

A guide to the Tight-Binding FITting (TBFIT) package

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This document is to provide explanation for the input file arguments of the TBFIT package.

System Requirements and installation

The program has been written by modern Fortran2008 language. If you want to deactivate the use of some module interfaces written in Fortran2008 syntax, please remove -DF08 option in your option tag of the makefile.

LAPACK library should be properly linked in the makefile. For the eigenvalue solver with sparse matrix, Inspector-executor Sparse BLAS Routines and Extended Eigensolver Routines in the Intel Math Kernel Library (Intel MKL) are referred. If the system size is very big, you can calculate band structure with energy window constraint. This is available with EWINDOW tag and -DMKL_SPARSE option. To use -DMKL_SPARSE option, make sure that mkl-splblas.f90 file is located in your \$MKLPATH/include folder.

To list up the space group information for the given geometry in the initial stages of the calculations, one can activate the use of space group library (Spglib). For this, put -DSPGLIB in your OPTION tag of the makefile, and provide appropriate library path in SPGLIB tag.

```
#-----|
# Compiler options and bin path      |
#-----|
OPTIONS= -fpp -DMPI -DF08 -DSPGLIB -DMKL_SPARSE
F90      = mpif90 $(OPTIONS)
FFLAG    = -O3 -heap-arrays -nogen-interfaces
BIN      = ~/code/bin
```

```
#-----|
# Dependencies: LAPACK, SPGLIB      |
#-----|
SPGLIB = -L/Users/Infant/code/lib/ -lsymspg
MKLPATH= $(MKLROOT)
LAPACK = -L$(MKLPATH)/lib/
          -lmkl_intel_lp64 -lmkl_sequential
          -lmkl_core -liomp5
_____ makefile example _____
```

- How to install:

```
> tar -xvf TBFIT-master.zip
> cd TBFIT-master
> make tbfit
```

- How to run:

In the **Example** directory, you can run a test cases, for example:

```
> cd TBFIT-master/Example/1H-MoS2/SOC
> tbfit < /dev/null | tee log.out
```

Note that the output log will be written in `log.out` file.

Part I.

User's Guide

1. INPUT tags of the INCAR-TB

GET_BAND *logical* Default: .TRUE. If .TRUE. **TBFIT** will perform tight-binding calculations for band structure evaluation.

TBFIT *logical* Default: .FALSE.

.TRUE. : Perform tight-binding parameter fitting which is defined in **PFILE**. After fitting is completed, whatever it is converged or not, additional tight binding calculations as defined in the INCAR-TB will be performed.

.FALSE. : Do not perform fitting procedures. In this case, regular tight binding calculations will be performed.

MITER *integer* Default: 100

Maximum number of iteration for the fitting procedures. If **GA** is set for **LSTYPE**, **MITER** represents the maximum number of generations.

MXFIT *integer* Default: 1

Maximum number of repeat for LMDIF procedures after **MITER** steps done. By checking convergence criteria defined by **FDIF** the variation of the fitness function, parameter constraints, i.e., upper or lower bounds defined by **SET CONSTRAINT** tags, **TBFIT** will determine to stop or not.

LSTYPE *integer* Default: LMDIF

Method for parameter fitting. Available tags are **LMDIF** and **GA**.

LMDIF method: Levenberg-Marquardt method^{1, 2} using finite-difference for Jacobian.

GA method: Genetic Algorithm³ based on PIKAIA library^{4,5,6,7}. To setup control parameters for the **GA**, see Sec. **GA**.

¹ Kenneth Levenberg, "A Method for the Solution of Certain Non-Linear Problems in Least Squares" *Quarterly of Applied Mathematics* 2, 164 (1944).

² Donald Marquardt, "An Algorithm for Least-Squares Estimation of Nonlinear Parameters" *SIAM Journal on Applied Mathematics* 11, 431 (1963).

³ D. E. Goldberg, "Genetic Algorithm in Search, Optimization, & Machine Learning" *Addison-Wesley* (1989).

⁴ P. Charbonneau and B. Knapp, "A user's guide to PIKAIA 1.0", (NCAR Technical Note 418+IA, 1995)

⁵ P. Charbonneau, "An introduction to genetic algorithm for numerical optimization" (NCAR Technical Note 450+IA, 2002)

⁶ P. Charbonneau, "Release notes for PIKAIA 1.2" (NCAR Technical Note 451+STR, 2002), <http://www.hao.ucar.edu/modeling/pikaia/pikaia.php>

⁷ Modern Fortran Edition of the Pikaia Genetic Algorithm. <https://github.com/jacobwilliams/pikaia>

PTOL & FTOL *real* Default: 0.00001

Tolerance of iteration of the fitting procedures for **LMDIF** method. **FTOL** is a tolerance for the difference between target and calculated data from tight binding method. **PTOL** is as tolerance for the tight binding parameters. Normally, both values below 0.00001 is sufficient to reach a local minima.

FDIFF *real* Default: 0.001

Tolerance of iteration of the fitting procedures for **LMDIF** method. **FDIFF** is a tolerance for the difference between fitness function of previous and last steps. After finishing **LMDIF** iterations, fitting procedures might start again if **CONSTRAINT** and **FDIFF** condition does not fulfill, and will stops by **MXFIT** criteria.

K_UNIT *string* Default: **ANGSTROM**

ANGSTROM : the unit of the k -point will be written in \AA^{-1} unit.

RECIPROCAL : the unit of the k -point will be written in reciprocal unit (fractional).

PFILE *string* File name for tight-binding parameters. Default: **PARAM.FIT.dat** For the details, see Sec.4.

Note 1: After fitting procedure is over, the **WEIGHT** information is written in **PFILE** so that one can restart fitting. To use **WEIGHT** information written in **PFILE**, one can add **USE.WEIGHT** tag as below:

```
PFILE  PARAM_FIT.dat  USE_WEIGHT
```

POFILE *string* Output file name for tight-binding parameters written after fitting procedures. Default: **PARAM.FIT.new.dat**

IS_SK or SLATER_KOSTER *logical*

.TRUE. : Slater-Koster type of hopping parameters will be assumed.

.FALSE. : User defined or direct hopping parameters will be assumed. *Warning* : This is experimental feature and on the development stages (do not set to **.FALSE.**).

SGPLIB *logical*

.TRUE. : Write space group information to the output log.

.FALSE. : Do not write space group information to the output log.

Note that this option is only applicable if you have put **-DSPGLIB** option in your makefile . See the details in **System Requirements and installation** section.

EFILE *string, integer*

File name for the *target* band structure for the fitting procedures. If the second *integer* n is followed by, **TBFIT** will read n -th column as a target band. Default is $n=2$.

EFILE DFT_BANDSTRUCTURE.dat 2

```
# 1st eigen value
# k-path  energy(eV)
0.000000 -12.36137
0.01693  -12.36162
0.03386  -12.36118
[...]
0.16932  -12.33324
0.18625  -12.32696
0.20319  -12.32014
```

```
# 2nd eigen value
# k-path  energy(eV)
0.000000 -12.36137
0.01693  -12.36041
0.03386  -12.35875
[...]
0.16932  -12.32136
0.18625  -12.31394
0.20319  -12.30600
```

[...]

EFILE DFT_BANDSTRUCTURE.out example

If **LORDER** = .TRUE. and **TBFIT** = .TRUE., re-ordered target energy information should be provided in parallel with the original energy, as below:

```
# k-path          energy(eV)      energy_ordered(eV) : 1st eig
0.000000000      -14.75638384      -14.75638384
0.04796527       -14.74941045      -14.74941045
[...]
2.95861071       -14.74708715      -14.74708715
3.01399626       -14.75638384      -14.75638384
```

[...]

```
# k-path          energy(eV)      energy_ordered(eV) : 3rd eig
0.000000000      -2.27711578       -2.27711578
0.04796527       -2.27002886       -2.27002886
[...]
2.95861071       -2.26767593       -0.44510940
3.01399626       -2.27711578       -0.44395430
```

[...]

EFILE DFT_BANDSTRUCTURE_ORDERED.out example

If the second argument is *VASP*, **TBFIT** will read **EFILE** which is indicated as the first argument and recognize this file as a *EIGENVAL* file of *VASP* code. (note: In this case, **LORDER** should be *.FALSE.*) For example,

```
EFILE EIGENVAL VASP
```

EFILE_EF *real*

The fermi level of **EFILE**. The energy will be shifted by the **EFILE_EF**, i.e., $\epsilon_{n,k}^{target} = \epsilon_{n,k}^{DFT} - \text{EFILE_EF}$, where $\epsilon_{n,k}^{DFT}$ is the eigenvalues provided by the **EFILE**.

GFILE *string* Default: *POSCAR-TB*

File name for the geometry and atomic orbital informations. The format is exactly same as *POSCAR* of *VASP* program. For the details of setting atomic orbitals, see Sec.3.

```
GFILE POSCAR-TB
```

The example file format of "GFILE" is as follows,

```
MoS2 # comment
1.0000000000000000 # scaling factor
3.1716343 0.000000 0.000000 # lattice vector a1
1.5858171 2.746715 0.000000 # lattice vector a2
0.0000000 0.000000 15.000000 # lattice vector a3
Mo S # atomic species
1 2 # number of atoms per species
Direct # coordinate type (direct or cartesian)
0.00000 0.00000 0.50000 dz2 dxy dx2 dyz dxz # coord, orbital
0.33333 0.33333 0.60645 s px py pz
0.33333 0.33333 0.39354 s px py pz
_____ POSCAR-TB example: MoS2 with Mo-d and S-sp _____
```

Note: **TBFIT** reads "GFILE" and reports it on to the screen in the parsing steps. If "PRINT_GEOM *.FALSE.*" tag is followed by, then program will not report the geometry informations, for the convenience.

```
GFILE POSCAR-TB PRINT_GEOM .FALSE.
```

KFILE *string* Default: *KPOINTS_BAND*

File name for the *k*-point setting. The format is exactly same as *KPOINTS* of *VASP* program.

```

k-points line mode example
40 ! intersections
Line-mode
Reciprocal
0.50000000 0.5000000 0 M
0.33333333 0.6666666 0 K

0.33333333 0.6666666 0 K
0.00000000 0.0000000 0 G

0.00000000 0.0000000 0 G
0.66666666 0.3333333 0 K'

```

_____ KPOINTS_BAND *line mode example* _____

```

k-points grid mode example
0
GMonkhorst-Pack #'G'amma centered grid mode
4 4 1 # grid nk_1 nk_2 nk_3
0 0 0 # shift

```

_____ KPOINTS_BAND *grid mode example* _____

Note1: In **VASP**, n k -points are generated along a k -path if n division is specified in the second line of KFILE. This will give $n \times m$ total k -points and $n - 1$ divisions along each k -path, where m represents the total number of k -path specified. And at the end of each line segment of k -path, same k -points are marked twice. However, some program, such as **FLEUR** uses different strategy in generating k -path, that is, $n + 1$ k -points along each path with only one k -points at the end of line segments. Hence, **EFILE** originated (or postprocessed) from **FLEUR** would have different format. This will give $n \times m + 1$ total k -points and n division of each k -path. You can read this kind of **EFILE** file as well, if you have also specify as below, letting **TBFIT** to recognize the type of generated k -path.

KFILE KPOINTS_BAND FLEUR

Note2: If your target band structure is originated from **FHI-aims**, the division between each k -path can be specified separately. For example, the typical way to specify band structure calculation tag in **FHI-aims** looks as follows:

```

output band 0.00 0.00 0.00 0.50 0.00 0.00 70 G X
output band 0.50 0.00 0.00 0.50 0.50 0.00 20 X M
output band 0.50 0.50 0.00 0.00 0.50 0.00 70 M Y

```

Here, each k -path is divided with 70, 20, and 70 divisions. In this case, you can specify each numbers (70 20 70) to your second line of [KFILE](#).

```
k-points line mode example
  70 20 70 ! intersections
Line-mode
Reciprocal
  0.0  0.0 0.0 G
  0.5  0.0 0.0 X

  0.5  0.0 0.0 X
  0.5  0.5 0.0 M

  0.5  0.5 0.0 M
  0.0  0.5 0.0 Y
_____ KPOINTS_BAND line mode (FHI-aims type) _____
```

KREDUCE *integer* Default: 1

For some cases, the target [EFILE](#) contains too many k -points with larger n of divisions between each line segment. In this case, you can reduce the number of k -points to be read by skipping k -points except every nk_{reduce} .

For example, if it has been divided with 10 k -points between each symmetry points in your [EFILE](#), you can reduce by factor of 2 or 5 by specifying

```
KREDUCE      2
or
KREDUCE      5 .
```

In this case, if [KREDUCE](#) is 2, then the total number of divisions will become 5, and this value should be same as number of k -point division which is specified in second line of your [KFILE](#). Note that [KREDUCE](#) should be one of prime number of the k -point division of [EFILE](#).

LOCCHG *logical* Default: .FALSE.

Setting tag for local potential. If .TRUE., one should give proper local potential parameter in your [PFILE](#) and should properly setup [LOCAL.POT](#) tag in your [GFILE](#). For the details, see the explanation of [LOCAL.POT](#) in Sec.4.

TYPMAG *string* Default: NONMAG

Setting tag for magnetic moment: `nonmagnetic`, `collinear`, `noncollinear` If `collinear` and `noncollinear` tag is applied, [MOMENT](#) or [MOMENT.C](#) in the [GFILE](#) should be set up appropriately. For details, see [MOMENT](#) of the Sec.3.

LSORB *logical* Default: `.FALSE.`

Setting tag for spin-orbit coupling. If `.TRUE.`, *lambda_orb_spec* should be properly defined in the [PFILE](#). For details, see [Sec.4](#)

LORBIT *logical,string(optional),string(optional)* Default: `.TRUE.`

Setting tag for orbital decomposed output. If `.TRUE.`, the local orbital contribution will be printed out in `bandstructure_TBA.dat` file. If you write `rh` or `mx` or `my` or `mz` next to the logical text with `.TRUE.`, then, corresponding magnetization values, which represents the expectation value of pauli matrices σ_i where $i=\{0,1,2,3\}$, will be printed out. Here σ_0 is 2×2 identity matrix to print out local orbital contribution. For example,

```
LORBIT .TRUE. mz
```

will print out `<mz>`. If you write `re` or `im` next to the logical text with `.TRUE.`, then, `real` or `imaginary` part of the wavefunction coefficient will be printed out. Note that this option only applicable with `LSORB .FALSE.` in the current version.

```
LORBIT .TRUE. re
```

If you write `wf` next to the logical text with `.TRUE.`, then, the wavefunction coefficient will be printed out. The real and imaginary part for each orbital basis is written. If `LSORB .TRUE.`, the spinor-up and spinor-dn part will be written, so that four real values will construct wavefunction coefficient.

```
LORBIT .TRUE. wf
```

Note that the corresponding output file `bandstructure_TBA.dat` file will be basically written by `ascii` (formatted) format. If you want to write in `binary` (unformatted) format, specify by `bin` (complex*16; double precision) or `bin4` (complex*8; single precision) tag next⁸. For example,

```
LORBIT .TRUE. wf bin
or
LORBIT .TRUE. wf bin4
```

This tag will generate `band_structure_TBA.(up/dn).bin` file.

⁸In the current version, `bin` or `bin4` tag is only applicable when it is combined with `wf` option

PROJ_BAND *logical, integers* Default: .FALSE.

Setting tag for orbital/atom projected band structure output. The output will be written in separate file for each atom. The correct usage is as follows:

```
PROJ_BAND .TRUE. 1:4 7
```

then you can get `band_structure_atom.#.dat` file

```
band_structure_atom.1.dat
band_structure_atom.2.dat
band_structure_atom.3.dat
band_structure_atom.4.dat
band_structure_atom.7.dat
```

and additionally, `band_structure_atom.sum1.dat` file will be printed out as well, where projected local DOS for those atoms ($\{1,2,3,4,7\}$) are summed up in a single file.

If you write another PROJ_BAND tag specifying different atom sets in the separate line, for example,

```
PROJ_BAND .TRUE. 1:4 7
PROJ_BAND .TRUE. 5:8
```

then, you can get another set of files (`band_structure_atom.sum2.dat` and `band_structure_atom.{5..8}.dat`) as follows:

```
band_structure_atom.1.dat
band_structure_atom.2.dat
band_structure_atom.3.dat
band_structure_atom.4.dat
band_structure_atom.5.dat
band_structure_atom.6.dat
band_structure_atom.7.dat
band_structure_atom.8.dat
band_structure_atom.sum1.dat  (= 1+2+3+4+7)
band_structure_atom.sum2.dat  (= 5+6+7+8)
```

Note1: The atom index should be written in ascending order and should not exceed total number of atoms of your system.

Note2: Since in the `band.structure.atom.sum?.dat` file the projected local DOS for each orbital basis of the specified atoms are summed up, one should make sure that the specified atoms should have same orbital basis set. For instance, let's assume that you have atoms $A=\{1:4, 7\}$ with orbitals p_x, p_y, p_z , and atoms $B=\{5:8\}$ with orbitals s, p_x, p_y, p_z . Then it will work fine with "PROJ_BAND .TRUE. 1:4 7" tag, but not work fine with "PROJ_BAND .TRUE. 1:4 5:8".

LOAD_HOP *logical, string* Default: `.false.`

If `.true.`, one can load hopping file to read t_{ij} value. The following *string* should be the file name to be read. And the syntax of the file should be exactly same as the `hopping.dat` file, which is generated in the initial stages of the calculation. Hence, if you have pre-generated `hopping.dat` file (with `LOAD_HOP .FALSE.`), you can copy it with a different name and modify the elements of t_{ij} column, and rerun the code with following tag (for example, if you have copied `hopping.dat` → `hopping_modified.dat`):

```
LOAD_HOP .TRUE. hopping_modified.dat
```

Below, you can see that the original hopping element can be modified by changing values of the `t_IJ(eV)` column.

#	Iatom	Jatom	Rij			...	ORB_I	...	ORB_J	...	t_IJ(eV)	...
1	1	1	0.0	0.0	0.0	...	s	...	s	...	-4.0	...
1	1	1	0.0	0.0	0.0	...	s	...	px	...	0.0	...
1	1	1	-1.2	-0.7	0.0	...	s	...	s	...	-3.9	...
1	2	1	-1.2	-0.7	0.0	...	s	...	px	...	1.9	...
...												
...												

_____ hopping.dat example file _____

#	Iatom	Jatom	Rij			...	ORB_I	...	ORB_J	...	t_IJ(eV)	...
1	1	1	0.0	0.0	0.0	...	s	...	s	...	-2.0	...
1	1	1	0.0	0.0	0.0	...	s	...	px	...	0.0	...
1	1	1	-1.2	-0.7	0.0	...	s	...	s	...	-3.9	...
1	2	1	-1.2	-0.7	0.0	...	s	...	px	...	1.9	...
...												
...												

_____ hopping_modified.dat example file _____

IBAND *integer* Default: 1 (*deprecated*)

IBAND is the first eigenstate of the target data of `EFILE`. This value will be used in the `WEIGHT SET` section.

FBAND *integer* Default: NEIG (*deprecated*)

NEIG : number of orbital basis of the system. FBAND is the last eigenstate of the target data of **EFIELD**. This value will be used in the **WEIGHT SET** section.

SCISSOR *integer, real*

If set, in the fitting procedures, target energy $EDFT(n, k)$ will be shift by amount of the scissor operation. This operation works as follows: $E'_{target}(n, k) = E_{target}(n, k) + e_{scissor}$ if $n \geq i_{scissor}$. Note that this operation is only valied if **TBFIT** is **.TRUE..**

```
SCISSOR 29 0.2 # i_scissor = 29 and e_scissor = 0.2 (eV)
```

NN_MAX *integer* Default: 3

Determine how many times the cell will be repeated in searching hopping pairs. If your system is sufficiently larger than the maximal value of hopping distances of your system, this can be reduced to 1, otherwise just use default value.

```
NN_MAX 3 3 3
```

or

```
NN_MAX 3
```

both settings will give $3 \times 3 \times 3$ cell repeat.

ERANGE *integer* Default: 1 NEIG

If provided, the energy level between these energy window will be printed out in the **bandstructure_TBA.dat** file.

```
ERANGE 4400 4700
```

Above example means that the energy level from 4400^{th} to 4700^{th} will be printed. This is particularly useful if you calculate very large systems. By setting **ERANGE** tag, you can save disk space a lot if **LORBIT** tag is turned on where orbital component information takes huge memory for larger systems.

EWINDOW *real, integer* Default: not activated

The eigenvalues within the energy window [emin:emax] will be calculated and stored. This option also useful in dealing with huge system. The usage for this tag is as follows:

```
EWINDOW -5.0:5.0 NE_MAX 10
```

If provided, the energy level between these energy window will be printed out in the `bandstructure_TBA.dat` file.

In the above setting, the eigenvalue ($\{e\}$) within the energy window $[-5.0:5.0]$ will be calculated and stored. The `NE_MAX` represents the maximum number of eigenvalue to be searched within the window and usually should be larger than the number of actual eigenvalues (`NE`) within the range and should not exceed the total number of eigenvalue (`NE_TOT`) of the system. The optimal values for `NE_MAX` is about $1.5 \times \text{NE}$ ⁹. Since the `NE_MAX` is critical to the calculation speed, choosing the optimal values is essential. During the calculation, the program will find the optimal `NE_MAX` and update in every k-point loop.¹⁰

Note 1: If the tag is specified in your input file, the Hamiltonian matrix will be constructed with the sparse matrix format rather than dense matrix format. The libraries to dealing with the sparse matrix is referred from `Intel Math Kernel Library (MKL)`, please make sure that your library path is properly assigned. (suggest to use MKL version ≥ 11.3)

Note 2: If `NE_MAX` is not provided or exceeding `NE_TOT`, i.e., $\text{NE_MAX} \geq \text{NE_TOT}$, `NE_MAX` will be set to `NE_TOT` by default.

PRTSEPK *logical* Default: `.FALSE.`

If `.TRUE.`, band structure file, `band_structure_TBA.dat`, will be separated for each k -point, i.e., `band_structure_TBA.kp_1.dat`, `band_structure_TBA.kp_2.dat`, ..., etc. This tag is useful if you are dealing with very large system and many k -points, where due to the the memory problem, calculation get failed to be finished.

PRTHAMK *logical* Default: `.FALSE.`

If `.TRUE.`, hamiltonian matrix H_k will be written for each k -point into separate file `Matrix.Hk_Kik_SPis.dat`, where ik and is represents k -point and spin index, respectively.

LORDER *logical* Default: `.FALSE.`

If `.TRUE.`, band structure will be re-ordered by maximizing the overlap between neighboring k -points. The overlap can be defined by the inner product of the wavefunctions $\langle u_{n,k} | u_{m,k-1} \rangle$. The re-ordered band structure will be written in `band_structure_ordered.dat` file. If `OV_CUT` tag is also provided with *real* value, the cutoff for the overlap integral to be considered with the value. The bands above `OV_CUT` will be swapped. The default value is $\frac{\sqrt{2}}{2}$.

`LORDER .TRUE. OV_CUT 0.7`

⁹Eric Polizzi, "Density-matrix-based algorithm for solving eigenvalue problem" *Physical Review B* 79, 115112 (2009)

¹⁰Though, one need to provide reasonable `NE_MAX` to save the memory, since `NE_MAX` is used to reserve memory space for the eigenvector store internally.

NOTE: (important) If the `LORDER = .TRUE.` with `TBFIT = .TRUE.`, then the fitting will be done with re-ordered band structure. Therefore, re-ordered target energy information should be provided in parallel with the original energy in `EFILE`. Please check `EFILE` tag, for the instruction how to provide re-ordered energy in this case. To get re-ordered energy: for `VASP`, one can use `VaspBandUnfolding` tools for re-ordering; for `QE`, one can use `bands.x` postprocessing program. In this case, `WEIGHT` tag should be carefully adjusted according to the re-ordered band index.

LPHASE *logical* Default: `.TRUE.`

If `.TRUE.`, we construct Bloch basis functions $\chi_i^{\vec{k}}(\vec{r}) = \sum_{\vec{R}} e^{i\vec{k} \cdot (\vec{R} + \vec{t}_i)} \phi_i(\vec{r} - \vec{R})$.

If `.FALSE.`, the phase factor $e^{i\vec{k} \cdot \vec{t}_j}$ is not included in the definition of Bloch functions.

SET *string*

Setting tags for post processing, parameter constraints, and nearest neighbor setups, etc. Available list for the `SET` tags are as follows,

`GA` : for Genetic Algorithm setting

`CONSTRAINT TPARAM`

`NN_CLASS`

`RIBBON`

`BERRY_CURVATURE`

`ZAK_PHASE`

`WCC`

`Z2_INDEX`

`PARITY_CHECK`

`EFIELD`

`WEIGHT`

`DOS`

`EIGPLOT`

`STMPLOT`

`EFFECTIVE`

`REPLOT`

2. Details of the SET

Each SET tag should be ended up by END tag.

GA Setting of control parameters for the Genetic Algorithm used in parameter fitting procedures. This setting is only effective when **LSTYPE** is set to **GA**. Below you can check the default settings for GA procedures. You can modify as your purpose or comment out to use default setup as a input.

```

SET GA
  MGEN 100 # maximum number of iterations. (default:500)
  NPOP 100 # population in each generation. (default:100)
  NGENE 6 # number of genes in chromosomal encoding.
           # should be in between 2 to 9. (default:6)
  PCROSS 0.85 # crossover probability. [min:max]=[0.0:1.0]
  RMUTMIN 0.0005 # minimum mutation rate. [0.0:1.0]
  RMUTMAX 0.25 # maximum mutation rate. [0.0:1.0]
  RMUTINI 0.005 # initial mutation rate. [0.0:1.0]
  MUT_MOD 2 # mutation with 1: fixed rage
             # mutation with 2: fitness dependent
             # mutation with 3: distance dependent
             # mutation+creep with 4: fixed rate
             # mutation+creep with 5: fitness dependent
             # mutation+creep with 6: distance dependent
  FDIF 1.0 # relative fitness differential [0.0:1.0]
  IREP 3 # reproduction plan 1: Full generational replacement
         # 2: Steady-state-replace-random
         # 3: Steady-state-replace-worst
  IELITE 0 # elitism 0: off, 1: on
           # Note that this tag applies only if IREP=1 or 2.
  VERBOSE 1 # printed output 0/1/2=None/Minimal/Verbose
  CONVTOL 0.0001 # convergence tolerance (must be > 0.0).
  CONVWIN 20 # convergence window.
             # If CONVWIN consecutive solutions are found
             # convergence will be declaired.
             # Hence, give larger convergence window to reach minima.
  IGUESSF 0.1 # fraction of the initial population to set equal
              #to the initial guess. [0.0:1.0]
  ISEED 999 # random seed value (must be > 0).
END GA

```

_____ GA default setup example _____

STMPLOT Setting of integrated eigen state wavefunction $\Sigma |\psi_{nk}(r)|^2$ plot. Here, the summation runs over the eigen states within the energy window specified by **STM_ERANGE** or equivalently **STM_WINDOW**.

```

SET STMPLOT
  NGRID 40 40 80 # GRID for CHGCAR-STM output (default = 0.1 ang).
  STM_ERANGE -1.0:0.0 # energy window
  RCUT 6.0 # cut off radius(Å). Beyond this will not be calculated.
  REPEAT_CELL T T T # repeat orbital for each lattice vector?
    # this logical tag is especially useful if you only
    # consider center region of the very large cell.
    # If set "T T F", orbital contribution which is periodically
    # repeated in a3 direction will not be considered to calculate.
    # Try this option if you have very large cell and you are
    # especially interested unitcell center.
END STMPLOT
_____ STMPLOT setup example _____

```

EIGPLOT Setting of eigen state wavefunction $\psi_{nk}(r)$ or charge density $|\psi_{nk}(r)|^2$ plot.

```

SET EIGPLOT
  IEIG 3 5 # index(es) n of eigen state.
  IKPT 1 10 # index(es) k of k-point.
  NGRID 40 40 80 # GRID for CHGCAR output (default = 0.1 ang).
  RORIGIN 0.0 0.0 0.0 # shift of the origin of the cube file.
  WAVEPLOT .TRUE. # plot wavefunction (.true.) or charge density.
  RCUT 6.0 # cut off radius(Å). Beyond this will not be calculated.
END EIGPLOT
_____ EIGPLOT setup example _____

```

DOS Setting of Density of states (DOS).

```

SET DOS
  GKGRID 100 100 1 # set Gamma centered Monkhorst-Pack grid
  KSHIFT 0.0 0.0 0.0 # shift of k-grid (k-offset)
  PRINT_KPTS .TRUE. IBZKPT-DOS_TB # print k-point to the file
  PRINT_EIG .TRUE. 1:2 3 # print specified energy surface
  PRINT_UNIT RECIPROCAL # k-point unit (or ANGSTROM 1/Å)
  SMEARING 0.03 # gaussian smearing. Default = 0.025
  NEDOS 2000 # number of grid points in energy window (erange)
  DOS_EWINDOW -20.0:10.0 # energy window to be plotted
  DOS_NRANGE 1:NEIG # energy window to be calculated (integer)
  DOS_SPARSE .TRUE. # or .FALSE. use sparse matrix? Default=.FALSE.
  DOS_FNAME DOS_TB_projected.dat # output file name for DOS output
  PRINT_LDOS .TRUE. 1:8 12 # Print local density of states for given
    # atoms. Here, 1 to 8-th atoms and 12-th
    # atoms will be resolved.
  LDOS_FNAME LDOS_TB_projected # header for LDOS file name.

```



```

# atom index will be appended after.
# For example, for atom-1,
# LDOS_TB_projected_atom.1.dat file will
# be generated.
END DOS

```

DOS setup example

Note1: NEIG variable of the DOS_N RANGE tag indicates total number of states, i.e., $N_{\text{ORB}} \times \text{ISPINOR}$, where N_{ORB} is total number of atomic orbitals and $\text{ISPINOR} = 1$ ($\text{LSORB} = \text{.FALSE.}$) or 2 ($\text{LSORB} = \text{.TRUE.}$). If you want to reduce calculation loads, you can adjust DOS_N RANGE.

Note2: DOS_SPARSE tag is only available if `-DMKL_SPARSE` option is activated in the makefile. If set to `.TRUE.`, DOS_N RANGE should be as following:

```

DOS_N RANGE  1:NE_MAX
or
DOS_N RANGE  NE_MAX

```

Here, NE_MAX is integer value larger than zero and less equal than total number of states NEIG. This setting will reduce the resources required for hamiltonian matrix construction and time consuming for the eigenvalue problem by the energy window constraint in the help of sparse matrix eigen solver. See [EWINDOW](#) for more informations.

Note3: PRINT_EIG is only applicable if DOS_SPARSE = `.FALSE.`

EFIELD Setting of E-field.

```

SET EFIELD
EFIELD  0.0 0.0 0.1 # Efield along z direction
EF_ORIGIN  0.0 0.0 0.345690593 # (in fractional coordinate)
#EF_CORIGIN 0 0 0 # (in cartesian coordinate)
END EFIELD

```

EFIELD setup example

WEIGHT Setting of weight factor for the fitting procedures.

KRANGE *integer* : range of k-point where the weight factor is applied

TBABND *integer* : range of eigen states of the tight binding calculation

DFTBND *integer* : range of eigen states of the target energy bands

WEIGHT *real* : weighting factor

ORBT_I *integer* : orbital index. n^{th} orbital states will get a penalty

SITE_I *integer* : site index. ORBT_Ith orbital state at SITE_I atom will get a penalty. This prohibit certain orbital character to be stabilized from the fitting procedures.

```

SET WEIGHT
  KRANGE :          TBABND :    DFTBND IBAND:FBAND WEIGHT 1
  KRANGE :          TBABND 17:20 DFTBND 17:20          WEIGHT 6
  KRANGE 20:60 100:140 TBABND 17:20 DFTBND 17:20          WEIGHT 20
  KRANGE 1      TBABND 7      ORBT_I 1  SITE_I Mo1 PENALTY 200
END WEIGHT
_____ WEIGHT setup example _____

```

Note 1: After fitting procedure is over, the **WEIGHT** information is written in **PFILE** so that one can restart fitting. To use **WEIGHT** information written in **PFILE**, one can add **USE_WEIGHT** tag in your **PFILE** tag. Please find this information in **PFILE** tag.

CONSTRAINT TBPARAM Setting for parameter constraints for the fitting and calculation. The value of the specified two parameter will be kept same during the fitting and tight-binding calculations. If you are using **GA** method for the fitting procedures (**LSTYPE**), you are encouraged to give upper bound and lower bound for each parameters to minimize parameter search field in the randomize procedures of **GA** method. The default lower/upper bound for every parameter is -20.0/20.0. Note that imposing the upper/lower bound for the parameter is not supported for **LMDIF** method in the current version.

```

SET CONSTRAINT
  e_py_S = e_px_S # e_py_S is enforced to be same as e_px_S.
  e_px_S <= 5.0   # upper bound for e_px_S (applied in GA)
  e_px_S >= -5.0  # lower bound for e_px_S (applied in GA)
END CONSTRAINT
_____ CONSTRAINT setup example _____

```

If the second argument '=' is replaced by '==' and the third argument is not present, then this parameter will not be fitted and its initial guess as defined in **PFILE** will be fixed during the fitting procedures. Note that, exactly same effect can be achieved by putting 'FIXED' tag at the parameter specification line of the **PFILE**, and the detailed explanation can be found in **Fixing parameter** of Sec.4.

NN_CLASS Setting for nearest neighbor set up.

If the distance between two atomic species (For example, Mo and S) are 1st nearest type, and its upper limit is 3.2 angstrom (e.g., below this value will be regarded as the pair), then we can set as follows,

```
Mo-S : 3.2  R0 3.171634
```

Here, number of dash '-' occurrence between two atomic species indicates the distance class n , and the above example represents 1st nearest hopping between Mo

and S. The following R0 tag defines optimal bonding distance between two neighbor pair. This value will be used in calling the scaling function to get the distance dependent hopping parameter.

```
SET NN_CLASS
  Mo-Mo : 3.2   R0 3.171634
  S-S   : 3.28  R0 3.171634
  S--S  : 3.2   R0 3.193724
  Mo-S  : 2.5   R0 2.429624
END NN_CLASS
```

_____ NN_CLASS setup example _____

RIBBON Setting for nanoribbon calculations.

At the initial stages of the calculations, TBFIT will generate GFILE-ribbon with the settings bellow.

NSLAB *integer* : multiplication of unitcell along each direction

VACUUM *real* : vacuum spacing along each direction.

KFILE_R *real* : KFILE for ribbon band structure. Default: KFILE

PRINT_ONLY_R *logical* : if .TRUE. the geometry file will be generated with -ribbon suffix to the GFILE and the program will imediatly stops. Default: .FALSE.

```
SET RIBBON
  NSLAB      1 20  1
  VACUUM     0 20  0
  KFILE_R    KPOINTS_RIBBON
  PRINT_ONLY_R .FALSE. or . TRUE.
END RIBBON
```

_____ Ribbon calculation setup _____

Z2_INDEX Automatic calculations for topological index $[\nu_0 \ \nu_1, \nu_2, \nu_3]$ for 3D or \mathbb{Z}_2 for 2D via WCC method. The output will be written at Z2.WCC.*plane_index*.dat and Z2.GAP.*plane_index*.dat. Here, *plane_index* indicates one of six B_i - B_j plane with $B_k = 0$ or π . For example, if *plane_index* = 0.0-B3.B1-B2-PLANE, then it contains WCC information of B1-B2 plane with $k_z = \pi$.

```
SET Z2_INDEX
  Z2_ERANGE  1:28 # upto occupied
  Z2_DIMENSION 3D # or 2D:kz (2D WCC plane perpendicular to kz)
  Z2_NKDIV   21 21 # k-grid for KPATH and k-direction for WCC
  Z2_CHERN   .TRUE. # 1st Chern number of given bands with ERANGE
END Z2_INDEX
```

_____ Z2 index calculation using WCC method _____

WCC Wannier Charge Center calculation settings

```

SET WCC
WCC_ERANGE 1:28 # upto occupied
WCC_FNAME WCC.OUT.dat
WCC_FNAME_GAP WCC.GAP.dat # largest gap will be written
WCC_KPATH 0 0 0 1 0 0 # k_init -> k_end (ex, along b1)
WCC_KPATH_SHIFT 0 0 0.5 # kpoint shift along b3 direction
WCC_DIREC 2 #k-direction for WCC evolution (1:b1,2:b2,3:b3)
WCC_NKDIV 21 21 # k-grid for KPATH and k-direction(odd number)
WCC_CHERN .TRUE. # 1st Chern number of given bands with ERANGE
END WCC

```

_____ Wannier charge center (WCC) setup: kz 0.5 (shift) _____

ZAK_PHASE Setting for Zak phase calculations.

```

SET ZAK_PHASE
ZAK_ERANGE 1:28 # upto occupied
ZAK_FNAME ZAK_PHASE.OUT.dat
ZAK_KPATH 0 0 0 1 0 0 # k_init -> k_end (ex, along b1)
ZAK_DIREC 2 #k-direction for Zak phase evolution (1:b1,2:b2,3:b3)
ZAK_NKDIV 21 21 # k-grid for KPATH and k-direction
END ZAK_PHASE

```

_____ Zak phase setup _____

BERRY_CURVATURE Setting for Berry curvature calculations.

```

SET BERRY_CURVATURE
BERRYCURV_METHOD KUBO # .or. RESTA(not yet supported)
BERRYCURV_ERANGE 17:18
BERRYCURV_FNAME BERRYCURV.17-18 # output will be BERRYCURV_FNAME.dat
BERRYCURV_DIMENSION 2D:B3 # 2D plane perpendicular to kz)
END BERRY_CURVATURE

```

_____ Berrycurvature setup _____

PARITY_CHECK Setting for Parity eigenvalue calculations for given *k*-points.

```

SET PARITY_CHECK
PARITY_KP 0.0 0.0 0.0 G # Gamma (reciprocal unit)
PARITY_KP 0.5 0.0 0.0 M1 # M1 (reciprocal unit)
PARITY_KP 0.0 0.5 0.0 M2 # M2 (reciprocal unit)
PARITY_KP 0.5 0.5 0.0 M3 # M3 (reciprocal unit)
PARITY_ORIGIN 0.0 0.0 0.0 # origin of the system (direct coord)
PARITY_OP1 -1 0 0 # Rotation matrix (R) for inversion
PARITY_OP2 0 -1 0 # => R*X=-X (invert coordinate)
PARITY_OP3 0 0 -1 # => X:direct coord ; R: integer 3x3 array
NOCC 10 # 10 occupied states

```

```

PRINT_HAMILTONIAN .FALSE. # print out H(k) for each k-point
END PARITY_CHECK
_____ Parity check setup _____

```

Note:

- You can add (or remove) `PARITY_KP` tag if you want to get the parity information for another TRIM (time reversal invariant momenta: $-k=k+G$) point.
- To use this functionality and to get the meaningful results, your system should have inversion symmetry.
- The `ROTATION` tag is optional, the default is

$$R = \begin{bmatrix} PARITY_OP1 \\ PARITY_OP2 \\ PARITY_OP3 \end{bmatrix} = \begin{bmatrix} -1 & 0 & 0 \\ 0 & -1 & 0 \\ 0 & 0 & -1 \end{bmatrix}$$

SYMMETRY_EIG Setting for Symmetry eigenvalue calculations for given k -points.

```

SET SYMMETRY_EIG
SYMMETRY_KP 0.0 0.0 0.0 G # Gamma (reciprocal unit)
PARITY_KP 0.6666667 0.6666667 0.0 M3 # M3 (reciprocal unit)
SYMMETRY_ORIGIN 0.0 0.0 0.0 # origin of the system (direct coord)
SYMMETRY_OP1 -1 -1 0 # Rotation matrix (R) for 2/3pi
SYMMETRY_OP2 0 1 0 #
SYMMETRY_OP3 0 0 1 #
ROT_ANGLE 120 # rotation angle counterclockwise
NOCC 10 # 10 occupied states
PRINT_HAMILTONIAN .FALSE. # print out H(k) for each k-point
END PARITY_CHECK
_____ Parity check setup _____

```

EFFECTIVE Setting for evaluating effective hamiltonian and its eigenvalues. This job will be performed by the Löwdin downfolding technique¹¹. Note that in the current version, only the *energy*-dependent effective Hamiltonian will be constructed, where the *energy* is representing one's interested region.

```

SET EFFECTIVE HAM
EFF_ORB C:pz # downfolding will be performed on these orbitals
EFF_EWINDOW -2:2 # energy window of interest (e_center=-2+2/2)
END EFFECTIVE HAM
_____ Effective Hamiltonian construction _____

```

REPLOT Setting for replotting where DOS/LDOS/PBAND represents density of states (DOS), local density of states (LDOS), and atom-projected band structure (PBAND) by reading `band_structure.dat` or `band_structure.up(dn).dat` file, respectively.

¹¹ P.-O. Löwdin, *J. Chem. Phys.* **19**, 1396 (1951)

E. Zurek, O. Jepsen, O. K. Anderson, *Chem. Phys. Chem.* **6**, 1934 (2005)

```

SET REPLOT
FILE_FORMAT bin # let code know what kind of
                  # band_structure_TBA file to be read.
                  # if bin : band_structure_TBA.(up/dn).bin
                  # if dat : band_structure_TBA.(up/dn).dat
                  # will be loaded. Default: dat
REPLOT_BAND .TRUE. wf # replot band structure
                  # with wavefunction coefficient (with tag wf). Instead of
                  # wf tag, one can also request rh, mx, my, mz, where the
                  # meaning of each tag can be found in LORBIT tag.
                  # If no additional tag is specified, set to rh by default.
                  # If no tag is specified, only energy band without orbital
                  # information will be printed out. The output file will be
                  # written in band_structure_TBA.replot_wf.(up/dn).dat file
                  # with ascii format.
                  # Note that to activate this tag, FILE_FORMAT tag should be
                  # set to bin and corresponding file band_structure_TBA.replot
                  # .(up/dn).bin should be exist in the folder.
REPLOT_PROJ_BAND .TRUE. 1:8 12 # replot projected band structure
                               # for given atoms and their sum
REPLOT_DOS .TRUE. # Recalculate DOS using pre-calculated
                  # band_structure file, e.g.,
                  # band_structure.dat (nonmagnetic or
                  # non-collinear) or band_structure.up/dn.dat
                  # (spin polarized case).
REPLOT_LDOS .TRUE. 1:8 12 # Print local density of states for
                          # given atoms. For example, here,
                          # 1st to 8-th atoms and 12-th
                          # atoms will be resolved.
REPLOT_DIDV .TRUE. # Print local density of states for given
                  # discrete energy level within DOS_EWINDOW.
                  # The outputs will be stored in
                  # ./didv/DIDV.replot.dat.#i where #i=[1:NEDOS]
SMEARING 0.03 # gaussian smearing. Default = 0.025
NEDOS 2000 # number of grid points in energy window (erange)
DOS_EWINDOW -20.0:10.0 # energy window to be plotted

REPLOT_SLDOS .TRUE. # spatial LDOS within EWINDOW
REPEAT_CELL 20 20 1 # if REPLOT_SLDOS = .TRUE.,
                   # cell periodicity for visualization
RORIGIN 0.0 0.0 0.0 # shift of origin of atomic coordinates
                   # (fractional to unit vector a1, a2, a3,

```

```

                                # respectively).
    BOND_CUT 1.8 # bond length <= bond_cut will not be written in
                                # BOND.replot.dat Default: 3.0 (ang)
    END DOS

```

DOS setup example

Note 1: This tag is useful if you want to get series of DOS/LDOS calculations with respect to the **SMEARING** and energy window. If this **SET** is activated, other calculations will be ignored and the program stops immediately after the calculation.

Note 2: If **REPLOT_DOS** = **.TRUE.** or **REPLOT_LDOS** = **.TRUE.** or **REPLOT_SLDOS** = **.TRUE.**, then it is encouraged to set **SMEARING**, **NEDOS**, **DOS_EWINDOW**, otherwise the default values will be used.

Note 3: If **REPLOT_SLDOS** = **.TRUE.**, then, **REPEAT_CELL**, **RORIGIN**, **BOND_CUT** should be set together, otherwise the default values will be used.

Note 4: The output file names are as follows:

- if **REPLOT_DOS** = **.TRUE.** → **DOS.replot.dat**
- if **REPLOT_LDOS** = **.TRUE.** → **LDOS.replot.ATOM.INDEX.dat**, where **ATOM.INDEX** is the atom number. The example can be found in the “**Example/Graphene/DENSITY_OF_STATE/replot**” of your example folder.
- if **REPLOT_DOS** = **.TRUE.** → **SLDOS.replot.dat** and **BOND.replot.dat**. The example can be found in the “**Graphene/QSH/NANORIBBON/zigzag_ribbon/SPATIAL_LDOS_REPLOT**” of your example folder.

Note 5: The multiple declaration of **REPLOT_BAND**, **REPLOT_PROJ_BAND** and **REPLOT_LDOS** tag result in multiple **band_structure.TBA.replot_??**.dat, **band_structure.TBA.atom.sum#**.dat and **LDOS.replot.sum#**.dat files, respectively, where **??** represents one of {**rh**, **mx**, **my**, **mz**, **wf**} tag you specified and **#** represents the order of declaration of the tag. The concept of multiple declaration is same as in **PROJ_BAND** tag.

Note 6: The purpose of **REPLOT_BAND** tag is clear as it only read **.bin** file and write **.dat**. That is, for converting binary file format into human readable ascii format. **PROJ_BAND**.

Note 7: If you add **bin** or **bin4** tag at the end of **REPLOT_BAND** tag, for example,

```
REPLOT_BAND .TRUE. rh bin (or bin4)
```

then the result will be written with unformatted format with single precision. This is only available if your target file is already written in **bin** (or **bin4**; single precision) (see the **LORBIT** tag for the details). Using this tag, ascii formatted file can be saved in unformatted file, e.g., (**band_structure.TBA.dat** → **band_structure.TBA.bin**).

3. Details of the format of GFILE

Atomic orbital setup *string*

Hydrogen-like atomic orbital can be specified for the orbital basis. The possible orbital bases are¹²:

s px py pz dz2 dxy dx2 dxz dx2

```
0 0.0 0.0 s px py pz # s, px, py, and pz orbitals at ATOM_A
0 0.0 0.5 s px py pz # s, px, py, and pz orbitals at ATOM_B
```

_____ setup of atomic orbital basis in GFILE _____

Customized atomic orbital setup *string*

If someone does not want to use Slater-Koster type interatomic hopping parameter, customized atomic orbital can be defined instead. In this case, distance and hopping pair dependent parameterization should be properly defined in the PFILE.

Warning : This is experimental feature and on the development stages (do not use).

```
0 0.0 0.0 cp1 # cp1 orbital at ATOM_1
0 0.0 0.5 cp1 # cp1 orbital at ATOM_2
```

_____ setup of customized atomic orbital name cp1 _____

MOMENT tag *real*

Magnetic moment for Each atomic orbital can be assigned as follows,

collinear case: 0.0

noncollinear case: 0.0 0.0 0.0 [M θ ϕ]

```
0 0.0 0.0 px py pz moment 0 0 1 # spin-up for pz
0 0.0 0.5 px py pz moment 0 0 -1 # spin-dn for pz
```

_____ usage of *moment* tag in GFILE with *collinear* magnetism _____

```
0 0.0 0.0 px py pz moment 0 0 0 0 0 0 1 0 0 # spin-up for pz
0 0.0 0.5 px py pz moment 0 0 0 0 0 0 -1 0 0 # spin-dn for pz
```

_____ usage of *moment* tag in GFILE with *noncollinear* magnetism _____

¹²Please note that current version does not support the f orbitals. However, we will include f in the future release of TBFIT. For the Slater-Koster tables of f orbitals, please see [K. Lendi, *Phys. Rev. B* 9, 2433 (1974)].

MOMENT.C tag *real*

Similar to **MOMENT** but in noncollinear case, the 1st, 2nd, and 3rd value represents, m_x , m_y , and m_z , respectively. Here, x , y , and z represents the cartesian axis.

noncollinear case: 0.0 0.0 0.0 [M_x M_y M_z]

```
0 0.0 0.0 px py pz moment.c 0 0 0 0 0 0 0 0 1 # spin-up for pz
0 0.0 0.5 px py pz moment.c 0 0 0 0 0 0 0 0 -1 # spin-dn for pz
```

— usage of *moment.c* tag in **GFILE** with *noncollinear* magnetism —

4. Details of the format of PFILE

ONSITE parameters *real*

Onsite parameters for each atomic orbital should have the prefix **e_** and joint with the name of the orbital. The suffix should be the atomic species where the orbital placed.

e_dx2_Mo -0.34

HOPPING parameters *real*

The tight binding hopping parameter used in the calculations.

case1.) **IS_SK** .TRUE.

In this case, Slater-Koster type parameter should be specified properly. The syntax is as follows:

hopping-type_nn-class_AB

hopping-type will have one of following prefix: { *ss*, *sp*, *sd*, *pp*, *pd*, *dd* }, and one of following suffix: { *s*, *p*, *d* }, which implies σ -, π -, and δ -type interaction. **nn-class** specifies the distance class. See **NN_CLASS** for the details. **AB** specifies the two atomic species (**A** and **B** atoms) where the orbital hopping take place. For example, for the *dd δ* Slater-Koster parameter involved with the hopping process between the d_{z^2} orbital in **Mo** atom and d_{yz} orbital in **Mo**, and they are 2nd neighbor pair, then the parameter should be the following form:

ddd_2_MoMo -0.2

For the overlap integral parameters, one can add **o_** prefix, for example,

o_ddd_2_MoMo -0.2

Note that to activate the use of overlap integral, i.e., assuming the use of non-orthogonal basis, one should put `USE_OVERLAP .TRUE.` tag into your [PFILE](#).

To activate the use of scaling functions, i.e., distance dependent rescaling of parameters, one should set corresponding scaling parameters, for example,

```
s_ddd_2_MoMo    -0.2
```

for the `ddd_2_MoMo` parameter. Note again that to apply same rule for the overlap integral parameters, one should put `os_` prefix instead, for example,

```
os_ddd_2_MoMo    -0.2
```

case2.) `IS_SK .FALSE.`

Warning : This is experimental feature and on the development stages (do not set to `.FALSE.`).

In this case, the customized atomic orbital is assumed and the following scheme should be applied:

```
hopping-type_nn-class_AB
```

Here, the basic structure is same as *case1.*), however, the syntax of `hopping-type` is slightly different. That is: the prefix should have `cc` since this indicates *customized* hopping parameters. For the suffix, one should put user defined letter that characterize the hopping. For example,

```
cca_2_BiBi      0.01
```

represents the hopping between 2nd neighbor Bi atoms with the '*a*' type of *rule* which characterizes hopping pair. If you want to setup the *rule*, you have to write the conditions to the source code: `get_cc_param.f90`.

```
# SET UP THE 'USER' DEFINED HOPPING 'RULE'
# NOTE: In THIS example, hopping between Bi-Bi atom along
# x-direction characterized by hopping distance at around
# 8.6 Å (cca_2_BiBi) with nn_class = 2 will be considered.
# Following 'if' routine will find the parameter named
# cca_2_BiBi in the 'PFILE' and will assign its number as
# the 'parameter_index'.

[...]
elseif( (dij .gt. 8.5) .and. (dij .lt. 8.7) .and. &
        (ci_atom .eq. cj_atom) ) then
    call get_param_name(cc_custom, param_class, 'a', &
```

```

nn_class, ci_atom, cj_atom, &
flag_scale)

[...]

```

source code example: get_cc_param.f90

LOCAL POTENTIAL: LOCAL.POT parameters *real*

If you want to apply local potential to the particular atomic site or particular orbital, then you can simply turn on **LOCCHG** (.TRUE.) and write **local.pot** tag together with the amount of local potential to be applied for each atomic orbitals in the **GFILE**. Next, you have to provide proper scaling parameter (U_{onsite}^i) for the local potential, since the local potential is applied on your Hamiltonian as: $e_{onsite}^i = e_{onsite}^i + e_{loc.pot}^i \times U_{onsite}^i$, i.e., it modifies onsite energy e_{onsite}^i to e_{onsite}^i . Here, U_{onsite}^i should be defined in your **PFILE** so that the syntax is **local_U_orbital-type_atom-name**. **orbital-type** is one of *s*, *p*, or *d* type of orbital and **atom-name** is the name of atomic species you want to apply the local potential.

```

0 0.0 0.0 px py pz local.pot 1 1 1 # positive loc.pot
0 0.0 0.5 px py pz local.pot -1 -1 -1 # negative loc.pot

```

example of **local.pot** tag in **GFILE**

```

local_U_p_S 1.0

```

example of **local.pot** parameter in **PFILE**

SOC parameters *real*

case1.) **IS_SK** .TRUE.

Every spin-orbit coupling parameters in **Slater-Koster** method should have the prefix with **lambda_** and proper orbital information *p_*(as a joiner, for example *p* orbital) and species information **_S**(as a suffix, for example **Sul**pur atom) to precisely indicating the atomic orbital where the SOC effect will be applied.

```

lambda_p_S 0.2

```

case2.) **IS_SK** .FALSE.

In the case of user defined hopping parameter (orbital prefix start with *c*, see Sec.3 for the details) has been defined in the **GFILE**, **SOC** can be considered by setting up the Rashba and in-plane spin-orbit interaction. For Rashba type **SOC**, the prefix **lrashba_** should be joint with nearest neighbor class *n* and hopping pair as follows.

```

lrashba_c_2_BiBi 0.2

```

Above setting represents, Rashba type spin-orbit coupling between the custom type orbitals with *c*-prefix of the atom Bi and Bi.

Fixing parameter

If one want some parameters not to be fitted during the fitting procedures, one can fix those parameters by adding **FIXED** or **F**. For example, if you want **lambda_p_S** to be kept as its initial value, then, set this parameter as follows,

```
lrashba_c_2_BiBi    0.2 FIXED
```

Example of PFILE

```
e_dz2_Mo      -0.34636955
e_dx2_Mo      -0.70447045
e_dxy_Mo      -0.70447045
e_dxz_Mo      -0.17913534
e_dyz_Mo      -0.17913534
e_pz_S        -2.96500556
e_px_S        -1.47877518
e_py_S        -1.47877518
e_s_S        -10.51138070
dds_1_MoMo    -1.04598377
ddp_1_MoMo     0.44731993
ddd_1_MoMo     0.10237760
pps_1_SS      0.62323972
ppp_1_SS      0.03251328
pds_1_MoS     -2.32384045
pdp_1_MoS      0.97229680
sss_1_SS      -0.57287106
sps_1_SS      -0.33278732
sss_2_SS      -0.45573348
sps_2_SS      -0.21906117
sds_1_MoS      2.66111706
lambda_d_Mo    0.08014531  Fixed
lambda_p_S     0.07567002  Fixed
```

_____ example of PFILE: PARAM_FIT.dat for MoS₂ (IS_SK .TRUE.) _____

```
e_cp1_Bi      -0.09222821
ccb_1_BiBi     0.01723235
cca_2_BiBi     0.13290800
ccy_3_BiBi     -0.0
ccx_4_BiBi     -0.03544401
```

```
lrashba_c_1_BiBi    -0.01119142  
lrashba_c_2_BiBi     0.04914549  
lrashba_c_3_BiBi    -0.00632175  
lrashba_c_4_BiBi    -0.00636364
```

example of PFILE: PARAM_FIT.dat for Bi/Si(110) (IS_SK .FALSE.)

Part II.

Examples

1. Graphene with s and p orbitals

1.1. Parameter fitting

1.1.1. Prepare main control file: INCAR_TB

TBFIT reads **INCAR_TB** in the initial stages of the calculations to set up basic control parameters. In addition, **GFILE**, **KFILE**, and **PFILE** is mandatory for the normal run, and it should be predefined in your **INCAR_TB**. For the fitting procedures, **TBFIT** should be **.TRUE..** Then, one has to choose the fitting algorithm **LSTYPE** among **LMDIF** and **GA**. In this example, we will take **LMDIF** as a fitting algorithm. For the **GA** method, please find the example in "Example/Graphene/BAND_FIT/Step_1.genetic_algorithm/" of your example folder.

The users must pay some time to "**SET WEIGHT**" which is quite important in fitting procedures. If you want to fit more tightly than the other regions of your target band structure, you can put much higher value for that particular region. In this example, we have 16 atomic orbitals ($2 \text{ atoms} \times 4 \text{ orbitals per atom} \{s, p_x, p_y, p_z\} \times 2 \text{ spinors}$) in total. The target band structure, which is calculated by **VASP**, also have 16 band structure. In the **INCAR_TB** file below, we give 5 weights.

The first line,

```
KRANGE : TBABND : DFTBND 1:16 WEIGHT 1
```

indicates that the all the k-range (:), and all the tight binding band structure (:), and first sixteen bands (1:16) of DFT target band structure will be weighted with "1".

And the second line,

```
KRANGE : TBABND 1:8 DFTBND 1:8 WEIGHT 7
```

indicates that the all the k-range (:), and first eight tight binding bands (1:8) will be targeted to the first eight (1:8) of DFT band structure with weight of "7". Hence, the valence bands will be much more tightly fitted.

And the third line,

```
KRANGE 10:51 TBABND 5:10 DFTBND 5:10 WEIGHT 27
```

indicates that the particular k-range (10:51, around M - K region), and 5-th to 10-th tight binding bands (5:10) will be targeted to those of DFT band structure with much larger weight of "27". The bands near the Fermi level and near the Dirac point will be fitted tightly. For the other lines, the same rules can be applied.

Next, the basic control tags should be informed. For example, **MITER**, **PTOL**, **FTOL**, **PFILE**, **POFILE**, **EFILE** ..., etc.

And then, one should specify whether your system is one of followings: *nonmagnetic*, *noncollinear*, *collinear*, which can be defined by `TYPMAG`, together with `LSORB` which is for the spin-orbit coupling effect. If you have put some `LOCAL.POT` tag in your `PFILE` to consider some local potential, you should turn on `LOCCHG` to `.TRUE.`, and add some relevant parameters (see `LOCAL.POT` for the details) into the `PFILE` to manage the strength of the local potential. The tag `IS_SK` is to make sure that the hopping integral evaluation will follow the Slater and Koster's rule¹³. Note that in the current version, `IS_SK = .FALSE.` is experimental and under developing for the ease of use, so recommend to leave it to `.TRUE.`.

Now you have to make some rule for the nearest neighbor (*nn*) hoppings by setting up “`SET NN_CLASS`” which defines interatomic hopping. Once you set *nn* pair, the necessary hopping parameter for those hopping will be automatically determined and `TBFIT` will try to find those parameters in your `PFILE`. The detailed syntax for the naming of hopping parameters can be found in Section-4: `PFILE`-detail.

Finally, with “`SET CONSTRAINT TBPARAM`” tag, one can add some constraint rule between parameters or restrict the magnitude of the parameters by applying upper/lower bound to them. For example, here, we have assumed that every *p* orbitals shall have same onsite energy. So by setting “`e_px_C = e_pz_C`”, during the calculations, `e_px_C` value will be kept same as `e_pz_C`.

INCAR_TB : control tags

```
TBFIT      .TRUE.
LSTYPE     LMDIF
MITER      300
PTOL       0.000000001
FTOL       0.000000001

GFILE      POSCAR-TB
KFILE      KPOINTS_BAND
PFILE      PARAM_FIT.dat
EFILE      DFT_BAND.dat
POFILE     PARAM_FIT.new.dat

LOCCHG     .TRUE.
TYPMAG     noncollinear
LSORB      .TRUE.
LORBIT     .FALSE.

IS_SK      .TRUE.
```

¹³J. C. Slater and G. F. Koster, ‘‘Simplified LCAO Method for the Periodic Potential Problem’’, *Phys. Rev.* **94**, 1498 (1954)

```

SET WEIGHT
  KRANGE :          TBABND :          DFTBND 1:16  WEIGHT 1
  KRANGE :          TBABND 1:8      DFTBND 1:8    WEIGHT 7
  KRANGE 10:51      TBABND 5:10     DFTBND 5:10   WEIGHT 27
  KRANGE 20:40      TBABND 1:4      DFTBND 1:4    WEIGHT 50
  KRANGE 1:8 53:80  TBABND 3:6      DFTBND 3:6    WEIGHT 10
END WEIGHT

SET NN_CLASS
  C-C    : 1.8    R0 1.4145
END NN_CLASS

SET CONSTRAINT TBPARAM
  e_px_C    = e_pz_C
  e_py_C    = e_pz_C
  e_s_C     >= -10
  e_px_C     >= -10
  e_py_C     >= -10
  e_pz_C     >= -10
  sss_1_CC  >= -10
  sps_1_CC  >= -10
  pps_1_CC  >= -10
  ppp_1_CC  >= -10
  lambda_p_C >= -10
  e_s_C     <= 10
  e_px_C     <= 10
  e_py_C     <= 10
  e_pz_C     <= 10
  sss_1_CC  <= 10
  sps_1_CC  <= 10
  pps_1_CC  <= 10
  ppp_1_CC  <= 10
  lambda_p_C <= 10
END CONSTRAINT TBPARAM

```

example of INCAR-TB for Graphene

1.1.2. Prepare parameter file: PARAM_FIT

PARAM_FIT.dat : [PFILE](#)

```

PRINT_INDEX = .TRUE. # control tag for indexing parameters
                  # (not affected on your actual calculations)
USE_OVERLAP = .TRUE. # control tag for the use of overlap integral
                  # parameters that specified with "o_" prefix.

```


# index	param_name	parameter
1	e_s_C	-5.50250547
2	e_px_C	0.27589107
3	e_py_C	0.27589107
4	e_pz_C	0.27589107
5	sss_1_CC	4.14407741
6	sps_1_CC	5.06877443
7	pps_1_CC	-4.33297737
8	ppp_1_CC	2.54569565
9	o_sss_1_CC	0.02586060
10	o_sps_1_CC	-0.04261519
11	o_pps_1_CC	0.05063120
12	o_ppp_1_CC	0.01711425
13	lambda_p_C	0.00000000

example of [PFILE](#) for Graphene

POSCAR-TB : [GFILE](#)

# Graphene with honeycomb lattice				
1.0000000000000000				
2.45	0.0000000000000000	0.0		
1.2250000000000000	2.1217622392718746	0.0		
0.0000000000000000	0.0000000000000000	15.0		
C				
2				
Direct coordinate				
0.16666666667	0.16666666667	0.0	s px py pz	
-0.16666666667	-0.16666666667	0.0	s px py pz	

example of [GFILE](#) for Graphene

Here, we have set s and p (p_x , p_y , and p_z) orbital basis for each carbon atom.

KPOINTS_BAND : [KFILE](#)

# k-points along high symmetry lines				
20	# number of division between each line segment.			
Line-mode				
Reciprocal				
0 0 0				G
0.50000000	0.500000000	0		M
0.50000000	0.500000000	0		M
0.3333333333333333	0.6666666666666667	0	K	
0.3333333333333333	0.6666666666666667	0	K	
0.00000000	0.000000000	0		G

0.00000000	0.00000000	0	G
0.00000000	0.00000000	0.5	A

example of [KFILE](#) for Graphene

Note that the file syntax is exactly same as KPOINTS file of [VASP](#) program. See [here](#) for the details.

DFT_BAND.dat : [EFILE](#)

For the details of the EFILE, please go to [EFILE](#) section and also please find the example file in "Example/Graphene/BAND_FIT/Step_2.lmdif_method/" of your example folder.