

# MOKIT Manual

version 1.2.2 2020-12-23

jxzou

<b>1 Introduction.....</b>	<b>3</b>
1.1 Introduction to MOKIT.....	3
1.2 Citation.....	4
<b>2 Installation .....</b>	<b>4</b>
2.1 Pre-built Windows executables .....	4
2.2 Installation under Linux .....	5
2.2.1 Prerequisite.....	5
2.2.2 How to compile .....	7
2.2.3 Environment variables .....	7
2.2.4 Test .....	8
2.3 Installation on Cluster .....	8
<b>3 Quickstart for MOKIT.....</b>	<b>9</b>
3.1 Which method should I use? .....	9
3.2 Which basis set should I use?.....	10
<b>4 User's Guide .....</b>	<b>10</b>
4.1 Syntax Rules of AutoMR .....	10
4.2 Memory and Parallel Settings .....	11
4.3 Keywords of supported methods in AutoMR.....	12
GVB .....	12
CASSCF .....	12
CASCI.....	12
DMRGSCF.....	13
DMRGCI.....	13
NEVPT2.....	13
CASPT2 .....	13
MRMP2.....	13
MRCISD .....	13
MCPDFT.....	13
4.4 List of AutoMR Keywords.....	14
4.4.1 readrhf.....	14
4.4.2 readuhf .....	14
4.4.3 readno.....	15
4.4.4 ist.....	15
4.4.5 LocalM .....	16

4.4.6 CIonly.....	16
4.4.7 Force.....	16
4.4.8 Cart.....	16
4.4.9 GVB_prog.....	17
4.4.10 CASCI_prog.....	17
4.4.11 CASSCF_prog.....	17
4.4.12 DMRGCI_prog .....	18
4.4.13 DMRGSCF_prog .....	18
4.4.14 CASPT2_prog.....	18
4.4.15 NEVPT2_prog.....	18
4.4.16 MRCISD_prog .....	18
4.4.17 MRMP2_prog .....	19
4.4.18 CtrType.....	19
4.4.19 MaxM.....	19
4.4.20 hardwfn .....	20
4.4.21 crazywfn.....	20
4.4.22 no10cycle .....	20
4.4.23 charge .....	20
4.4.24 OtPDF .....	21
4.4.25 DKH2 .....	21
4.4.26 X2C .....	21
4.5 List of Utilities in MOKIT .....	21
4.5.1 add_bgcharge_to_inp .....	22
4.5.2 bas_fch2py .....	23
4.5.3 bas_gms2molcas .....	23
4.5.4 bas_gms2molpro .....	23
4.5.5 bas_gms2py.....	24
4.5.6 dat2fch.....	24
4.5.7 extract_noon2fch.....	25
4.5.8 fch2com.....	25
4.5.9 fch2inp .....	25
4.5.10 fch2inporb .....	26
4.5.11 fch2mkl.....	27
4.5.12 fch_mo_copy.....	27
4.5.13 fch_u2r .....	27
4.5.14 frag_guess_wfn .....	27
4.5.15 gvb_sort_pairs .....	28
4.5.16 mkl2fch .....	28
4.5.17 orb2fch .....	29
4.5.18 mo_svd.....	30
4.5.19 solve_ON_matrix .....	30
4.5.20 fch2py.....	30
4.5.21 py2fch.....	30
4.5.22 xml2fch .....	31

<b>5 Examples.....</b>	<b>31</b>
------------------------	-----------

<b>Appendix.....</b>	<b>31</b>
----------------------	-----------

A1 Frequently Asked Questions (FAQ) .....	31
A2 Limitations and Suggestions .....	33
1. Basic knowledge of multi-reference methods .....	33
2. Symmetry .....	34
3. The validity of MOs obtained by AutoMR for excited state calculations .....	34
4. Possible multiple solutions of UHF .....	34
5. Density in the .fch file .....	35
A3 Bug Report .....	35
A4 Acknowledgement.....	35

## 1 Introduction

### 1.1 Introduction to MOKIT

The full name of MOKIT is **Molecular Orbital KIT**. MOKIT offers various utilities and modules to transfer MOs among various quantum chemistry software packages. Besides, the **AutoMR** program in MOKIT can set up and run common multi-reference calculations in a block-box way.

With MOKIT, one can perform multi-reference calculations in a quite simple way, and utilize the best modules of each program. E.g.

```

UHF(UNO) -> CASSCF -> CASPT2
Gaussian    PySCF    OpenMolcas
or
UHF(UNO) -> GVB    -> CASSCF -> NEVPT2
Gaussian    GAMESS   PySCF    PySCF

RHF    ->    GVB    -> CASSCF    -> ic-MRCISD+Q
Gaussian    GAMESS   PySCF    OpenMolcas

```

Negligible energy loss (usually  $< 10^{-6}$  a.u., for the same wave function method in two programs) are ensured during transferring MOs, since the basis order of angular momentum up to H (i.e.  $l=5$ ) is explicitly considered.

Note that although MOKIT aims to make the multi-reference calculations block-box, the users are still required to have practical experiences of quantum chemistry computations (e.g. familiar with routine calculations in Gaussian). You are encouraged to learn how to use Gaussian first if you

are a fresh hand. See Appendix A2 for more information.

## 1.2 Citation

If you use any module or utility of MOKIT in your work, you **MUST CITE** the GitLab page of MOKIT, just like

[1] Molecular Orbital Kit (MOKIT), <https://gitlab.com/jxzou/mokit> (accessed month day, year)

If any of the keyword `ist=0,1,3` (see Section 4.4.4) in program AutoMR is used, please **ALSO CITE** the following two papers

[2] J. Chem. Theory Comput. 2019, 15, 141-153. DOI: 10.1021/acs.jctc.8b00854

[3] J. Phys. Chem. A 2020. DOI: 10.1021/acs.jpca.0c05216.

Besides, you need to **CITE** all quantum chemistry software packages called in your AutoMR job(s). For example, the file

mokit/examples/automr/00-h2o\_cc-pVDZ\_1.5.gjf

is a CASSCF job. 3 software packages will be called:

- (1) Gaussian will be called to perform RHF/UHF;
- (2) GAMESS will be called to perform GVB;
- (3) PySCF will be called to perform CASSCF.

Therefore, in this case you should also **cite** corresponding references of Gaussian, GAMESS and PySCF, as well as possible references of electronic-structure methods and basis sets.

In the future version of MOKIT, there will be a CITATION.txt file generated after your computations terminated. You can simply copy citation information in that plain text file.

## 2 Installation

The installation of MOKIT does not require any root privilege.

### 2.1 Pre-built Windows executables

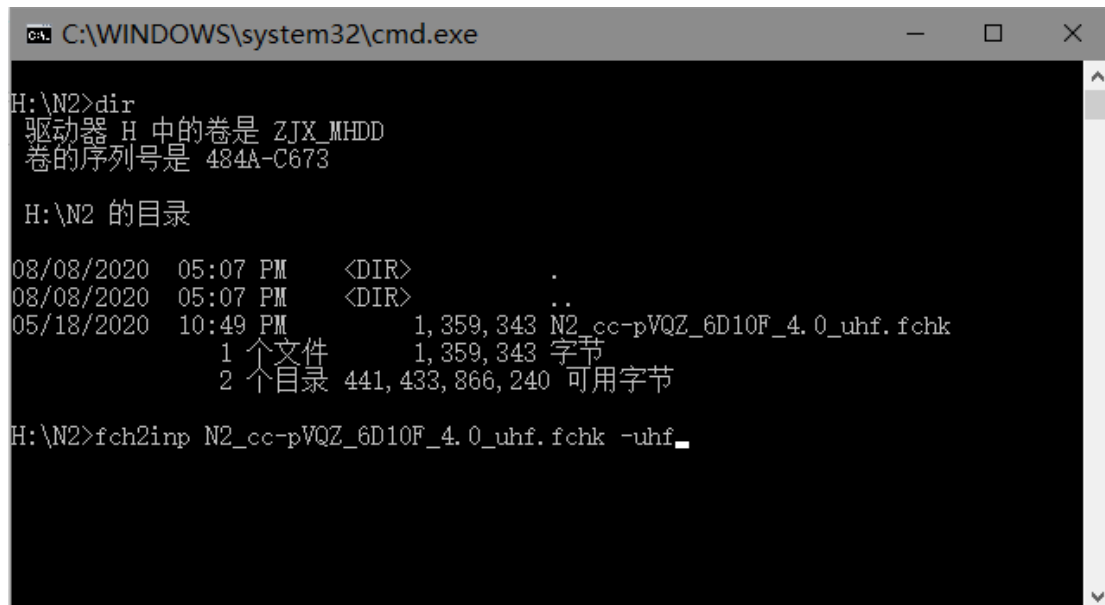
If you only want to use some utilities of MOKIT (e.g. transfer MOs among various programs, generate input files of various programs), the most convenient way is probably to use the pre-built (or pre-compiled) Windows executables.

Only 16 out of all utilities in MOKIT are provided. These executables are compressed into a .zip file and can be downloaded at 'Project overview' -> 'Releases' on <https://gitlab.com/jxzou/mokit/>. Download, uncompress it, and set the environment variables, then these utilities can be used in any directory.

To set the environment variables, search 'environment' ('环境变量' in Chinese) in the

Windows search bar, then press **Enter** and click **Edit** to edit the PATH variables. Create a new path and type the path of MOKIT \bin into it. For example, on my computer the path is H:\Software\MOKIT\mokit\bin.

Press the combination keys **Win+R** on the keyboard, type 'cmd' to prompt CMD, and **change into the directory where your .fch(k) file holds**, simply run like



```
C:\WINDOWS\system32\cmd.exe
H:\N2>dir
驱动器 H 中的卷是 ZJX_MHDD
卷的序列号是 484A-C673

H:\N2 的目录

08/08/2020  05:07 PM    <DIR>          .
08/08/2020  05:07 PM    <DIR>          ..
05/18/2020  10:49 PM             1,359,343  N2_cc-pVQZ_6D10F_4.0_uhf.fchk
                1 个文件             1,359,343  字节
                2 个目录  441,433,866,240  可用字节

H:\N2>fch2inp N2_cc-pVQZ_6D10F_4.0_uhf.fchk -uhf
```

## 2.2 Installation under Linux

### 2.2.1 Prerequisite

1. Intel compiler (for ifort and MKL library)
2. [Anaconda Python3](#) (for python, f2py, numpy, etc)

It is strongly recommended to install **Intel compiler** and **Anaconda Python3** on your computer/node. Although the two packages are big, they meet all prerequisites of compiling MOKIT. Note that the Intel compiler is free of charge for academic use.

If you want to use any Fortran compiler other than ifort (e.g. gfortran), you need to install the MKL library (or equivalently, LAPACK/BLAS, OpenBLAS, etc) on your node. And then **uncomment** the first few lines in mokit/src/Makefile for gfortran settings. And of course, use '#' to comment lines of ifort in that Makefile. The recommended version of gfortran is  $\geq 4.8.5$  but  $< 8.0$ . If you had compiled MOKIT before, and assuming you want to use another compiler, REMEMBER to run 'make clean' before compiling.

If you want to use [Python3](#) or [Miniconda](#) instead of Anaconda Python3, you need to ensure that the **f2py** wrapper is valid. For example, run 'which f2py' in Shell to see whether f2py exists.

The filenames of \*.so files compiled by f2py from Python3 are shorter than those from Anaconda Python3, but they are OK to be used.

The AutoMR program/executable in MOKIT is an integrated interface program connecting common quantum chemistry software packages. The AutoMR itself does not contain any code for computing electron integrals, it just transfers MOs among software, sometimes read one-electron integrals from some package, and call various packages to do specified computations. Therefore, the users are assumed to have successfully installed these common software packages, which are [Gaussian](#), [PySCF](#), [GAMESS](#), [OpenMolcas](#), [Molpro](#) and [ORCA](#). Some recommended versions are given below

PySCF:  $\geq 1.6.5$  ( $\geq 1.7.5$  preferred)

GAMESS:  $\geq 2017$  (2017 preferred)

Gaussian: G09 or G16

OpenMolcas:  $\geq v20.10$

Older versions are not tested by the author jxzou, so that they may work or may not. OpenMolcas v18.09 has also been tested, but you need to take care of a problem, see Section A1, Q5 in Appendix.

Of course, not all packages will be called in an AutoMR job. It depends on the job type and the program specified by users (see Section 4.4.9 ~ 4.4.17 for details). Usually three software packages (Gaussian, PySCF and GAMESS) are used extensively in routine computations. Thus you are recommended to install at least these three packages. If you have any difficulty in installing software, please read their corresponding manuals carefully. Or you can find answers from their official site, forums, Github/Gitlab page, etc.

If you can read Chinese, the following installation instructions or tutorials of common software packages on the WeChat Official Accounts ‘quantumchemistry’ (微信公众号 “量子化学”) are strongly recommended:

1. 《Linux 下 Gaussian 16 安装教程》 <https://mp.weixin.qq.com/s/ffGo6eOEacfgqg3sYbrLJA>
2. 《ORCA 软件安装教程》 <https://mp.weixin.qq.com/s/9j3U5v0wBaAabRk-uo4EhQ>
3. 《GAMESS 编译教程》 <https://mp.weixin.qq.com/s/w689PJc4c2H8sWj03zsUBA>
4. 《离线安装 PySCF 程序（1.5 及更高版本）》  
<https://mp.weixin.qq.com/s/QZPG5jRFZ5s1it2OaBGJqw>
5. 《OpenMolcas 与 QCMAquis 的安装》 [https://mp.weixin.qq.com/s/ldhxz3I3txmlDxjk\\_3a5bw](https://mp.weixin.qq.com/s/ldhxz3I3txmlDxjk_3a5bw)
6. 《Block-1.5 的编译和安装》 <https://mp.weixin.qq.com/s/EUZKLYSqbuIUL9-zlySfbQ>
7. 《Boost.MPI 的编译》 <https://mp.weixin.qq.com/s/AMYUTB5pTNLFZ8NEtFIG-Q>
8. 《安装基于 openmpi 的 mpi4py》 <https://mp.weixin.qq.com/s/f5bqgJYG5uAK1Zubngg65g>

Note that the original GAMESS source code can only deal with GVB up to 12 pairs. To go beyond that (which is routine type of calculation in AutoMR of MOKIT), please read Section 4.4.9 carefully. After re-compiling GAMESS (followed by instructions in Section 4.4.9), an executable ‘gamess.01.x’ will be generated. This is the executable to be called in automr.

## 2.2.2 How to compile

Assuming you've already [downloaded](#) the MOKIT .zip package, just run

```
unzip mokit-master.zip
```

to uncompress it. Note that do not uncompress the package in Windows\* OS, but uncompress it in Linux\* OS. Then simply run the following three command lines in Shell

```
mv mokit-master mokit
cd mokit/src
make all
```

to compile MOKIT. This will take about 2 minutes, There is no need to 'make install'. If you do not need automr, and only want to compile one or several modules, e.g. fch2inp, for Gaussian -> GAMESS orbital transferring. Then you simply need to run

```
make fch2inp
```

Be careful with hints on the screen, some modules depend on other modules, thus a compilation of two or three modules is necessary sometimes.

## 2.2.3 Environment variables

After successful compilation, you need to add the following environment variables into your ~/.bashrc file:

```
export MOKIT_ROOT=/home/$USER/software/mokit
export PATH=$MOKIT_ROOT/bin:$PATH
export PYTHONPATH=$MOKIT_ROOT/lib:$PYTHONPATH
export ORCA=/home/$USER/software/orca-4.2.1/orca
export GMS=/home/$USER/software/games/rungms
```

Note that do not mistake 'PYTHONPATH' for 'LD\_LIBRARY\_PATH'. Please modify the above paths to **suit your situations**. Since PySCF is run by `python`, OpenMolcas is run by `pymolcas`, and Molpro is run by `molpro`, there is no extra variable to be exported here. The configuration file 'program.info' is no longer used since MOKIT 1.2.1. After writing environment variables, a logout and re-login on your terminal is strongly recommended.

The scratch directory (in Chinese, 临时文件存放目录) is not determined by MOKIT or AutoMR, but by each quantum chemistry package (Gaussian, OpenMolcas, GAMESS, etc). Please do not submit two computations with the same input filename (even in different work directories) at the same time, since their temporary files may be overwritten by each other. For example, GAMESS, OpenMolcas and Molpro jobs are sensitive to the files in the scratch directory, while

Gaussian, PySCF and ORCA are not that sensitive.

## 2.2.4 Test

Change into the example directory, and pick up a .gjf file to test whether the automr program works. For example,

```
cd $MOKIT_ROOT/examples/automr/  
automr 00-h2o_cc-pVDZ_1.5.gjf >& 00-h2o_cc-pVDZ_1.5.out &
```

If you encounter any errors in output, please search your problem in Section A1 FAQ of Appendix first. Some common questions have been listed. For bug reporting, please read Section A3.

## 2.3 Installation on Cluster

Installing MOKIT on a cluster (in Chinese, 集群或超算) is somewhat troublesome (also for other software packages). If you can write environment variables freely into ~/.bashrc, then there is nothing different with installation on your local Linux computer.

However, sometimes you are not allowed, or unwilling to modify ~/.bashrc. And usually environment variables of various packages (e.g. ifort, python, etc) are controlled by the ‘module’ function. For example, if you need some version of python (other than system default), you have to run ‘module load python/...’ to make it accessible. In such case, you have to firstly load proper versions of Intel compiler and Python before installing MOKIT. For example,

```
module avail          # find which version you can use  
module load intel/2019u5 # load the version you want to use  
module load python/3.7.6 # load the version you want to use  
make all              # compile MOKIT
```

The first line finds which versions of software packages you can choose. The 2<sup>nd</sup> and 3<sup>rd</sup> lines load the corresponding software. And the 4<sup>th</sup> line is just the installing of MOKIT. This is just a simple example telling you how to load modules on a cluster. For detailed questions, please consult the administrator of your node, or the cluster. Moreover, a good choice to running automr is that you should create a Shell script, e.g. `run.sh`, with

```
module load intel/2019u5  
module load python/3.7.6  
gjfname=$1  
outname=${gjfname%.*}.out  
automr $gjfname >& $outname
```

written in this script. If you are allowed to submit jobs to the current node, then you can run



```
chmod +x run.sh
./run.sh 00-h2o_cc-pVDZ_1.5.gif &
```

However, usually you are not allowed to submit any job in the main node or login node. And there exists a queue system or batch system on your cluster, e.g. 'bsub' in LSF batch or 'qsub' in PBS batch, which distributes your job to a proper computation node. Taking 'bsub' as an example, you should write a Shell script like

```
#!/bin/sh
#BSUB -q ...    # queue name
#BSUB -n ...    # number of cores
module load intel/2019u5
module load python/3.7.6
gjfname=$1
outname=${gjfname%.*}.out
automr $gjfname >& $outname
```

Then you can run

```
bsub run.sh 00-h2o_cc-pVDZ_1.5.gif
```

If you still encounter problems, please consult the administrator of your cluster. This is beyond the scope of this manual.

## 3 Quickstart for MOKIT

See examples in \$MOKIT\_ROOT/examples/. More details to be added.

### 3.1 Which method should I use?

For practical use, e.g. to properly compare results with those from experiments, NEVPT2/CASPT2/MRCISD is recommended. The GVB and CASSCF methods are often qualitatively correct. For high accuracy results, dynamic correlation is necessary. Additional general recommendations are provided below:

- (1) NEVPT2 is free of the intruder-state problem, thus is preferable to CASPT2.
- (2) If you find NEVPT2/CASPT2 is too expensive for your system, consider the MC-PDFT method.
- (3) If you find the computation cost of NEVPT2/CASPT2 is acceptable for your system and you want higher accuracy, consider ic-MRCISD or FIC-MRCISD. For very small systems such as two or three atoms, the uncontracted MRCISD in ORCA is a good choice.

## 3.2 Which basis set should I use?

For testing or debug, you can use any type of basis sets. You can, of course, use a small basis set like def2-SVP to test whether AutoMR works. However, for practical use or to obtain publishable data, please use at least triple-zeta basis set, e.g. cc-pVTZ, def2-TZVP, def2-TZVPP or def-TZVP. Results obtained from combinations like MRCISD/def2SVP, NEVPT2/6-31G(d) are almost useless. Additional general recommendations are provided below:

- (1) If your system is large ( $>700$  basis functions), you should consider properly simplify your system or use mixed basis sets for different elements/atoms. For example, use cc-pVTZ for important atoms and cc-pVDZ (or even 6-31G(d)) for other atoms.
- (2) Pople-type basis set like 6-311G(d,p) is less recommended.
- (3) If pseudopotential (PP) is desired, better to use cc-pVTZ-PP, def2-TZVP. Be careful with the built-in basis set (with PP) SDD in Gaussian software for elements  $\geq$  the 4<sup>th</sup> period. Often there is no  $d, f$  polarization functions in the built-in SDD basis set of Gaussian (although the PP part seem pretty good), but the  $d, f$  polarization functions are usually important for high-accuracy computations. If you insist on the usage of SDD, you should search in previous papers the data of  $d, f$  polarization functions of SDD for your atoms, and add the data to the .gjf file manually.
- (4) If your molecule is an anion, e.g.  $\text{MnO}_4^-$ , it is strongly recommended to use basis set with diffuse functions, such as aug-cc-pVTZ, def2-TZVPD. Similar to (1), if your system is large, you can use basis set with diffuse functions for atoms with significant negative charges, and use no diffuse functions for other atoms. If the atoms involving significant negative charges are not so important in your study, you can just use aug-cc-pVDZ.
- (5) If all-electron relativistic calculations are desired (DKH2 or X2C), do remember to use basis sets like cc-pVTZ-DK, x2c-TZVPall or ANO-RCC-VDZ series. All-electron relativistic computations using CASSCF/cc-pVTZ or cc-pVTZ-PP with DKH2 is almost non-sense.

Currently AutoMR cannot read user-defined basis sets or pseudopotentials in .gjf file, so you have to provide a Gaussian .fch(k) file and use one of the three options 'readrhf', 'readuhf', 'readno'. See Section 4.4.1~4.4.3 for related information.

## 4 User's Guide

### 4.1 Syntax Rules of AutoMR

Syntax rules of the input file of AutoMR is almost identical to those of Gaussian software. Therefore, it takes little time to become familiar with the usage of AutoMR. A simple input example is shown below

```
-----  
%mem=4GB  
%nprocshared=4  
#p CASSCF/cc-pVQZ
```

```
mokit{readuhf='N2_cc-pVQZ_6D10F_4.0_uhf.fchk',ist=1,car}
```

---

For the memory and parallel settings, please read Section 4.2. For the theoretical method and basis set, please read Section 4.3. Here we focus on the keywords in mokit{ }.

1. All keywords must be written in the curly bracket of 'mokit{ }' in the Title Card line of a .gif file.
2. Using upper or lower case of keywords in AutoMR makes no difference. For example, the following two lines have identical meanings:

(1) MOKIT{readuhf='a,fchk',ist=1,LocalM=Boys}

(2) mokit{readuhf='a,fchk',ist=1,localm=boys}

3. If 'readrhf', 'readuhf', or 'readno' keyword is used, a filename of the provided .fch(k) file must be included in a pair of single quotation marks '. Do not use double quotation marks "" or no quotation marks.
4. If pure Cartesian functions of basis set are used in the provided .fch(k) file, you need to write keyword 'cart'. The default is pure spherical harmonic functions. And you do not need to write any keyword about this if you provide a .fch(k) file in which pure spherical harmonic functions are used.
5. Use a comma to separate different keywords. Do not use other symbols (like spacing).
6. User-defined basis sets (i.e. gen) and pseudopotentials (i.e. genecp) are not supported in the .gif file currently. To use that, you can write one of the keywords 'readrhf', 'readuhf', or 'readno', and provided a .fch(k) file (in which the data of basis sets and pseudopotentials are recorded).

## 4.2 Memory and Parallel Settings

The settings of memory and the number of processors are identical to that in Gaussian. For example, the following syntax

```
%chk=16GB
```

```
%nprocshared=8
```

requests a AutoMR calculation use 16GB (maximum) memory and 8 processors. Note that only the unit GB and %nprocshared is supported. Some DON'T things are listed below:

- (1) Do not use unit MB, MW, GW, or %cpu..
- (2) Do not write %chk since it is useless for AutoMR.

Since multireference computations often require large memory, it is recommended to use at least %mem=1GB for even a small molecule. Note that memory and parallel settings of OpenMolcas is controlled by variables in your ~/.bashrc (export MOLCAS\_NPROCS, export MOLCAS\_MEM),

not by AutoMR. You should refer to (Open)Molcas manual for details.

The memory and parallel settings are passed into various programs called by AutoMR (e.g. PySCF, Gaussian, etc). The AutoMR itself only needs negligible memory and usually run in a serial mode.

## 4.3 Keywords of supported methods in AutoMR

Currently, the keywords of all supported methods in AutoMR are: **GVB**, **CASCI**, **CASSCF**, **DMRGCI**, **DMRGSCF**, **NEVPT2**, **CASPT2**, **MRMP2**, **MRCISD**, and **MCPDFT**. More multi-configurational and multi-reference methods will be supported in the future. These terms should be written in the '#p ...' line in the .gjf file.

There must be a '/' symbol between the method and the basis set, e.g. CASSCF/cc-pVTZ. AutoMR does not allow the use of a spacing to separate the method and basis set (which is allowed in Gaussian). When 'readrhf', 'readuhf', or 'readno' is used in mokit {}, the basis set after '/' symbol is actually useless, since the geometry and basis set data will be read from the given .fch(k) file. Note that, however, the user still needs to provide a basis set name, although it is not used in this case.

For the methods listed below, AutoMR can automatically determine the active space, thus you need not specify that. If you do not want the automatically determined one, you can manually specify it, such as CASSCF( $m,n$ ) or NEVPT2( $m,n$ ), with  $m$ ,  $n$  being the number of active electrons and active orbitals, respectively. While for GVB, you may specify GVB( $n$ ), where  $n$  is the number of pairs. Manually specifying is only recommended for experienced users.

### GVB

Generalized Valence Bond theory.

Note that the original GAMESS source code can only deal with GVB up to 12 pairs. To go beyond that (which is routine type of calculation in AutoMR of MOKIT), you need to modify the GAMESS source code, please read Section 4.4.9 carefully.

### CASSCF

Complete Active Space Self-consistent Field.

### CASCI

Complete Active Space Configuration Interaction.

CASCI can be viewed as the 0-th step of the CASSCF step, i.e. CASSCF without orbital optimization. It is always recommended to perform CASSCF rather than CASCI, except for those who wish to compare the quality of different initial guesses, and/or do not want the CASSCF result.

## DMRGSCF

Here the term DMRGSCF actually means the DMRG-CASSCF method. Please also read Section 4.4.13 for related information.

## DMRGCI

Here the term DMRGCI actually means the DMRG-CASCI method. Please also read Section 4.4.12 for related information.

DMRGCI can be viewed as the 0-th step of the DMRGSCF step, i.e. DMRGSCF without orbital optimization. It is always recommended to perform DMRGSCF rather than DMRGCI, except for those who wish to compare the quality of different initial guesses, and/or do not want the DMRGSCF result.

## NEVPT2

Second order *N*-Electron Valence state Perturbation Theory based on the CASSCF reference.

## CASPT2

Second order Perturbation Theory based on CASSCF reference.

## MRMP2

Second order Multi-reference Perturbation Theory based on CASSCF reference. After CASSCF converged, AutoMR will call the GAMESS program to perform MRMP2 calculation. No other program is supported. Also, DMRG-MRMP2 is not supported and AutoMR will abort in that case.

## MRCISD

Multi-reference Configuration Interaction Singles and Doubles, based on CASSCF reference. Please also read Section 4.4.16 for related information.

## MCPDFT

Multi-configurational Pair Density Functional Theory, based on CASSCF reference. Note that **MCPDFT** is a keyword in AutoMR but **MC-PDFT** is the method name. Do not mix them up.

Note that if the active space is larger than (14,14), the MC-PDFT will be automatically

switched to DMRG-PDFT. In this special case you need to install the QCMAquis package (interfaced with OpenMolcas) for DMRG computations.

**\*\*\*\*\*YOU MUST ALSO READ\*\*\*\*\***

Note that usually there is no need to write DMRGCI or DMRGSCF, the users can just write CASCI or CASSCF. Once AutoMR detects the size of active space is larger than (14,14), it will switch from CASCI/CASSCF to DMRGCI/DMRGSCF automatically. Similarly, the NEVPT2/CASPT2/MC-PDFT will be automatically switched into DMRG-NEVPT2/DMRG-CASPT2/DMRG-PDFT when the active space is larger than (14,14). The only exception is that the users just want to perform a DMRG calculation with active space smaller than (14,14), then the DMRGCI or DMRGSCF must be specified.

Usually the automatically determined active space is reasonable. However, when you are studying a potential energy curve/surface, the automatically determined active space may be not the same size for each geometry. For example, for  $N_2$  molecule at  $d(N-N) = 1.15 \text{ \AA}$ , the CAS(4,4) may be automatically determined by AutoMR, but for  $d(N-N) = 4.0 \text{ \AA}$ , the active space turns into CAS(6,6). Thus, if you want to keep the size to be CAS(6,6), you need to specify CASSCF(6,6), NEVPT2(6,6), MRCISD(6,6), etc.

## 4.4 List of AutoMR Keywords

If any of the 'readrhf', 'readuhf', and 'readno' keywords is used, there is no need to write Cartesian coordinates in .gjf file (in fact AutoMR will not read coordinates in such case), since the geometry is already provided in the specified .fch(k) file.

### 4.4.1 readrhf

Read RHF (or ROHF) orbitals from a specified .fch file. If you provide a UHF-type .fch file, only the Alpha MO section will be read.

### 4.4.2 readuhf

Read UHF orbitals from a specified .fch file. MOKIT will generate UHF natural orbitals (UNO) using the input UHF orbitals. It is strongly recommended to check the stability of UHF wave function (using keyword 'stable=opt' in Gaussian). An instable or not-the-lowest UHF solution may lead to improper GVB or CASSCF results.

The author does not recommend the usage of UDFT orbitals. But in case you have to do that (e.g. forced by your BOSS or driven by your curiosity), remember to add an extra keyword 'no10cycle' (see 4.4.22 for no10cycle).

Note: do not provide a UNO .fch file with this keyword. If you want to use any type of NOs as the initial guess, see ‘readno’ in the following section.

### 4.4.3 readno

Read natural orbital occupation numbers (NOON) and natural orbitals (NO) from a specified .fch file. In this case, you must ensure that the ‘Alpha Orbital Energies’ section in the .fch file is occupation numbers, not energy levels or something else, since the size of the active space will be determined according to the (threshold of the) occupation numbers.

With this keyword, you may try different NOs as the initial guess, like MP2 NOs, CCSD NOs, or some type of NOs generated by your own program. You may also use UNOs from UHF as the initial guess. In this case, it is equivalent to use the keyword ‘readuhf’ to read in the UHF orbitals and generate UNOs by MOKIT.

### 4.4.4 ist

Request the use of the *i*-th strategy. Default is 0. This means: (1) if the spin of the target molecule is singlet, MOKIT will call the Gaussian software to perform RHF and UHF computations, then determine whether to change ‘ist’ to 1 or 3. If the  $E_{\text{UHF}} = E_{\text{RHF}}$ , ist will be changed to 3. If  $E_{\text{UHF}} < E_{\text{RHF}}$ , ist will become 1. (2) if not singlet, ist will be changed to 1 immediately.

For simple organic molecules which have multireference characters (like diradicals), the UHF performed by MOKIT (calling Gaussian) can usually find the lowest (and stable) UHF solution. But for complicated systems like binuclear transition metal complex, there often exist multiple UHF solutions. And the UHF solution found by MOKIT is not necessarily the lowest one. In this case you are recommended to do UHF computations by yourself and use ist=1 to read in the Gaussian .fch file. See a practical guide for advanced UHF computations on <http://gaussian.com/afc/>. If you can read Chinese, you are recommended to read Sobereva’s blog <http://sobereva.com/82>.

Currently, there are 6 allowed values for ist:

- 0: if RHF wfn is stable, use strategy 3; otherwise use strategy 1
- 1: UHF -> UNO -> associated rotation -> GVB -> CASCI/CASSCF -> ...
- 2: UHF -> UNO -> (associated rotation ->) CASCI/CASSCF -> ...
- 3: RHF -> virtual orbital projection -> localization -> pairing -> GVB -> CASCI/CASSCF -> ...
- 4: RHF -> virtual orbital projection -> CASCI/CASSCF -> ...
- 5: NOs -> CASCI/CASSCF -> ...

The value 0 or 1 is recommended, if you do not know which one to choose.

### 4.4.5 LocalM

Specify the orbital localization method. Only the Boys (also called Foster-Boys) localization and Pipek-Mezey (PM) localization method are supported. The corresponding keywords are 'LocalM=Boys' and 'LocalM=PM'. By default, the PM localization is used.

Note: the Boys method will mix  $\sigma$  and  $\pi$  orbitals, while the PM method tends to keep them separated. These two methods make no difference when the target molecule contains only  $\sigma$  bonds (and possibly a few isolated  $\pi$  bonds). But if you are dealing with multiple  $\pi$  bonds or conjugated  $\pi$  systems like oligoacene (benzene, naphthalene, etc), or if you want the active space to contain only  $\pi$  orbitals, please use the PM method. The GVB and CASSCF optimized orbitals will be affected by the localization method sometimes.

For people who are keen on comparing initial guesses generated from different methods/algorithms, 'Local=Boys' should also be taken into considerations, to see whether a lower CASCI or CASSCF energy occurs.

### 4.4.6 CIonly

Skip the CASSCF orbital optimization in the CASPT2 or NEVPT2 job. Obviously, this keyword only applies to CASPT2 or NEVPT2 case. Writing CIonly means a CASCI  $\rightarrow$  CASPT2 or CASCI  $\rightarrow$  NEVPT2 job. In fact, the CASSCF orbital optimization is always recommended to be performed, unless it is too time-consuming, or you happen to want this type of result.

Note: if you simply need a CASCI computation, do not use CIonly in a CASSCF job, but simply write CASCI/basis\_set in the keyword line of .gjf file.

### 4.4.7 Force

Request a calculation of the analytical nuclear gradient. Currently this keyword only applies to CASSCF. Geometry optimization is currently not supported, but you can use the generated files to perform optimization using corresponding software. Numerical gradient is not supported.

Note that this keyword do not have any attribute value, i.e. do not write 'force=.True.' but only 'force' in {}. Also keep in mind that force is negative gradient.

### 4.4.8 Cart

Request the use of Cartesian type atomic basis functions. The default basis type in AutoMR (i.e. spherical harmonic functions) will then be disabled. These two types of basis functions correspond to '6D 10F' (Cartesian functions) and '5D 7F' (spherical harmonic functions) in Gaussian. It is recommended to use spherical harmonic functions, especially in all-electron relativistic computations (DKH2, X2C, etc).

Note that for computations involving the ORCA program, this keyword cannot be used since ORCA only support spherical harmonic functions.



If you don't know the meaning of 5D or 6D, you are referred to Schlegel and Frisch's paper (DOI: 10.1002/qua.560540202), and a good explanation from Chemissian <http://www.chemissian.com/ch5>. If you can read Chinese, you are recommended to read Sobereva's blog <http://sobereva.com/51>.

#### 4.4.9 GVB\_prog

Specify the GVB program. Default is GAMESS, and this is the only program supported currently. The second-order SCF (SOSCF) algorithm in GAMESS is used to converge the GVB wave function. The GAMESS version  $\geq 2017$  is strongly recommended. Older versions of GAMESS may work or may not, since they are not tested by the author jxzou.

Note the original GAMESS can only do GVB up to 12 pairs. Nowadays we can do a black-box GVB computation with hundreds of pairs. So, to go beyond 12 pairs, you need to modify and re-compile the source code of GAMESS.

MOKIT offers a Shell script to help you automatically handle this. Assuming you've compiled GAMESS before (i.e. all \*.o files are still in **gamess/object/** directory of GAMESS), now you simply need to copy two files (modify\_GMS1.sh and modify\_GMS2.f90) from mokit/src/ into **gamess/source/** directory, and run './modify\_GMS1.sh'. The script will modify source code and re-compile GAMESS, taking about 2 minutes. The linked GAMESS executable will be gamess.01.x. If you already had an executable named gamess.01.x, please rename it to another filename. Otherwise it will be destroyed and replaced during re-compilation.

Besides, the original GAMESS only supports 32 CPU cores. If your machine has more cores (and if you want to use  $>32$  cores), you need to modify the source code. See a simple guide in file src/modify\_GMS\_beyond32CPU.txt.

#### 4.4.10 CASCI\_prog

Specify the program for performing the CASCI calculation, e.g. CASCI\_prog=PySCF. Supported programs are PySCF(default), GAMESS, OpenMolcas, Gaussian, ORCA and Molpro.

#### 4.4.11 CASSCF\_prog

Specify the program for performing the CASSCF calculation, e.g. CASSCF\_prog=PySCF. Supported programs are PySCF(default), GAMESS, OpenMolcas, Gaussian, ORCA and Molpro. If you want to use a CASSCF program instead of PySCF, I recommend OpenMolcas, Molpro or GAMESS.

#### 4.4.12 DMRGCI\_prog

Specify the program for performing DMRG-CASCI calculation, e.g. DMRGCI\_prog=PySCF. Currently only PySCF is supported and it is the default program.

Note that in fact the DMRG-CASCI calculations are performed by [Block-1.5](#) and PySCF, not only by PySCF. Thus you should install the Block-1.5 program. And you should also cite corresponding reference of the Block-1.5 program. Also note that the MPI version used by Block may be contradicted with MPI used by ORCA, you have to comment one version of MPI environment variables at a time. See Section 2.1 for related information.

#### 4.4.13 DMRGSCF\_prog

Specify the program for performing DMRG-CASSCF calculation, e.g. DMRGSCF\_prog=PySCF. Currently only PySCF is supported and it is the default program.

Note that in fact the DMRG-CASSCF calculations are performed by [Block-1.5](#) and PySCF, not only by PySCF. Thus you should install the Block-1.5 program. And you should also cite corresponding reference of the Block-1.5 program.

Also note that the MPI version used by Block is probably contradicted with MPI version used by ORCA, you have to comment one version of MPI environment variables at a time. See Section 2.1 for related information.

#### 4.4.14 CASPT2\_prog

Specify the program for performing CASPT2 calculation, e.g. CASPT2\_prog=OpenMolcas. Currently only OpenMolcas(default) and Molpro are supported. All core orbitals are not frozen. Note that a default IP-EA shift 0.25 a.u. will be applied and it cannot be modified. If your CASPT2 results are sensitive to the IP-EA shift, it implies that CASPT2 is not suitable to your problem. Another two types of shift (the real or imaginary shift) is not supported.

#### 4.4.15 NEVPT2\_prog

Specify the program for performing NEVPT2 calculation, e.g. NEVPT2\_prog=PySCF. Currently only PySCF is supported and it is the default program. All core orbitals are not frozen.

The NEVPT2 method in PySCF is actually SC-NEVPT2, where 'SC' for strongly contracted.

#### 4.4.16 MRCISD\_prog

Specify the program for performing MRCISD calculation. By default, MRCISD\_prog=OpenMolcas. Currently, AutoMR supports the interfaces of 3 variants of the MRCISD method: (1) uncontracted MRCISD; (2) internally contracted MRCISD (ic-MRCISD); (3)

fully internally contracted MRCISD (FIC-MRCISD). And AutoMR is able to call OpenMolcas/Molpro/ORCA/Gaussian programs to perform MRCISD. All core orbitals are not frozen. MRCISD based on the DMRG reference is not supported currently.

If MRCISD\_prog=OpenMolcas, only variants (1) and (2) are supported. The Davidson correction for size-consistency can only be calculated for (2).

If MRCISD\_prog=ORCA, only (1) and (3) are supported. The Davidson correction can be provided for both methods. However, only spherical harmonic functions of basis sets are supported in ORCA. But this is often not a problem, since it is recommended to use spherical harmonic functions than Cartesian functions.

If MRCISD\_prog=Gaussian, only (1) is supported and no Davidson correction is given.

If MRCISD\_prog=Molpro, only (2) is supported. The Davidson correction energy will also be printed. Note that the MRCIC program of Molpro will be called to perform ic-MRCISD. This ic-MRCISD is not exactly identical to that of OpenMolcas, so their electronic energies are different with (but close to) each other. If you want to compare (relative) electronic energies of two molecules, please choose the same type of ic-MRCISD, i.e. both using Molpro or both using OpenMolcas.

The ic- and FIC-MRCISD are both approximations of uncontracted MRCISD. If the Davidson correction energy is added, then it should be denoted as MRCISD+Q. It is recommended to use ic- or FIC-MRCISD+Q in practical calculations since the uncontracted MRCISD is very expensive.

You must also specify a contraction type, please read Section 4.4.18 carefully.

#### 4.4.17 MRMP2\_prog

Specify the program for performing MRMP2 calculation. Only GAMESS is supported and this is the default.

#### 4.4.18 CtrType

Specify the contraction type of the MRCISD method. The default value is 0. When you specify the MRCISD method and the MRCISD\_prog, you must assign an integer for this variable, where

1 for uncontracted MRCISD

2 for ic-MRCISD

3 for FIC-MRCISD.

Generally, the ic- and FIC-MRCISD methods are recommended. If your calculation involves Cartesian functions, then you cannot use FIC-MRCISD in ORCA. In such case, you should choose ic-MRCISD in OpenMolcas instead.

#### 4.4.19 MaxM

Specify the bond dimension MaxM in DMRG-related calculations. The default values is 1000 (e.g. MaxM=1000). When maxM increases, the DMRG-CASCI energy will become closer to the CASCI energy, but the computational cost increases as well. The value 1000 is suitable for common

cases. But do check whether it is valid for your system. For example, three computations using different MaxM (e.g. 500, 1000, 1500) may be conducted to study whether the energy converges with MaxM.

#### 4.4.20 hardwfn

This option can only be applied to CASCI/CASSCF calculations using PySCF or GAMESS. By specifying 'hardwfn', AutoMR will add extra keywords into the CAS input files to ensure a better convergence. Note that normally you do not need this keyword, and it is useless if you specify other programs as the CAS solver.

#### 4.4.21 crazywfn

This option can only be applied to CASCI/CASSCF calculations using PySCF or GAMESS. By specifying 'crazywfn', AutoMR will add extra keywords (more than those of 'hardwfn') into the CAS input files to ensure a better convergence. Note that usually you do not need this keyword, and it is useless if you specify other programs as the CAS solver.

For example, when the N<sub>2</sub> molecule is stretched to  $d(\text{N-N}) = 4.0 \text{ \AA}$ , this is a system which features strong correlation and requires a CAS(6,6) active space. The Davidson iterative diagonalization in determinant CASCI (using GAMESS) may not find the singlet state in the lowest 5 states. In this case, specifying 'crazywfn' will increase the NSTATE to 10, so that the singlet state can be found.

#### 4.4.22 no10cycle

Skip the 10 cycles of SCF calculations after importing MOs. By default, AutoMR will do several (up to 10) cycles of RHF or UHF after importing MOs from .fch file. This has two advantages: (1) check whether the SCF converges immediately. If not, the MO in .fch file may be wrong, or there exists some bug of fch2py (which has never been observed by the author). (2) it will slightly improve the orthonormality of the input MOs, although the orthonormality is already good. Thus usually you do not need to write this keyword.

If you start with MOs which are not RHF or UHF MOs (e.g, NOs, UDFT MOs, etc), you must specify 'no10cycle' in mokit{}. Because any iteration of input MOs will change them, which is not what you want.

#### 4.4.23 charge

This keyword has identical meaning with the same keyword in Gaussian software, i.e. including background point charges in calculations. This keyword is supported for all methods in AutoMR.

The including of background point charges is useful for QM/MM calculations or fragmentation-based linear scaling methods (like GEBF, Many-body expansion, etc).

Note: **WRITE** this keyword in mokit{}. **DO NOT WRITE** this keyword in the Route Section of .gjf file (i.e. '#p ...' line).

#### 4.4.24 OtPDF

The choice of the on-top pair density functional. This keyword has identical meaning with the keyword **KSDFT** in OpenMolcas/Molcas software. Currently available functionals are tPBE, tBLYP, tLSDA, trevPBE, tOPBE, ftPBE, ftBLYP, ftLSDA, ftrevPBE and ftOPBE. For more details please refer to the Molcas manual. Note that the available functionals depends on your version of OpenMolcas/Molcas. Old versions may not support some of the functionals.

#### 4.4.25 DKH2

Request the 2<sup>nd</sup> order scalar relativistic Douglas–Kroll–Hess (DKH2) correction to the one-electron Hamiltonian. Note that: (1) the two keywords **DKH2** and **X2C** are mutually exclusive; (2) you should use all-electron basis sets like 'cc-pVTZ-DK', 'x2c-TZVPall' or 'ANO-RCC-VDZ' for all-electron relativistic calculations; (3) it is strongly not recommended to use Cartesian-type function of basis set (severe numerical instability observed), please just use the default spherical harmonic functions.

Currently only the point nuclei charge distribution is supported.

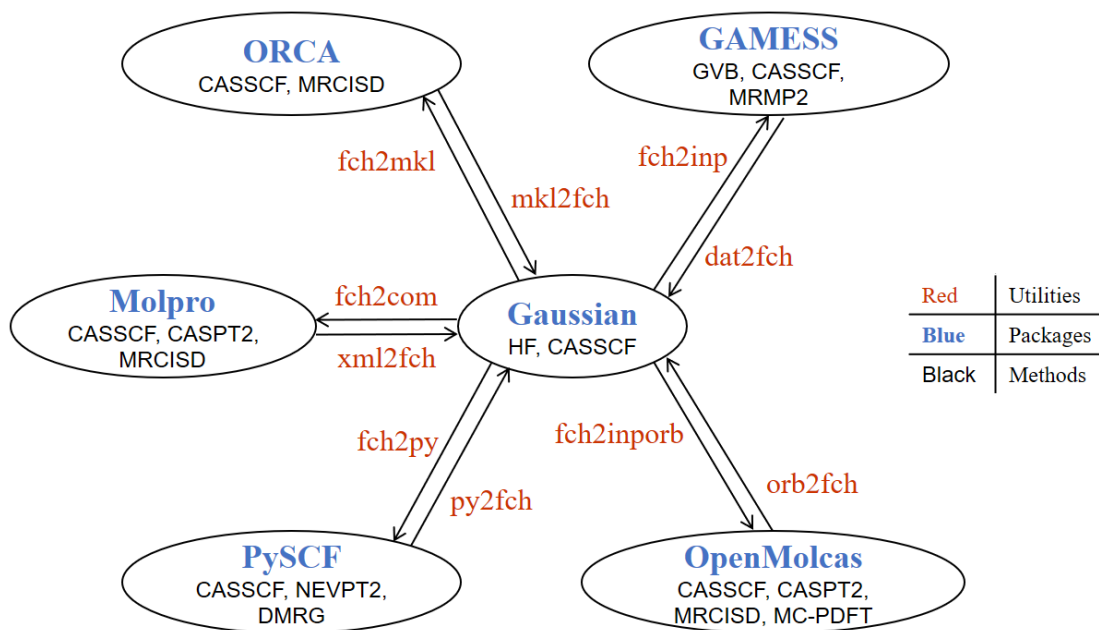
#### 4.4.26 X2C

Request the scalar relativistic X2C (eXact-two-Component) corrections to the one-electron Hamiltonian. Note that: (1) the two keywords **DKH2** and **X2C** are mutually exclusive; (2) you should use all-electron basis sets like 'cc-pVTZ-DK', 'x2c-TZVPall' or 'ANO-RCC-VDZ' for all-electron relativistic calculations; (3) it is strongly not recommended to use Cartesian-type function of basis set (severe numerical instability observed), please just use the default spherical harmonic functions.

Also note that the RHF/UHF is performed using Gaussian called by AutoMR, and GVB is performed using GAMESS called by AutoMR. Since Gaussian and GAMESS do not support X2C, in these steps the X2C will be replaced by DKH2. According to the limited tests of the author jxzou, MOs resulting from DKH2 and X2C are similar and often converge in few cycles.

### 4.5 List of Utilities in MOKIT

The utilities of transferring MOs are summarized in the following figure:



For detailed explanations of all utilities, please read the following subsections.

#### 4.5.1 add\_bgcharge\_to\_inp

This utility is designed to add background charges to the input file of various software packages. If you do not use background charges in your computation, you can skip this section. But if you do use them (e.g. in subsystems of fragmentation-based or embedding methods), they are not recorded in any .fch(k) file. This can be viewed as a defect of the .fch(k) file. Therefore, the generated input file by utilities `fch2com`, `fch2inp`, `fch2iporb`, or `bas_fch2py` will contain no background charges either.

To add background charges into the input file, you have to provide a .chg file which contains information of those charges. An example of such file is shown below

```
2
4.0  0.0  0.0  0.0  0.1
-4.0  0.0  0.0  0.0  0.1
```

The first line holds the number of point charges. While the charges are written starting from the second line, with format *x,y,z,charge*.

Note that in all computations of the AutoMR program, this situation is explicitly considered. This utility will be automatically called if needed. The only situation when you need this utility is merely using utilities `fch2com`, `fch2inp`, `fch2iporb`, or `bas_fch2py` (and of course, with background charges).

## 4.5.2 bas\_fch2py

Generate a PySCF .py file from a Gaussian .fch file. The Cartesian coordinates and basis set data are written in the .py file. Note: AutoMR does not use any built-in basis sets of PySCF, but always generates the basis set data from .fch file. This procedure ensures an (almost) exactly identical setting of basis set in Gaussian and PySCF.

This utility is in fact a wrapper of two utilities 'fch2inp' and 'bas\_gms2py'. So if you only want to compile this utility, you have to compile 'fch2inp' and 'bas\_gms2py' additionally.

Note that if you use background charges in your studied system, the background charges are not recorded in the .fch(k) file. So there are no background charges in the generated .py file, either. To add background charges, you need to use the utility add\_bgcharge\_to\_inp (see Section 4.5.1).

## 4.5.3 bas\_gms2molcas

Generate an (Open)Molcas .input file from a GAMESS .inp or .dat file. The Cartesian coordinates and basis set data are written in the .input file.

Two examples are shown and explained below

### (1) bas\_gms2molcas a.inp

Generate .inp file, in which the keywords 'Cartesian' of each atom are written (in order to use pure Cartesian type of basis functions)

### (2) bas\_gms2molcas a.inp -sph

Generate .inp file, in which the keywords 'Cartesian' of each atom are not written (in order to use pure spherical harmonic type of basis functions).

## 4.5.4 bas\_gms2molpro

Generate a Molpro .com file from a GAMESS .inp or .dat file. The Cartesian coordinates and basis set data are written in the .com file.

Two examples are shown and explained below

### (1) bas\_gms2molpro a.inp

Generate .inp file, in which the keyword 'Cartesian' is written (in order to use pure Cartesian type of basis functions)

### (2) bas\_gms2molpro a.inp -sph

Generate .inp file, in which the keyword 'Cartesian' is not written (in order to use pure spherical harmonic type of basis functions).

### 4.5.5 bas\_gms2py

Generate a PySCF .py file from a GAMESS .inp or .dat file. The Cartesian coordinates and basis set data are written in the .py file.

Two examples are shown and explained below

(1) `bas_gms2py a.inp`

Generate .inp file, in which the keyword 'mol.cart = True' is written (in order to use pure Cartesian type of basis functions)

(2) `bas_gms2py a.inp -sph`

Generate .inp file, in which the keyword 'mol.cart = True' is not activated (in order to use pure spherical harmonic type of basis functions).

### 4.5.6 dat2fch

Transfer MOs from GAMESS (.inp/.dat file) to Gaussian .fch file. Note that dat2fch can not generate a .fch file from scratch. The user must provide a .fch(k) file, and MOs in that file will be replaced. Five examples are shown and explained below

(1) `dat2fch a.dat a.fch`

This is used for transferring RHF, ROHF or CASSCF orbitals.

(2) `dat2fch a.dat a.fch -uhf`

This is used for transferring UHF orbitals.

(3) `dat2fch a.dat a.fch -gvb 5`

This is used for transferring GVB orbitals for spin singlet molecule. The order of GVB orbitals is different between Gaussian and GAMESS. Thus you must specify '-gvb [npair]' to tell the utility the number of GVB pairs, so that dat2fch can adjust the order of MOs.

(4) `dat2fch a.dat a.fch -gvb 5 -open 1`

This is used for transferring GVB orbitals for non-singlet molecule. In this way, you tell the utility the number of GVB pairs and singly-occupied orbitals, so that dat2fch can adjust the order of MOs.

(5) `dat2fch a.dat a.fch -no 5 10`

This is used for transferring natural orbitals (NOs) of CASCI/CASSCF. In this way, you tell the utility the beginning index and final index of NOs in .fch file, so that dat2fch can work correctly.

NOTE: the recommended way is to firstly use Gaussian to generate a .fch file (with keywords 'nosymm int=nobasistransform'), then generate the .inp file from .fch file. After GAMESS computations finished, you can transfer MOs from .dat back to .fch file. This procedure seems a little bit tedious, but it ensures an exact reproduce of energy in GAMESS.



This utility supports two types of basis functions: (1) pure spherical harmonic functions; (2) pure Cartesian functions. To transfer MOs from Gaussian to GAMESS, see Section 4.5.9.

### 4.5.7 extract\_noon2fch

Extract natural orbital occupation numbers (NOONs) from (1) .out file of PySCF or (2) .dat file of GAMESS, and write NOONs into a given .fch file. This is for the convenience of visualizing NOONs in GaussView.

### 4.5.8 fch2com

Generate a Molpro .com file from a Gaussian .fch(k) file, with alpha MOs written in a .a file. Two examples are shown and explained below

(1) `fch2com a.fch`

This is used for transferring RHF, ROHF or CASSCF orbitals.

(2) `fch2com a.fch -uhf`

This is used for transferring UHF orbitals. Besides, a new file with suffix '.b' will be generated, with beta MOs written in.

This utility will call another two utilities 'fch2inp' and 'bas\_gms2molpro'. So if you want to compile fch2com, you have to compile 'fch2inp' and 'bas\_gms2molpro' additionally.

Note that in Windows\* OS, any file with .com suffix/extension may be automatically associated with system, in which case double click of the mouse to open this file does not work. You have to right click on the .com file and choose 'open with'. You can modify the suffix/extension to .inp if you do not like that.

Note that if you use background charges in your studied system, the background charges are not recorded in the .fch(k) file. So there are no background charges in the generated .com file, either. To add background charges, you need to use the utility add\_bgcharge\_to\_inp (see Section 4.5.1).

### 4.5.9 fch2inp

Generate a GAMESS .inp file from a Gaussian .fch(k) file, with MOs written in the .inp file. The keywords in .inp file is already suitable for common simple calculations, but do check or modify it if you have additional requirements.

Note that due to the different types of MOs (RHF, UHF, GVB, and CASSCF orbitals), the fch2inp offers different options. Four examples are shown and explained below

(1) `fch2inp a.fch`

This is used for transferring RHF, ROHF or CASSCF orbitals.

(2) `fch2inp a.fch -uhf`

This is used for transferring UHF orbitals.

(3) `fch2inp a.fch -gvb 5`

This is used for transferring GVB orbitals for spin singlet molecule. The order of GVB orbitals is different between Gaussian and GAMESS. Thus you must specify ‘-gvb [npair]’ to tell the utility fch2inp the number of GVB pairs, so that fch2inp can adjust the order of MOs.

(4) `fch2inp a.fch -gvb 5 -open 1`

This is used for transferring GVB orbitals for non-singlet molecule. In this way, you tell the utility fch2inp the number of GVB pairs and singly-occupied orbitals, so that fch2inp can adjust the order of MOs.

This utility supports two types of basis functions: (1) pure spherical harmonic functions; (2) pure Cartesian functions. To transfer MOs from GAMESS back to Gaussian, see Section 4.5.6.

Note that if you use background charges in your studied system, the background charges are not recorded in the .fch(k) file. So there are no background charges in the generated .inp file, either. To add background charges, you need to use the utility `add_bgcharge_to_inp` (see Section 4.5.1).

## 4.5.10 fch2inporb

Transfer MOs from Gaussian to OpenMolcas/Molcas. A .input file and a .INPORB file will be generated. The .input file is the input file of OpenMolcas/Molcas, and it contains the geometry, basis set data and keywords. The .INPORB file contains the MOs. Three examples are shown and explained below

(1) `fch2inporb a.fch`

This is used for transferring RHF, ROHF or CASSCF orbitals.

(2) `fch2inporb a.fch -uhf`

This is used for transferring UHF orbitals.

(3) `fch2inporb a.fch -no`

This is used for transferring NOs.

Note: the default option is to transfer RHF MOs. If you want to transfer UHF MOs, use ‘`fch2inporb a.fch -uhf`’. There is also another option ‘-no’, which means reading NOONs and NOs from .fch(k) file and printing them into the .INPORB file. The NOONs written in the .INPORB file does not affect the calculations in OpenMolcas at all. It just make the file appear more readable.

This utility will call another two utilities ‘fch2inp’ and ‘bas\_gms2molcas’. So if you want to compile fch2inporb, you have to compile ‘fch2inp’ and ‘bas\_gms2molcas’ additionally.

Note that if you use background charges in your studied system, the background charges are

not recorded in the .fch(k) file. So there are no background charges in the generated .inp file, either. To add background charges, you need to use the utility `add_bgcharge_to_inp` (see Section 4.5.1).

### 4.5.11 fch2mkl

Transfer MOs from Gaussian to ORCA. A .inp file and a .mkl file will be generated. The .inp file of ORCA holds the geometry, basis set data and keywords. The .mkl file contains the MOs. Similarly, add an argument ‘-uhf’ for transferring UHF MOs.

**Note 1:** you need to run ‘`orca_2mkl a.mkl -gbw`’ to generate the ORCA .gbw file since ORCA cannot read .mkl file directly.

**Note2:** the default keywords in .inp file does not contain any RI approximations, and settings of VeryTightSCF are written (the author does this to ensure an exact reproduce of energy in ORCA). You can modify keywords as you wish, but note that an exact reproduce of energy may not be assured.

Note that if you use background charges in your studied system, the background charges are not recorded in the .fch(k) file. So there are no background charges in the generated .inp or .mkl file, either. To add background charges, you need to use the utility `add_bgcharge_to_inp` (see Section 4.5.1).

### 4.5.12 fch\_mo\_copy

Copy MOs from one .fch file into another .fch file. An example is shown below

```
./fch_mo_copy a.fch b.fch
```

The default is to copy Alpha MOs in a.fch to Alpha MOs in b.fch. There are 4 optional parameters ‘-aa’, ‘-ab’, ‘-ba’, ‘-bb’. For example, ‘-ab’ means copying Alpha MOs from a.fch to Beta MOs in b.fch.

### 4.5.13 fch\_u2r

Transform a UHF-type .fch file into a RHF-type one. Only alpha MOs are retained.

### 4.5.14 frag\_guess\_wfn

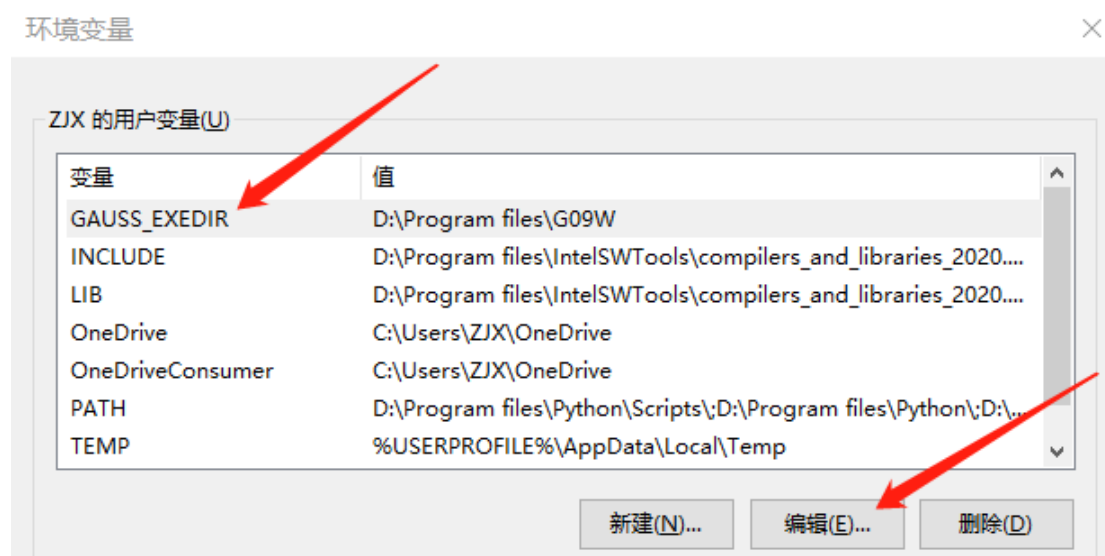
This is a utility designed to perform a SCF (i.e. HF or DFT) computation using initial guess constructed from molecular orbitals of fragments. The Gaussian software package will be called to perform SCF computation for each fragments (and only Gaussian is supported). The input file is exactly the Gaussian .gif file, in which the atoms, charge and spin multiplicities of each fragment are properly defined.

The SCF computations of radicals and transition-metal-containing molecules often suffers from multiple UHF/UKS solutions. Using a proper fragment guess (i.e., the ‘guess(fragment=*N*)’ keyword in Gaussian), one can then obtain a desired SCF solution or a lower energy solution after SCF converged and a check of wavefunction stability of the whole system. However, the wavefunction stability of each fragment in the initial guess cannot be assured in Gaussian, thus not efficient for complicated molecules. This utility – frag\_guess\_wfn – can ensure the wavefunction stability of each fragment and allow the usage of RHF/UHF (or RKS/UKS) for different fragments, which would improve the quality of initial guess and save time for subsequent SCF computation of the whole system. Examples of the fragment guess can be found at <http://gaussian.com/afc>. If you can read Chinese, a nice introduction to this topic from Sobereva’s blog

《谈谈片段组合波函数与自旋极化单重态》 <http://sobereva.com/82>

is recommended.

The Windows pre-built executable frag\_guess\_wfn is provided at [Releases](#). Note that you should define the environment variable %GAUSS\_EXEDIR% (in Windows\* OS) before using this utility, since Gaussian program would be called to perform SCF computations. For example, search “environment variable” in your Windows search bar and click **Edit** to add a new environment variable, and set it as the correct G03W, G09W or G16W directory. A screenshot is shown below



#### 4.5.15 gvb\_sort\_pairs

Sort (part of) MOs in descending order of the pair coefficients of the 1st natural orbital in each pair. This utility is designed only for the GAMESS .dat file. A new .dat file will be generated, in which the sorted MOs and pair coefficients are held.

#### 4.5.16 mkl2fch

Transfer MOs from ORCA .mkl file into Gaussian .fch(k) file. A .fch(k) file must be provided

by the user, in which the geometry and basis set data are valid (i.e. specifying 'noysmm int=nobasistransform 5D 7F' in Gaussian).

Note that the number of digits in .mkl file is only 7, and the scientific notation is not used. Therefore, the transferred MOs will not be very accurate. This should be sufficient for visualizing orbitals and common wavefunction analysis, but may cause up to  $10^{-5}$  a.u. error on electronic energy in further computations. This can be viewed as a defect of the orca\_2mkl utility in ORCA program. You are recommended to bring up an issue or request in the ORCA forum (<https://orcaforum.kofo.mpg.de>), to suggest ORCA developers to fix this. If the scientific notation is not used, then 10 digits of MO coefficients should be sufficient for further computations.

Three examples are shown and explained below

(1) `mkl2fch a.mkl a.fch`

This is used for transferring R(O)HF orbitals.

(2) `mkl2fch a.mkl a.fch -uhf`

This is used for transferring UHF orbitals.

(3) `mkl2fch a.mkl a.fch -no`

This is used for transferring NOs.

## 4.5.17 orb2fch

Transfer MOs from OpenMolcas \*Orb file (e.g. .ScfOrb, .RasOrb.1, .UnaOrb, .UhfOrb, etc) to Gaussian .fch(k) file. A .fch(k) file must be provided by the user, in which the geometry and basis set data are available. Five examples are shown and explained below

(1) `orb2fch a.ScfOrb a.fch`

This is used for transferring RHF orbitals.

(2) `orb2fch a.RasOrb a.fch`

This is used for transferring CASCI/CASSCF or RASCI/RASSCF (pseudo)canonical orbitals.

(3) `orb2fch a.UnaOrb a.fch -no`

This is used for transferring UNOs.

(4) `orb2fch a.UhfOrb a.fch -uhf`

This is used for transferring UHF alpha and beta MOs.

(5) `orb2fch a.RasOrb.1 a.fch -no`

This is used for transferring CASCI/CASSCF or RASCI/RASSCF NOs.

### 4.5.18 mo\_svd

Output the singular values of the overlap matrix between two sets of MOs. This utility will first read the atomic overlap matrix from a given file, then calculate the overlap matrix between two sets of MOs. Finally, perform singular value decomposition (SVD) on the molecular orbital overlap matrix and print information about singular values. The first two command line arguments can be both Gaussian .fch files, or both OpenMolcas orbital files (.INBORB, .RasOrb, etc). The third argument is a Gaussian .log file or a OpenMolcas output file, in which the atomic overlap matrix is written.

The singular values can be used to measure the overlap or similarity of two sets of MOs. If all singular values are close to 1, the compared two sets of MOs are very similar. Any singular value being close to 0 means there exists at least 1 distinct orbital.

### 4.5.19 solve\_ON\_matrix

Compute the occupation number matrix (a non-diagonal matrix) of a set of MOs. Assuming you have a .fch(k) file which holds some kind of MOs, and another .fch(k) file which holds some kind of NOs and corresponding NOONs, then this utility can compute the occupation numbers of this set of MOs (transformed from NOs and NOONs). Of course, in this case the occupation number matrix of MOs is not a diagonal matrix, only the diagonal elements are written into the 'Alpha Orbital Energies' section of the file which holds MOs.

The utilities below are compiled by **f2py**, which is a Fortran to Python interface generator. These utilities are not executable files, but dynamic libraries \*.so in \$MOKIT\_ROOT/lib. They can only be called in a Python script. And this is the reason that why one of the environment variables of MOKIT is 'PYTHONPATH', not 'LD\_LIBRARY\_PATH'.

### 4.5.20 fch2py

Transfer MOs from Gaussian to PySCF. By importing fch2py, PySCF Python script is able to read alpha and/or beta MOs from a provided .fch file.

### 4.5.21 py2fch

Export MOs from PySCF to a Gaussian .fch file. Note that py2fch cannot generate a .fch file from scratch. The user must provide one .fch file, in which the 'Alpha Orbital Energies' and 'Alpha MOs' sections will be replaced by occupation numbers and MOs from PySCF.

The provided .fch file must contain exactly the same geometry and basis set data as those data

of PySCF. To obtain a valid .fch file, it is strongly recommended to use the `bas_fch2py` utility to generate a .py file from a .fch file first, and then import `py2fch` in this generated .py file. These descriptions seem a bit of tedious. But a rigorous transferring of MOs between two programs or two files is ensured.

#### 4.5.22 xml2fch

Transfer MOs from Molpro .xml file to Gaussian .fch(k) file. Note that `xml2fch` cannot generate a .fch file from scratch. The user must provide one .fch file, in which the ‘Alpha Orbital Energies’ and ‘Alpha MOs’ sections (and possibly Beta sections) will be replaced by occupation numbers and MOs from Molpro .xml file. Three examples are shown and explained below

(1) `xml2fch a.xml a.fch`

This is used for transferring R(O)HF orbitals.

(2) `xml2fch a.xml a.fch -uhf`

This is used for transferring UHF orbitals.

(3) `xml2fch a.xml a.fch -no`

This is used for transferring NOs.

## 5 Examples

See examples in `$MOKIT_ROOT/examples/`. More details to be added.

## Appendix

### A1 Frequently Asked Questions (FAQ)

#### Q1: Find errors like ‘xxx: command not found’. What is the solution?

**A1:** This is simply because you haven’t installed the corresponding software, or you didn’t write environment variables correctly. Two examples are shown below:

Example 1: the error ‘-bash: f2py: command not found’ means there is no `f2py` on your computer, see Section **2.1 Prerequisite** for details.

Example 2: assuming you’ve compiled MOKIT successfully, but got the ‘-bash: automr: command not found’ error. Then you should check the MOKIT paths in your `~/.bashrc`. See Section **2.3 environment variables** for details.

#### Q2: Is there any Windows/Mac OS pre-compiled or pre-built version of MOKIT?

**A2:** The author offers 16 utilities of Windows\* OS pre-built executables, which are released as a [.zip file](#). See instructions for download and setting environment variables in Section 2.1.

The AutoMR module is not included in pre-compiled executables, since multi-reference calculations are usually performed on high-performance computers/platforms, which usually contain Unix/Linux systems. However, if you really need all modules or utilities under Windows, you can compile the source code on your laptop/computer/node by yourself. The Mac OS pre-compiled executables will never be considered by the author.

**Q3: Why the utilities `dat2fch`, `py2fch`, `mkl2fch` and `orb2fch` cannot generate a .fch file from scratch, but require the user to provide one?**

**A3:** Strictly speaking, to correctly transfer MOs between different programs requires 'int=nobasistransform nosymm' (and also possibly '5D 7F' or '6D 10F') keywords in Gaussian, and equivalent keywords in other quantum chemistry programs. This rule also applies to other programs/software which claim they can transfer MOs or support file transformation.

However, the utility/subroutine (which transfers MOs) cannot detect whether the users have truly specified 'int=nobasistransform nosymm' (and also possibly '5D 7F' or '6D 10F') keywords, or equivalent keywords in other programs. Then transferring MOs in such case is very dangerous, i.e. correctness cannot be assured. For example, using the built-in basis sets in other programs instead of basis sets generated by MOKIT is dangerous, since the built-in basis sets in other programs are generally not exactly identical to those generated by MOKIT.

Therefore, the author jxzou has to require the users to provide a .fch file, to remind the users that proper keywords must be used in Gaussian. And the most recommended approach is to use utilities in MOKIT (e.g. `fch2inp`, `bas_fch2py`, etc) to generate input files of other quantum chemistry programs. The users use these generated input files to perform their desired computations. After jobs finished, use `dat2fch` and `py2fch` to transfer MOs back to the .fch file. Such an approach is already applied in AutoMR.

**Q4: Can MOKIT support more types of files? Transferring MOs between other programs like QChem, NWChem is possible?**

**A4:** The author jxzou wishes to make the MOKIT recognize all kinds of MO files of quantum chemistry programs, but he is not likely to be familiar with all programs. Therefore, if you are very familiar with any program (other than supported ones in MOKIT), and you happens to need a transferring of MOs, please contact jxzou and tell him the information in the MO file of that program. With the help from experienced users, the development will be much easier.

**Q5: Why there is a keyword error in OpenMolcas output when using DKH2 Hamiltonian? Two possible errors are given: (1) ERROR: RELATIVISTIC is not a keyword!, Error in keyword. (2) ERROR: R02O is not a keyword!, Error in**



## **keyword.**

**A5:** This is due to a recent update of OpenMolcas. If version  $\leq 18.09$ , the keyword for DKH2 is simply `R02O`; but for version  $\geq 20.10$ , this keyword become `RELAtivistic = R02O`. For version  $> 18.09$  and  $< 20.10$ , the author jxzou has no manual and thus it is not tested (but you can test if you like).

If you encounter any of the two errors, you have two choices: (1) update your OpenMolcas to a newer version, e.g.  $\geq 20.10$ ; (2) modify the source code of MOKIT and re-compile it. If you choose (2), you will need to modify the words ‘RELAtivistic = R02O’ to ‘R02O’ in file `src/automr.f90`, and run ‘make automr’ in Shell to re-compile the program automr.

## **Q6: How does AutoMR read the paths of Gaussian, OpenMolcas, PySCF, ORCA, and GAMESS?**

**A6:** For Gaussian, the paths of executable files are read from the environment variables `$GAUSS_EXEDIR`. For PySCF and OpenMolcas, the ‘python’ and ‘pymolcas’ executable files are used directly, assuming the user had installed the corresponding programs correctly. For ORCA and GAMESS, the user must define the `$ORCA` and `$GMS` environment variables in his/her `~/.bashrc` file, such that the automr program can find corresponding paths.

## **Q7: What are the possible reasons and solutions of the following errors**

**(1) ‘\*\*\*\*\* ERROR \*\*\*\* DIMENSIONS EXCEEDED \*\*\*\*\*’**

**(2) ‘PAIR=   xx MAX=   12’**

**(3) ‘DDI Error: Could not initialize xx shared memory segments.’**

**(4) ‘DDI was compiled to support 32 shared memory segments.’**

**(5) ‘The GAMESS executable gamess.01.x or else the DDIKICK executable ddikick.x could not be found in directory...’**

**in GAMESS .gms file (where xx is an integer  $> 12$ )?**

**A7:** Please read Section 4.4.9 carefully.

**Q8: Errors like ‘semget errno=ENOSPC -- check system limit for sysv semaphores’ found in the .gms file. Why? How to solve?**

**A8:** Please read [FAQ of GAMESS](#) carefully.

## **A2 Limitations and Suggestions**

### **1. Basic knowledge of multi-reference methods**

Although MOKIT is a useful tool for black-box multi-reference computations, the users are

assumed to know basic knowledge of multi-reference methods. If he/she does not even know the meaning of  $CAS(m,n)$ , then the results of MOKIT are meaningless to he/she, and even wrong explanations may be made from the results. Therefore, if you know little about the multi-reference methods, I recommend you the following materials:

(1) the ORCA CASSCF-tutorial (<https://orcaforum.kofo.mpg.de/app.php/dlxt/?cat=4>), which is a quickstart guide (but also detailed) for CASSCF computations. To download this .pdf file, you may need to (register and) login to the forum.

(2) to be added.

## 2. Symmetry

Unfortunately, molecular point group symmetry cannot be taken into consideration in any module of MOKIT. This is due to: (1) use of symmetry may change the orientation of the target molecule, and the MO coefficients will be changed accordingly; (2) localized orbitals are used in almost all modules of AutoMR, this usually contradicts with symmetry.

## 3. The validity of MOs obtained by AutoMR for excited state calculations

When you use AutoMR to perform a ground state CASSCF calculation, the obtained CASSCF MOs (whether pseudo-canonical MOs or NOs) is supposed to be excellent for the ground state electronic structure of the target molecule. And you can use this set of MOs (held in a .fch file) to further conduct excited state calculations like state-averaged CASSCF (SA-CASSCF). And moreover, NEVPT2, CASPT2 or MRCISD, if you wish.

However, the resulting excitation energies and excited state MOs (e.g. state-averaged NOs) are not necessarily excellent. Here ‘not necessarily excellent’ means for some molecules you may get good results while may be unsatisfactory for some other molecules. The reason is simple: the current algorithms in AutoMR focus on the multi-reference characters in the ground state of the molecule. Thus AutoMR ‘finds’ excellent active orbitals of the ground state. But the active orbitals of excited states are not necessarily the same as those of the ground state. And the orbital optimization in SA-CASSCF does not guarantee leading to good MOs for excited states. This problem actually exists in almost all methods which feature block-box or automatic multi-reference calculations.

## 4. Possible multiple solutions of UHF

There may exist multiple UHF solutions when a covalent bond cleavages homolytically, or in a transition-metal-containing molecule. In these special cases, if you use  $ist=0$ , the UHF calculated by AutoMR may be not the lowest UHF solution (but it is stable). You may need to perform several

UHF computations (by yourself) using various initial guesses. After you identify the lowest UHF solution, you can use keywords `ist=1` and `'readuhf'` to read in the desired UHF .fch file.

## 5. Density in the .fch file

In the current version of MOKIT, the CASCI or CASSCF NOs are stored in the corresponding \*\_NO.fch files after CASCI or CASSCF job finished. However, the density in any \*\_NO.fch file ('SCF Density' Section) may be wrong, they are possibly not CASCI or CASSCF density!!! In MOKIT 2.0, this defect will be removed. The exception is that you use the Gaussian as the CASCI/CASSCF solver, so that the density in .fch file is right.

To conclude, if you need CASCI or CASSCF density (to perform population analysis, wave function analysis, etc), USE THE GAUSSIAN SOFTWARE PACKAGE AS THE CASCI OR CASSCF PROGRAM (i.e. `cascli_prog=Gaussian` or `casscf_prog=Gaussian`).

## A3 Bug Report

If you find any bug frequently occurs, you can contact the author jxzou via E-mail [njumath\[at\]sina.cn](mailto:njumath[at]sina.cn), with your input file (.gjf, .fch) and output files attached. Or you can open an issue on gitlab page of MOKIT (<https://gitlab.com/jxzou/mokit/>). The author may not answer or update code frequently since he is being postponed due to his PhD program.

## A4 Acknowledgement

Thanks Mr. Shirong Wang for constructive suggestions and bugs report.