LegBuilder Documentation

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CONTENTS

contents

CHAPTER

ONE

DISCRETIZATION MODULE

Discretize the continuous hybridization function into a discretized model(DiscModel). checking method is also provided.

class discretization.**DiscHandler**(*token, Lambda, N, D=[-1.0, 1.0], Gap=[0.0, 0.0]*)
Bases: object

Handler for discretization of hybridization function.

token: the token of this handler, which is a string for saving/loading data.

Lambda: scaling factor.

N: the maximum discretization index.

D: the band range, [-1,1] for default.

z: number of z.

Gap: the gap range.

check_mapping2(*rhofunc*, *Efunc*, *Tfunc*, *scalefunc*, *sgn*, *Nx=1000*, *Nw=200*, *smearing=0.02*)
check the mapping quality - the multi-band Green's function version.

rhofunc: the original hybridization function.

Efunc/Tfunc: the representative energy/hopping term as a function of x.

scalefunc: scale function.

sgn: the branch.

Nx/Nw: number of samples in x(index)- and w(frequency)- space.

smearing: smearing constant.

get_Efunc(*wxfunc*, *sgn*, *bandindex=0*, *N=100000*, *rk=False*)
get representative Energy function E(x) -the python version.

wxfunc: a function of w(x), which is equal to t(x)^2.

sgn: the positive branch if sgn>0, else the negative one.

bandindex: the band index.

N: the number of samples for integration.

rk: use Ronge-Kutta if True(in this version, it's better to set False).

get_Efunc2(*Efuncs*, *Ufunc*)
Get the Efunc for multi-band system.

Efuncs: energy functions for individual bands.

Ufunc: U function.

get_Tfunc2(*wxfuncs*, *Ufunc*)
Get the hopping term for multi-band system.

wxfuncs: functions of weights for individual bands, t=sqrt(w) in 1-band system and this is for multi-band.

Ufunc: U function.

get_Ufunc2(*Efuncs*, *sgn*)
get the U(x) function.

Efuncs: the energy functions.

get_discrete_model(*funcs*, *z=1.0*, *append=False*)
get a discrete set of models for specific zs.

funcs: a super tuple -> (scalefunc_positve,Efunc_positive,Tfunc_positive),(scalefunc_negative,Efunc_negative,Tfunc_negat

z: z or a list of zs.

append: append scale datas.

get_scalefunc_log(*sgn*)
get logarithmic scale tick function. epsilon(x)=Lambda^(2-x)

sgn: return the scale function for the positive branch if sgn>0, else the negative one.

get_scalefunc_sclog(*sgn*)
get logarithmic scale tick function suited for superconductor(logarithmic for normal part).

sgn: return the scale function for the positive branch if sgn>0, else the negative one.

get_wxfunc(*scalefunc*, *sgn*, *bandindex=0*, *N=10000*)
Get weight function w(x), which is equal to int^e(x)_e(x+1) d(w,bandindex) dw

scalefunc: the function for scale ticks.

sgn: specify the branch.

bandindex: the bandindex.

N: the number of samples.

quick_map2(*tick_type='log'*, *NN=1000000*)
Perform quick mapping(All in one suit!) for 2 x 2 hybridization matrix.

tick_type: the type of tick, *log*->logarithmic tick, *sclog*->logarithmic ticks suited for superconductor.

NN: the number of samples for integration over rho(w).

return: a super tuple -> (scalefunc_positve,Efunc_positive,Tfunc_positive),(scalefunc_negative,Efunc_negative,Tfunc_nega

set_rhofunc(*rhofunc*, *NW=50001*)

rhofunc: the hybridization function.

NW: the number of ws for rho(w).

unique_token
return a unique token, for saving/loading datas.

class discretization.**DiscModel**(*Elist*, *Tlist*, *z=1.0*)
Bases: object

discrete model.

Elist/Tlist: a list of on-site energies and hopping terms. The shape is (2N,nz,nband,nband)

z: the twisting parameters.

N
: number of particles for each branch(positive or negative).

nband
: number of bands.

nz
: number of twisting parameters.

CHAPTER

TWO

CHAINMAPPER MODULE

Map a discretized model into a Chain by the method of (block-)lanczos tridiagonalization. checking method is also provided.

class chainmapper.**Chain**(*t0*, *elist*, *tlist*)

Bases: object

NRG chain.

t0: the coupling term of the first site and the impurity.

elist/tlist: a list of on-site energies and coupling terms.

class chainmapper.**ChainMapper**(*prec=3000*)

Bases: object

A Chain Model Mapper for NRG.

prec: the precision in mapping process.

check_spec(*chain*, *dischandler*, *rhofunc*)

check mapping quality.

chain: the chain after mapping.

dischandler: discretization handler.

rhofunc: hybridization function.

map(*model*)

Map discretized model to a chain model using lanczos method.

model: the discretized model(DiscModel instance).

return: a Chain object

CHAPTER

THREE

TRIDIAGONALIZE MODULE

Tridiagonalization methods for both scalar(tridiagonalize) and block(tridiagonalize_qr) versions. Some test functions are also included.

tridiagonalize.**check_tridiagonalize**(*H0*, *trid*)

check the quality of tridiagonalization.

H0: the original hamiltonian.

trid: tridiagonalization result, a tuple of (data,offset).

tridiagonalize.**tridiagonalize**(*A*, *q*, *m=None*, *prec=None*, *getbasis=False*)

Use m steps of the lanczos algorithm starting with q to generate eigenvalues for the sparse symmetric matrix A.

A: a sparse symmetric matrix.

q: the starting vector.

m: the steps to run.

getbasis: return basis vectors if True.

return: (data,offset,vectorbase)

Use scipy.sparse.diags(res[0],res[1]) to generate a sparse matrix

tridiagonalize.**tridiagonalize_qr**(*A*, *q*, *m=None*, *prec=None*)

Use m steps of the lanczos algorithm starting with q - the block version with QR decomposition.

Note: we need to specify a two-column starting vectors here (q0,q1) with q0,q1 orthogonal to each other.

A: a sparse symmetric matrix.

q: the starting othogonal vector q=(q0,q1).

m: the steps to run.

return: (data,offset), the trdiagonal matrix can be generated by scipy.sparse.diags(data,offset).

CHAPTER

FOUR

UTILS MODULE

Author: Jinguo Leo Date : 8 September 2014 Description : physics utility library

utils.**H2G**(*h*, *w*, *tp='r'*, *geta=0.01*, *sigma=None*)
Get Green's function g from Hamiltonian h.

h: an array of hamiltonian.

w: the energy(frequency).

tp: the type of Green's function. 'r': retarded Green's function.(default) 'a': advanced Green's function. 'matsu': finite temperature Green's function.

geta: smearing factor. default is 1e-2.

sigma: additional self energy.

utils.**eigh_pauliv_npy**(*a0*, *a1*, *a2*, *a3*)
eigen values for pauli vectors - numpy version.

a0/a1/a2/a3: pauli components.

utils.**mpconj**(*A*)
get the conjugate of matrix A(to avoid a bug of gmpy2.mpc.)

A: the input matrix.

utils.**ode_ronge_kutta**(*func*, *y0*, *tlist*, ***kwargs*)
Integrate use Ronge Kutta method.

func: the function of (x,y).

y0: the starting y.

tlist: a list of t.

****kwargs:** additional arguments for scipy.ode.set_integrator

utils.**qr2**(*A*)
analytically, get the QR decomposition of a matrix.

A: the matrix.

utils.**s2vec**(*s*)
Transform a 2 x 2 matrix to a 4 dimensional vector, corresponding to s0,sx,sy,sz component.

s: the matrix.

utils.**vec2s**(*n*)
Transform a vector of length 3 or 4 to a pauli matrix.

n: a 1-D array of length 3 or 4 to specify the *direction* of spin.

CHAPTER

FIVE

HYBRI_SC MODULE

Get the hybridization function of a conventional superconductor. wide-band approximation(get_hybri_wideband) version and finite-band width(get_hybri) version are available.

hybri_sc.**get_hybri**(*Gap*, *Gamma*, *D0=1.0*, *mu=0.0*, *eta=1e-10*)

D(w) for superconducting surface.

Gap: the Gap value.

Gamma: the overall strength.

D0: the band width of normal part.

mu: chemical potential.

eta: the smearing factor.

hybri_sc.**get_hybri_wideband**(*Gap*, *Gamma*, *D=1.0*, *mu=0.0*, *eta=1e-10*)

D(w) for superconducting surface, taking wide-band approximation.

Gap: the Gap value.

Gamma: the overall strength.

D: the band width.

mu: chemical potential.

eta: the smearing factor.

CHAPTER

SIX

INDICES AND TABLES

- genindex
- modindex
- search

c

d

h

t

u