database transfer
Prepare constraints/restraints
Refine structure
Refine charge density
Deconstrain charge density
Refine all parameters
Publish
Run MoPro

Select molecular p	arameters file	×
Look In: 📑 alam	et_tutorial	A A A B B
alamet.lhkl		
Select Directory :	alamet.lhkl	
Files of <u>T</u> ype:	Reflections file *hkl	-
		Open Cancel

h k l lobs sigma(lobs)



gof_F gof_Ffree RF_fr wR2F_fr

> C# L#

3

2

3

3

3

WRIT FOUR

Scan mopro.out

Kill MoPro

6

3.832

0

Step 6 Preparation of constraints & restraints

e.g. H-X distances for Hydrogen atoms

	MoProGUI - D:\Users\Christian\Desktop\jelsch_pavia\alamet_tutorial					
	<u>File Edit MoPro V</u> MoF	Pro MoProV <u>i</u> ewer Molly <u>n</u> x	Help			
	MoPro Input File 🗙					
MoPro Guide	 mopro.inp Files Options Verbose Preparation 	Files ✓ Molecular structure	thymidine_01.par	Browse	Edit	< previous next >
Set molecular file Display molecule		✓ Reflections hkl	alamet.lhkl	Browse		
Set hkl file	thymidine_09.par	Bulk solvent Fhki		Browse		
Database transfer		✓ Atomic Table	D:\MoProSuite\LibMoPro\mopro.tab	Browse	Edit	
Prepare constraints/restraints Refine structure		✓ Wave Functions	D:\MoProSuite\LibMoPro\WAVEF	Browse	Edit	
Refine charge density		Anomalous asf_Kissel	D:\MoProSuite\LibMoPro\asf_Kissel.dat	Browse		
Deconstrain charge density Refine all parameters	Comment/Activate Remove	Constraints	CONSTRAIN.txt	Browse	Edit	
Publish Run MoPro	Add Run MoPro	Restraints	RESTRAIN.txt	Browse	Edit	

Edit and have a look at the generated CONSTRAIN.txt & RESTRAIN.txt files

Step 7 Refine structure

SCA XYZ UIJ *are selected* SCAle factor, Positions & Thermal motion parameters

	MoProGUI - D:\Users\Christian\Desktop\jelsch_pavia\alamet_results	
MoPro Guide	Eile Edit MoPro VMoPro MoProViewer Mollynx Help	
	MoPro Input File X MoPro Output File	
	= mopro.inp Refinement block name	A
Set working directory	- Files SET	
Import molecular file	Verbose RESOLUTION SELECTION (applies until a new selection is made) Refinement struct Resolution Range d(A) 0.25 Output Reciprocal Resolution sin θ / Λ (A-') 0.00	
Set molecular file	MANUAL SELECTION OF PARAMETERS TO REFINE	
Display molecule	Use file : Browse Edit	
Set hkl file	Selection OF PARAMETERS TO REFINE	>
Refine scale factor	Occupation Factors Anharmonicity Extinction Valence Expansion/Contraction Spherical KP1 Multipolar KP2	
Database transfer	Valence populations Multipoles All DIP QUA OCT HEX	
Prepare constraints/restraints	SELECTION OF CONCERNED ATOMS	
Refine structure	Isotropic only Anisotropic only Water only exclude	
Refine charge density	Hydrogen only exclude	
,	Chemical type only exclude	
Deconstrain charge density	Disorder Only exclude	
Refine all parameters	Limitation on thermal B-Factor \square Beq > 0.0 A^2 \square Beq < 0.0 A^2	
	Manual Selection	
Publish	Combination of selections 🗹 + 🗋 +	
Run MoPro	REFINEMENT OPTIONS	
Don't show this guide on startup	Full Matrix Inversion	
	Comment/Activate Conjugate gradients Sparse Matrix Distance cutoff(A) 5	k diagonal
	Remove Number of refinement cycles 10 ÷ Damping factor of parameters shifts 0.7 ÷	
	Add Run MoPro Guide Convergence test max(parameter_shift/sigma) > 0.1	



MoProViewer - thymidine_00.par	X	
File Options Tools View Help	\sim	
	LABEL CENTER INFO	- Fourier Density e/A3: thymidine_02.FOUR of: thymidine_00.par ; Z = 0.00000
Generate Ortep : 55501 Generate Symmetry op. : x, y, z	+ Cell translations: a 0 🜩 b 0 🜩 c 0 👳	
Switch to : thymidine_00.par previous next		
Map Properties Plane Parameters		
Map		
Property : Fourier Synthesis	\mathbf{X}	
Of type : Deformation (full deformation)		
Critical Points		
Type of critical points : Bond •	\rightarrow	
Around:		
CP file name : cp.dat Auto-load file		
Fourier Map		
Use Fourier file amet_results/alamet_02.FOUR Browse		Iso-contours Atoms, CPs and bonds Labels
Data are Totally merged		Positive Negative Zero Dash Color Dash Color
Resolution range 0.0 < sin(q)/l < 2.0 A-1		Minimum value Maximum value Standard contour levels -0.301555 0.702811 0.05
Use coefficients 1.0 Fobs - 1.0 Fcalc		Advanced contours settings
	1	Use advanced contours
Output grid file grid IV Auto-Load grid file		Multiplier Increment Base Exponent Max contours 1.0 2.48 10 [-3] 2 1 17
Output Ps file plot1.ps Open VMoPro.out	Click on 3 atoms	
		Save Image Scale factor : 4,2 🔄 Open grid Close
Cancel Kill VMoPro Run VMoPro	to define a plane	

2D map:

Select Map Property : Fourier Synthesis Select Fourier file : alamet_02.FOUR Data are Merged

Click on "Run VMoPro" to start calculation

Step 9 HIGH ORDER refinement of structure

MoProGUI - D:\Users\Christian\Desktop\jelsch_pavia\alamet_results High resolution data d < 0.7 Å, File Edit MoPro VMoPro MoProViewer Mollynx Help MoPro Input File 🗙 MoPro Output File *mopro.inp* 🗙 Hydrogen not refined mopro.inp Refinement block name Files SET struct Options Verbose RESOLUTION SELECTION (applies until a new selection is made) Refinement struct Resolution Range d(A) 0.25 to 0.7 Reciprocal Resolution sin Refinement The MoPro commands Output MANUAL SELECTION OF PARAMETERS TO REFINE Use file : Browse... Edit... ! <refinement> structural SELECTION OF PARAMETERS TO REFINE RESO 0.25 0.7 Scale factors VVV XYZ ✓ Thermal parameters Occupation Factors Anharmonicity Extinction SFLF XYZ UU NOH Valence Expansion/Contraction Spherical KP1 Multipolar KP2 Valence populations Multipoles All DIP QUA OCT HEX RFFI CG 10 DAMP 0.7 SELECTION OF CONCERNED ATOMS WRIT RFAC Isotropic only Anisotropic only Water only exclude Hydrogen only ✓ exclude MoProGUI - D:\Users\Christian\Desktop\jelsch_pavia\alamet_results File Edit MoPro VMoPro MoProViewer Mollynx Help Write a Fourier reflections file MoPro Input File 🗙 *mopro.inp* 🗙 MoPro Output File mopro.inp Refinement block name for all resolution Files Options Verbose **RESOLUTION SELECTION (applies until a new selection is n** Refinement struct Resolution Range d(A) 0.25 to 900 Refinement Output MANUAL SELECTION OF DADAMETERS TO DEFINE

Step 10Compute a Fourier Residual Electron Densityafter High-Order refinement

MoProGUI - D:\Users\	Christian\Desktop\jelsch_pavia\alamet_results
<u>File Edit M</u> oPro <u>V</u> M	oPro MoProV <u>i</u> ewer Molly <u>n</u> x <u>H</u> elp
MoPro Input File 🗙	MoPro Output File *mopro.inp* 🛿
= mopro.inp	Refinement block name
- Files	
- Options	
- Verbose	- RESOLUTION SELECTION (applies until a new selection is r
- Refinement struct	RESULTION SELECTION TAPPIES INNEA NEW SELECTION IS I
Refinement	Resolution Range d(A) 0.25 to 900
Output	MANUAL SELECTION OF DADAMETERS TO DEFINE

ontour map				1
1ap Properties	Plane Par	ameters		
Мар				
Property	Fourier S	Synthesis		•
Of type :	Deforma	tion (full deforma	ation)	Ŧ
Critical Points				
Type of critical po	ints : E	Bond		~
Around:		ALL		-
CP file name :	cp.dat		Auto-lo	ad file 📃
Fourier Map				
Use Fourier file	amet	results/alamet_0	3.FOUR	Browse
Data are	Totally	/ merged	•	
Resolution range	0.0	< sin(q)/l <	1.2	A-1
Use coefficients	1.0	Fobs -	1.0	Fcalc
utput grid file gri	d		V Aut	to-Load I file
utput Ps file pla	t1.ps		Open	VMoPro.out



RESO 0.25 900. WRIT FOUR Slightly Stronger residual electron density visible on covalent bonds



Teo-contours Atoms (De and bonds Labols

Step 11 Compute a Fourier Residual map at LOW resolution

after High-Order refinement

$\sin\theta/\lambda < 0.8$ Å⁻¹

resolution

d > 0.6 Å

2D contour map		₽×
Map Properties	Plane Parameters	
Мар		
Property :	Fourier Synthesis	•
Of type : [Deformation (full deformatio	n) 🔻
Critical Points		
Type of critical poin	ts : Bond	-
Around:	ALL	-
CP file name :	cp.dat	Auto-load file
-Fourier Map		
Use Fourier file	amet_results/alamet_03.F	OUR Browse
Data are	Totally merged	•
Resolution range	0.0 < sin(q)/l <	0.8 A-1
Use coefficients	1.0 Fobs -	1.0 Fcalc
Output grid file grid		Auto-Load grid file
Output Ps file plot:	l.ps	Open VMoPro.out
Cancel	Kill VMoPro	Run VMoPro





Step 12 Refinement of charge density







* Block diagonal: variables are decorrelated and can be refined together

* Damping to avoid divergence

Have a look at resulting molecular .par file





Step 14 Refinement of all parameters

Refine all parameters Publish

Run MoPro



- Block diagonal & damp : refine all parameters together
- Else : refine them successively





Step 15 Deconstrain charge density

Removes

- •Atoms equivalencies : similar atoms have same charge density
- •Local symmetry of multipoles



Constraints Application

Step 16 Refinement of all parameters till convergence

MoPro Guide	
Set working directory	✓ Refine ALL parameters succesively ✓ Block diagonal
Import molecular file	SCA XYZ ULI VAL PLM KP1 KP2
Set molecular file	with High Order refinement of XUZ UIJ of non-H atoms
Display molecule	10 - number of times
Set hkl file	
Refine scale factor	Damping factor of parameters shifts 0.3
Database transfer	Convergence test max(parameter_shift/sigma) > 0.1
Prepare constraints/restraints	
Refine structure	✓ No High Order refinement
Refine charge density	
✓ Deconstrain charge density	
Refine all parameters	

Check *R*-factor evolution

Publish

Run MoPro

AT 1993 1993 1 IFF IF

Check max Shift/sigma evolution



Step 17 Check Static Deformation Electron Density 2D maps



Step 18 Fast Fourier Transform 3D map

MoProViewer - alamet_06.par	Construction of the owner	
File Options Tools View Help		
	MOVE X 22 Z X LABEL CENTER INFO	
Generate Ortep : 55501 Generate Symme	try op.: X, Y, Z	
Switch to : alamet_06,par previous ne	xt	
3D isosurface map	3D Maps Manager	
Map Properties 3D Box Parameters Surface Hirshfeld	Map File D:/Users/Christian/Desktop/jelsch_pavia/alamet_results/gridmap.xplor	7
Map	REMARK Fourier Density (e/A3): alamet_06.FOUR of alamet_06.par Isosurface 1 Maximum 0.550	Residual Electron Density
Property : Fast Fourier Transform Static Electron density Electrostatic Potential	Show I Isovalue 0.244 + Update Minimum -0.620 Average 0.000	map in unit cell
Fourier Synthesis Fast Fourier Transform Laplacian of Electron density Surface	Cull back W Two faces Invert Filled W Transp. : 0 Color Std. dev. 0.081 faces W lightning Filled W Transp. : 0 Color Nx, Ny, Nz 176 74 212 Dimensions 13.1x5.3x15.9	
Fourier Map	Color isosurrace 1 according to : None Extend (fractional coordinates)	
Use Fourier file amet_results/alamet_06.FOUR Browse	Limit surface print property on surface : print X : 0,00 \odot - 1,00 \odot Y : 0,00 \odot - 1,00 \odot - 1,00 \odot - 1,00 \odot	
Resolution range 0.0 < sin(g)/l < 2.0 A-1	Isosurface 2 Z: 0,00 ⊕ - 1,00 ⊕ Use PBC ♥ Use PBC ♥	
Use coefficients 1.0 Fobs - 1.0 Fcalc	Show 5 Isovalue 0.244 Update Show Box	
Oversampling 3.0	faces ightning normals Hied V Iransp.: U V Delete Map	
Qubut file name : arideza volar		
0/119 V Auto-Load map		
Cancel Kill VMoPro Run		

Step 19 Stereochemical analysis in MoPro

	Refinement block name	
MoProGUI - D:\Users\C	SET	Refine
<u>File Edit MoPro VMol</u>	RESOLUTION SELECTION (applies until a new selection is made)	at first
MoPro Input File 🗙	Resolution Range d(A) 0.25 to 900 Reciprocal Resolution sin θ / λ (at irst
= mopro.inp		Structure
- Files	MANUAL SELECTION OF PARAMETERS TO REFINE	(15)
Refinement	Use file : Browse Edit	
- Analysis	SELECTION OF PARAMETERS TO REFINE	to obtain
	✓ Scale factors ✓✓✓ XYZ ✓ Thermal parameters	sigmas
	Occupation Factors Anharmonicity Extinction	of distances
	Valence Expansion/Contraction Spherical KP1 Multipolar KP2	UT UISTAILLES
	Valence populations Multipoles All DIP QUA OCT HEX	
	REFINEMENT OPTIONS	
	Full Matrix Inversion	
MoPro Input File 🗙	○ Conjugate gradients □ Sparse Matrix Distance cutoff(A) 5 → □ Diagonal Matrix	Block diagonal
	Analysis	
- Files	Molecular Geometry	
Refinement	☐	
Analysis	Angles	
	Plane	
	Chiral volumes	
	Molecular Connectivity	
MoDro Output File X	refined	
	ATOM1 ATOM2 SYM2 DIST sigDIST xyz xyz	
	O1 thy 1 C1 thy 1 1.239082 0.000175 +++ +++	
	O2 thy 1 C2 thy 1 1.245673 0.000163 +++ +++	
	O3 thy 1 C6 thy 1 1.428634 0.000135 +++ +++	
	Etc	

Step 20 2D map of Electrostatic Potential

DIST of			BO		D
Generate Ortep :	5550	1 Gener	ate Symm	etry op. :	х, у,
Switch to : alame	t_06.par	▼ previous	r 🗌	next	
contour map				5	×
1ap Properties	Plane Para	ameters			_
Мар					
Property :	Electrosta	atic Potential		•	
Generated by :	Total Elec	tron Density (N	uc & Cor &	kPval & I 🔻	J
Critical Points					
Type of critical poin	nts : B	ond		*	
	ALL				
Around:	A	LL		~	
Around:	A	LL	1	*	
Around: CP file name :	Image: cp.dat	LL] Auto-lo	▼ ad file □	
Around: CP file name : Fourier Map	cp.dat	LL] Auto-lo	▼ ad file	
Around: CP file name : Fourier Map Use Fourier file	cp.dat	LL esults/alamet_0	Auto-lo	ad file Browse	
Around: CP file name : Fourier Map Use Fourier file Data are	cp.dat amet_ru Totally	LL esults/alamet_0 merged] Auto-lo 3.FOUR	ad file Browse	
Around: CP file name : Fourier Map Use Fourier file Data are Resolution range	cp.dat amet_ro Totally 0.0	LL esults/alamet_0 merged] < sin(q)/l <	Auto-lo 3.FOUR	ad file Browse A-1	
Around: CP file name : Fourier Map Use Fourier file Data are Resolution range Use coefficients	cp.dat amet_ro Totally 0.0 1.0	LL esults/alamet_0 merged] < sin(q)/l <] Fobs -	Auto-lo 3.FOUR 1.2 1.0	ad file Browse A-1 Fcalc	
Around: CP file name : Fourier Map Use Fourier file Data are Resolution range Use coefficients use coefficients	cp.dat amet_ru Totally 0.0 1.0	LL esults/alamet_0 merged < sin(q)/l < Fobs -	Auto-lo 3.FOUR 1.2 1.0 Auto-lo	ad file Browse A-1 Fcalc o-Load file	



Augment dimensions of plane for a wider picture

Step 21 Generate a dimer in MoProViewer

Click right on view



Step 22 Search Intermolecular critical points

MoProViewer - alamet_06.par	And in case of the owner owne
ïle Options Tools View Help	
Critical Points Search	
VMoPro MoProViewer	1
Critical Points Search using VMoPro	\prec
Property type	
Property : Static Electron density	
Of type : Total electron density (Cor & Pval & P00 & Plm) 🔻	
	LPC I
Contributing symmetry operations	
Use all currently active symmetric molecules	
Add / Del : 55501 Generate Molecules	for a fast
55501	calculation
	=> Search
Search options	arouna
Type of critical points : Intermolecular	1 atom only
НЗ	(e.g. H11)
Search options	MoProviewer shows CPs & bond pat
Output file name: co.dat Auto-load 🗸	
Cancel Kill VMoPro Run VMoPro	

Step 23 Compute electrostatic interaction energy of a dimer

SELECTED ATOMS

.



- 1) Click on *Energy* tool of MoProViewer
- 2) Select one molecule (shift+mouse) Right click, Selection / SAVE selection
- 3) Invert Selection
- 4) Run VMoPro energy calculation

Interaction Energy Tool				
Energy type	Total electrostatic energy			
Using method	Spherical integration / Buckingham summation			
First group is active selection (31 atoms) Second group is saved selection (31 atoms)				
VMoPro output file : Reload				
Energy Computation results : The energy DENS_TOT * POT_TOT is : -65.3077 kJ/mol sym:55501 * 46502 The energy DENS_TOT * POT_TOT is : -15.5985 kcal/mol The energy DENS_TOT * POT_TOT is : -0.0470 e^2/A/mol				
Selection :	Show saved selection Cancel Kill VMoPro Run VMoPro			



Step 24 Discover the Tools of MoProViewer

μ Dipole moment MoProViewer - alamet_07.par File Options Tools View Help ENERGY 3D INFO SLICE RB Uii CENTER CP MULT KAPPA TORSION LABEL ZX DIST 🗘 b 0 🌩 c 0 🌩 ▼ + Cell translations: a 0 Generate Ortep : 65602 Generate Symmetry op. : X, Y, Z Switch to : alamet_07.par 🔻 previous next Equivalence Show local Compute Compute Move Stereo-**Constraints** axes system 3D map 2D map atoms chemistry for multipoles of atomic Critical orientation charge points density Uij Thermal ellipsoids

Step 25 ELMAM2 Database transfer

Useful for a protein or an organic molecule structure at usual atomic resolution d > 0.6 Å or s < 0.8 Å⁻¹

MoPro Guide	MoProGUI - D:\cholesterol_oxid\Figure_POT	_ 🗆 🗙
	<u>File Edit M</u> oPro <u>V</u> MoPro MoProV <u>i</u> ewer Molly <u>n</u> x <u>H</u> elp	
Set working directory	MoPro Input File ×	
Import molecular file	mopro.inp Files	
Set molecular file	Database transfer	
Display molecule	✓ Database File: D:\MoProSuite\LibMoPro\ELMAM2.txt Bro	wse
Set hkl file	✓ Transfer	
Refine scale factor		
Database transfer	✓ Neutralize	
Prepare constraints/restraints		
Refine structure	Prepare X-H distance constraints	
Refine charge density		
Deconstrain charge density	Elongate X-H distances to neutron values	
Refine all parameters		
Publish	Comment/Activate	
Run MoPro	Add	
Don't show this guide on startup	Run MoPro	

Check the resulting Static Deformation Electron Densiy maps

Step 25 Discover the MoPro Menus

Commands are classified and visible in menus

MoProGUI - D:\Users\Christian\Desktop\jelsch_pa	wia\alamet_tutorial				
Eile Edit MoPro VMoPro MoProViewer Mo	ly <u>n</u> x <u>H</u> elp				
MoPro Input File 🛪					
mopro.inp Files Options Verbose					
Preparation	Files	Modification of Molecule			
	Preparation Verbose Options Database Transfer	Shake Molecular Structure Shake Image: All parameters XYZ Ulij KAPpa Kappa1 Kappa2 VALence PLM multipoles DIPoles QUAdrupole OCTupole HEXadecapole <shift>: 0.001 Atoms: HYDrogen only NO Hydrogen VIRtual only NO Virtual NO Virtual</shift>			
	Reset / Zero	Set number of scale Factors :			
	Modification	Neutralize Electrically. atoms selection			
	Constraints Restraints	Translate Sequence (Residue Number): Translate molecule by vector x 0.0 y 0.0 z 0.0 Unit: Bohr Angstrom Fractional			
	Refinement Automatic Refinement	Apply Symmetry Operator. Ortep code 55501 Enanthiomorph structure Atoms selection			
	Solvent	Isotropic ⇒ Anisotropic Add ▼ Clear			
Comment/Activate Remove Before selected item	Analysis Output	Set Uij positive definite			
Add After selected item	Manual Commands	Set Multipole Level: Chemical Types Monopole Dipole Quadrupole Octupole Hexadecapole			
Run MoPro	ADDR / GOTO / LOOP				
	Stop				
	Duplicate Block	27			