Manual for ANIPAR (Automatic Near-Infrared PARameter finder

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Abstract

This manual contains instructions to use all the routines included with ANIPAR. A detailed description of the associated files is included as well.

This folder contains every code required to create a grid of synthetic spectra, normalize the spectra of M dwarfs, selecting the best normalization for each star, running turbospectrum for that normalization, and determining stellar parameters for them.

The pipeline uses code from iSpec, the radiative transfer code Turbospectrum, and MARCS GES stellar models, together with a custom line list and a linemask, to determine these stellar parameters.

This file contains instructions on how to use the codes included with the pipeline, and can serve as step-by-step instruction booklet to obtain stellar parameters from raw spectra.

Contained are codes and instructions to download APOGEE spectra, converting them into usable iSpec format, normalizing them, finding the best normalization through χ^2 minimization, and finding Turbospectrum's best fit and final parameters for the spectra.

Chapter 1

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1.1 Python routines

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- Synthesize_SpectralGrid.py - creates a Grid of synthetic spectra from the combinations available in isochrones.dat
- normalized_Mdwarfs_grid.py - used for normalization of M dwarf spectra with the different template spectra
- ChiSqCalc.py - Calculates the χ^2 between the spectra in /normalized_spectra and the templates used to generate them, outputs list to a table
- BestTemplateCalc.py - Automatically finds best template per star + all other potential templates within a given margin, outputs list to a table
- ispec_ParameterFinder.py - Calculates best fits + parameters for spectra listed in a given table

1.2 Auxiliary files

- isochrones.dat - PARSEC isochrones calculated for 1Gyr, header deleted
- isochrones_header.dat - PARSEC isochrones calculated for 1Gyr, header included, not actually used in the code but important for reference
- linemask.txt - linemask created from star Ross-128, containing the lines best suited for parameter determination
- barber_Mdwarf_final.list - Final line list for M dwarfs, containing important elemental transitions and over 1 000 000 water lines relevant for M dwarf spectra
- My_stars.fits - example list of interesting stars for download (planet-host M dwarfs)

1.3 Folders

- /default_output/ - every code will place its output by default inside this folder
- /Grid/ - Contains a grid of synthetic spectra with the parameters from isochrones.dat; a new Grid can be created by running Synthesize_SpectralGrid.py again, with a new set of isochrones
- /input/ - contains files required for our run of ispec, do not edit unless you know what you are doing. **Copy the files from the abundances/MARCS.GES folder in your iSpec directory to the corresponding folder, as the files are too large to include in the github directory.**
- /ispec/ - Folder that should contain iSpec2020. **Please copy and paste your version of iSpec, as as the files are too large to include in the github directory. Keep only the synth/turbospectrum.py file and every file in synth/pycache, and substitute them in your iSpec distribution, as these routines must be edited for ANIPAR to work properly.**
- /synthesizer/ - Turbospectrum, do not edit unless you know what you are doing.
- /raw_spectra/ - place raw spectra (txt, ispec format) in this folder, normalizer_Mdwarfs_grid.py will take spectra from here as input
- /normalized_spectra/ - place normalized spectra (txt, ispec format) in this folder, code ChiSqCalc.py will take spectra from here as input

Chapter 2

How to use the code

This chapter includes a list of all the requirements needed to run the code, as well as an individual description of each of the routines, how it works, and what their outputs are. Each python routine is made to run individually, with the user needing to finish each step before initiating the following one. The routines are described in the order they are meant to be used, but an advanced user can run only their selected parts of the full code.

To run a routine, the user can simply load it in an IDLE environment, such as spyder or Anaconda, edit the variable names necessary, and then run it in an IPython console.

2.1 Requirements

The main requirements to run the full code are:

- An installation of Python 3.8 - see Van Rossum and Drake Jr ((1995)), preferably with an easy to edit IDLE environment, such as Spyder or Anaconda.
- An installation of iSpec_v2020.10.01 - see Blanco-Cuaresma et al. ((2014)) and Blanco-Cuaresma ((2019)). One is included with this distribution of the code. If using your own iSpec installation, replace the routines synth.py, lines.py and atmospheres.py with the custom edited ones included with this distribution.
- *Turbospectrum* - from Alvarez and Plez ((1998)) and Plez ((2012)) and MARCS.GES - see Gustafsson et al. ((2008)) stellar models with logg values up to 5.5. These files are included in the iSpec distribution and in this folder, but, if you are using a custom iSpec distribution, please make sure they are available.

Additionally, please make sure the following python modules are installed:

- os - `https://docs.python.org/2/library/os.html`
- sys - `https://docs.python.org/2/library/sys.html`
- logging - `https://docs.python.org/2.7/library/logging.html`

```
from math import *
import numpy as np

from astropy.io import fits

hdulist2 = fits.open('stars_not_found.fits') #file name containing stars for download
#must be in ASPCAP table format - table with all stars available at https://www.sdss.org/dr14/irspec/spectro_data/

tbdata2 = hdulist2[1].data
x2 = tbdata2['APOGEE_ID_1']
#y2 = tbdata2['LOCATION_ID']
z2 = tbdata2['FIELD']
t2 = tbdata2['TELESCOPE']
stri = '#'https://data.sdss.org/sas/dr16/apogee/spectro/aspcap/r12/l33/apo25m/' #DR14, must be changed if wanting to download spectra from other DR
ns = 100

for j,name in enumerate(x2):
    stri += 'https://data.sdss.org/sas/dr16/apogee/spectro/aspcap/r12/l33/'
   # name = name[10:]
   # loc = y2[j]
    fie = z2[j]
    tel = t2[j]
    stri += tel + '/' + fie + '/aspcapStar-r12-' + str(name) + '.fits'
    stri += '\n'

f = open('down_list_stars_not_found.txt', 'w') #saving to file
f.write(stri)
f.close()

#after running this code and creating the file, the spectra can be downloaded by opening a command line and executing the code:
#wget -i down_list_example.txt
#The spectra will appear in the folder where the code is executed
```

Figure 2.1: Code for the routine build_download_list_dr16.py

- numpy - `https://numpy.org/`
- multiprocessing - `https://docs.python.org/2/library/multiprocessing.html`
- matplotlib - `https://matplotlib.org/`
- astropy - `https://www.astropy.org/`
- scipy - `https://www.scipy.org/`
- shutil - `https://docs.python.org/2.7/library/shutil.html`

2.2 build_download_list.py

This first small routine is designed to create a download list for the stars the used wants to characterize. It takes as an input a list of stars in the format of ASPCAP's tables with the full results (download available at `https://www.sdss.org/dr16/irspec/spectro_data/`) and gives as an output a list of the stars online locations. The default name for the list is down_list_example.py. The full code is shown here in Fig.2.1.

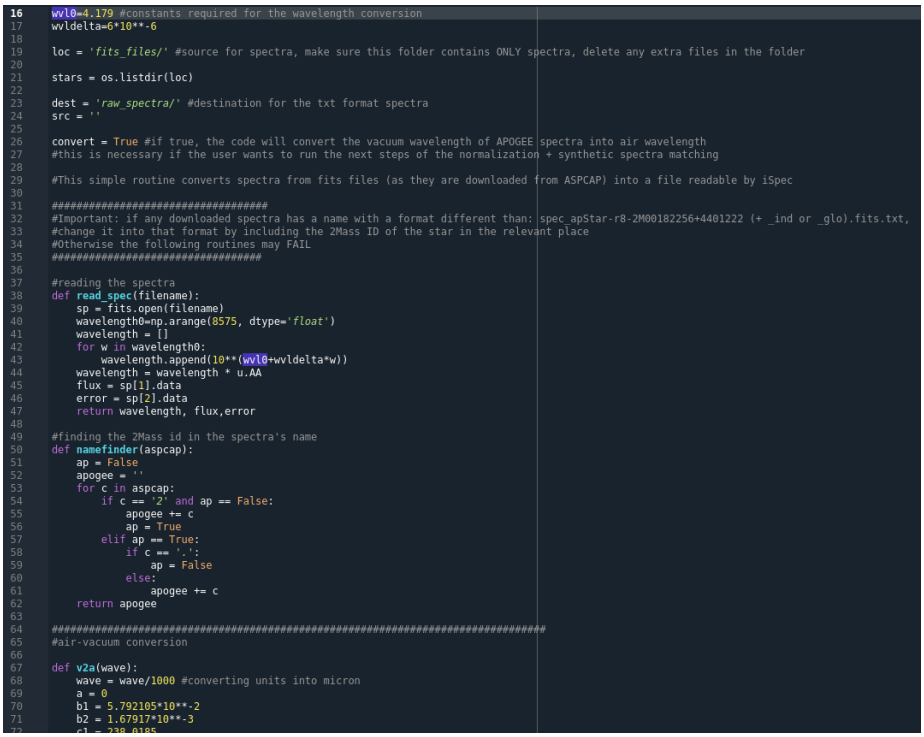
This version produces the locations of the spectra from APOGEE DR14, but it can be upgraded to the another Data Release by changing the default link. To do so, simply edit the "stri" variable to contain the new locations required.

After creating the download list, the files can be obtained by opening a command line and running the command:

```
wget -i down_list_example.txt
```

The command will download all spectra available to the directory the user is currently in. It is recommended that these files are saved in the folder "/fits_files/", as the following routines will call the spectra from that directory.

For downloading spectra from APOGEE DR16, the routine build_download_list_dr16.py is available as well. The format is similar to this one, but the paths are specific to that Data Release.



```
wvl0=4.179 #constants required for the wavelength conversion
wvldelta=6*10**-6

loc = 'fits_files/' #source for spectra, make sure this folder contains ONLY spectra, delete any extra files in the folder

stars = os.listdir(loc)

dest = 'raw_spectra/' #destination for the txt format spectra
src = ''

convert = True #if true, the code will convert the vacuum wavelength of APOGEE spectra into air wavelength
#this is necessary if the user wants to run the next steps of the normalization + synthetic spectra matching

#This simple routine converts spectra from fits files (as they are downloaded from ASPCAP) into a file readable by iSpec

##################################
#Important: if any downloaded spectra has a name with a format different than: spec_apStar-r8-2M00182256+4401222 (+ _ind or _glo).fits.txt,
#change it into that format by including the 2Mass ID of the star in the relevant place
#Otherwise the following routines may FAIL
##################################

#reading the spectra
def read_spec(filename):
    sp = fits.open(filename)
    wavelength0=np.arange(8575, dtype='float')
    wavelength = []
    for w in wavelength0:
        wavelength.append(10**(wvl0+wvldelta*w))
    wavelength = wavelength * u.AA
    flux = sp[1].data
    error = sp[2].data
    return wavelength, flux,error

#finding the 2Mass id in the spectra's name
def namefinder(aspcap):
    ap = False
    apogee = ''
    for c in aspcap:
        if c == '2' and ap == False:
            apogee += c
            ap = True
        elif ap == True:
            if c == '.':
                ap = False
            else:
                apogee += c
    return apogee

#################################################################################
#air-vacuum conversion

def v2a(wave):
    wave = wave/1000 #converting units into micron
    a = 0
    b1 = 5.792105*10**-2
    b2 = 1.67917*10**-3
```

Figure 2.2: Code for the routine fits_to_txt.py

2.3 fits_to_txt.py

This second routine is used to convert the spectra downloaded into a format that can be useable by iSpec. By default, spectra are taken from the folder "/fits_files/" and saved to "/raw_spectra/", but these destinations can be changed by renaming the variables "loc" and "dest", respectively.

The conversion of most downloaded APOGEE spectra will result in two different spectra being created, one with the suffix "ind" and one with "glo". These represent the individual and global weighting for the errors being considered in the spectra (more information at `https://www.sdss.org/dr16/irspec/spectra/`).

An important point to note here regarding some stars with weird APOGEE names, is that the names of the output files should follow the format

`spec_apStar-r8-2M00182256+4401222 (+ _ind or _glo).fits.txt`

. Otherwise, the following routines may fail to retrieve the proper 2mass ID from the name of the files.

2.4 Synthesize_SpectralGrid.py

This auxiliary routine is used to create synthetic spectra with a given parameter combination. It is based on the "synthesize_spectrum()" function available on iSpec's example.py file, and, as is, can create a grid of synthetic spectra based on the parameter combinations found on isochrones.dat.

```
save_loc = 'default_output/' #put your destination for the spectral grid here

#printing to file

import sys

###########################################################################
#Getting the isochrone values

iso_file = np.loadtxt('isochrones.dat') #isochrone sources, can be customizable. remember to delete file header first

teffs = [[[],[],[],[],[],[]],[[],[],[],[],[],[]],[[],[],[],[],[],[]],[[],[],[],[],[],[]],[[],[],[],[],[],[]],[[],[],[],[],[],[]]]
loggs = [[[],[],[],[],[],[]],[[],[],[],[],[],[]],[[],[],[],[],[],[]],[[],[],[],[],[],[]],[[],[],[],[],[],[]],[[],[],[],[],[],[]]]

age = iso_file[0][2]
age0 = iso_file[0][2]
ages = [age]

metal = iso_file[0][1]
metal0 = iso_file[0][1]
metals = [metal]

c = 0
r = 0

maxTeff = 4.00 #maximum value for the Teff used in the grid (/1000)
maxLogg = 4.5 #maximum value for the logg used in the grid

Combos = [] #this will contain the combinations used for the grid

#getting isochrone values, rounding to nearest multiples of 100K for Teff, 0.1 dex for [M/H] and logg
for k in iso_file:
    Teff = (10**k[7])/1000
    logg = k[8]
    if Teff < maxTeff and logg>maxLogg:
        NewCombo = [k[1],1000*round(Teff,1),round(logg,1)]
        if NewCombo not in Combos:
            Combos.append(NewCombo)
```

Figure 2.3: Code for the routine Synthesize_SpectralGrid.py

By default, the grid will use as limits the values of $T_{\rm eff} < 4000\,{\rm K}$ and $\log g < 4.5\,{\rm dex}$, but these values can be customized to create a grid with larger parameter coverage. By default, the output synthetic spectra will be saved to the folder "/default_output/", and should be moved to "Grid" if the user wants to use the newly generated spectra with another routine.

It is not necessary to run this routine for an user to derive stellar parameters, as an example grid of 103 synthetic spectra is available with the default distribution of the code, but it can be used to generate custom synthetic spectra with different parameter combinations. In order to do that, simply comment the final two lines of code:

```
for combo in Combos:

    synthesize_spectrum(teff = combo[1],logg = combo[2], MH = combo[0])
```

and call the function "synthesize_spectrum(teff, logg, mh)" with the intended parameter combinations to synthesize.

2.5 normalized_Mdwarfs_grid.py

This complicated routine is used to normalize the spectra generated with "fits_to_txt.py". It will take each spectrum in folder "/raw_spectra/" and normalize it using every template in "/Grid/", saving the normalized spectra to the folder "/normalized_spectra/". A fits table recording every star/template combination is saved by default to "Normalized_Mdwarfs_data.fits", and the user can customize the name of this output table changing the variable "filename" (see Figure 2.4).

The code used here is based on the function "normalise_spectra()", available in example.py, included with the iSpec distribution used.

```
21  #################
22  #input options
23
24  inputs = True
25
26  if inputs == True:
27
28      loc = ''#location for the normalized spectra and output, can be customized, using own folders by default
29
30      filename = 'Normalized_Mdwarfs_data.fits' #data for normalized M dwarfs will be stored here
31
32      #txt_folder = 'raw_txt/'
33      txt_folder = 'raw_spectra/' #location of raw spectra to normalize
34
35      #stars = os.listdir(loc + 'norm_stars_data/')
36      stars = os.listdir(loc + txt_folder)
37
38      norm = "Template" #renormalize the spectra?
39
```

Figure 2.4: Code for the routine normalized_Mdwarfs_grid.py - input section

```
316 ##########################################################################
317
318 if __name__ == '__main__':
319
320     print ('Starting by opening Aspcap')
321     #Aspcap = open_aspcap(True)
322     print( 'Creating fits')
323
324     MasterTable = create_fits()
325
326     stars.sort()
327
328     p = Pool(10) #this step parallelizes the process, set your number of parallel threads for the code here
329     table = p.map(Normalizing_Stars, stars)
330
```

Figure 2.5: Code for the routine normalized_Mdwarfs_grid.py - main section

The code can be parallelized for increased efficiency and speed. In order to do so, simply change the number in line 351

```
p = Pool(10)
```

to the number of parallel threads available for your computation (see Figure 2.5.

2.6 ChiSqCalc.py

The following two routines could have been implemented as a single one, but are separated for ease of customization. They are dedicated to the identification of the best templates to normalize each of the stars being characterized.

ChiSqCalc.py, the first routine, will calculate the χ^2 differences between each spectrum in folder "/normalized_spectra/" and the template used to normalize that spectrum. The routine will provide as an output a fits files summarizing both the χ^2 measured in a selected linemask and the χ^2 obtained by comparing the full available wavelength of the spectrum. This linemask is the one used developed specifically for M dwarfs, but can be customized by creating a new one and changing the variable "linemaskname" - see Figure 2.6. The output full table is saved to "Mdwarf_ChiSq_Table.fits" by default.

Due to the complexity and number of functions, you may want to test them before running the code for the stellar sample. In that case, simply set the

```
if __name__ == '__main__'
```

(line 164, see Figure 2.7) condition to 'different than'.

```
    ########################################
    #INPUT

    loc = ''

    filename = 'Mdwarf_ChiSq_Table.fits' #output table's file name

    linemaskname = 'linemask.txt'

    folder = 'normalized_spectra/' #source for normalized spectra

    stars = os.listdir(loc + folder)

    ########################################
```

Figure 2.6: Code for the routine ChiSqCalc.py - input section

```
####################################

BigTable = create_fits()

if __name__ == '__main__': #set this to false to test the functions themselves, without running the full code


    for i,star in enumerate(stars): #running across all normalized spectra

        print( star, i)

        starname, tef, mh, lg = extract_Params(star) #getting the template parameters from the name of the normalized spectra
        template = open_template(tef, mh, lg) #finding the template used to normalize the spectra
        spectra = ispec.read_spectrum(loc + folder + star) #opening the template

        linemasks = create_segments_around_linemasks(spectra) #applying the linemask to the spectra

        template = resample_spectrum(template) #resampling both template and normalized spectra for comparison
        spectra = resample_spectrum(spectra)

        waveobs = spectra['waveobs']
        comparing_mask = create_comparing_mask(waveobs, linemasks) #masking the compared regions according to linemask
        mask = np.where(comparing_mask==1.0)

        ChiSqMask = ChiSqCalc(spectra,template,mask) #calculating Chi Sq in linemask regions
        ChiSqFull = ChiSqCalc(spectra,template) #calculating Chi Sq in every wavelength region

        line = [starname, tef, mh, lg, ChiSqMask, ChiSqFull] #creating a line summarizing the results
        BigTable.add_row(line) #adding it to table

BigTable.write(loc + filename,overwrite=True) #writing table to file
```

Figure 2.7: Code for the routine ChiSqCalc.py - main section

```
20  #This small code finds the best templates for each star, according to the ChiSq values calculated by ChiSqCalc.py
21  #it can output not only the best template for each star, but also every template within a specified margin of ChiSq value
22
23  loc = ''
24
25  Output_filename = 'Mdwarf_BestTemplates.fits' #output table
26  Input_filename = 'Mdwarf_ChiSq_Table.fits' # Input table
27
28  margin = 1.10 #margin, set to 1.0 to include only best template per star
29  #margin will be multiplied by the lowest ChiSq to find all templates within those values
30
31  def open_aspcap():
32      hdulist = fits.open(Input_filename) #input table
33      tbdata = hdulist[1].data
34      return tbdata
35
36  def create_fits():
37      ####   create table
38      columns = ('APOGEE_ID','T_Norm','MH_Norm','logg_Norm','ChiSqMask','ChiSqFull')
39
40      dtypes = ('S20','f8','f8','f8','f8','f8')
41
42      MasterTable = Table(names = columns, dtype = dtypes)
43
44      return MasterTable
45
46  BigTable = open_aspcap()
47  NewTable = create_fits()
48
49  BigTable.sort()
50
51  CharStars = []
52  BestChiSq = []
53  BestFits = []
54
55  for line in BigTable: #finding best combination per star
56      if line['APOGEE_ID'] not in CharStars:
57          BestFits.append(line)
58          CharStars.append(line['APOGEE_ID'])
59          BestChiSq.append(line['ChiSqMask'])
60      elif line['ChiSqMask'] < BestChiSq[-1]:
61          BestFits[-1] = line
62          CharStars[-1] = line['APOGEE_ID']
63          BestChiSq[-1] = line['ChiSqMask']
64
65  for line in BigTable: #adding other combinations within the margin used
66      star = line['APOGEE_ID']
67      for k,comp_star in enumerate(CharStars):
68          if comp_star == star:
69              if line['ChiSqMask'] < BestChiSq[k]*margin and line['ChiSqMask'] != BestChiSq[k]:
70                  BestFits.append(line)
71
72  for line in BestFits:
73      NewTable.add_row(line)
74
75  NewTable.write(loc + Output_filename,overwrite=True) #writing results to file
```

Figure 2.8: Code for the routine BestTemplate.py

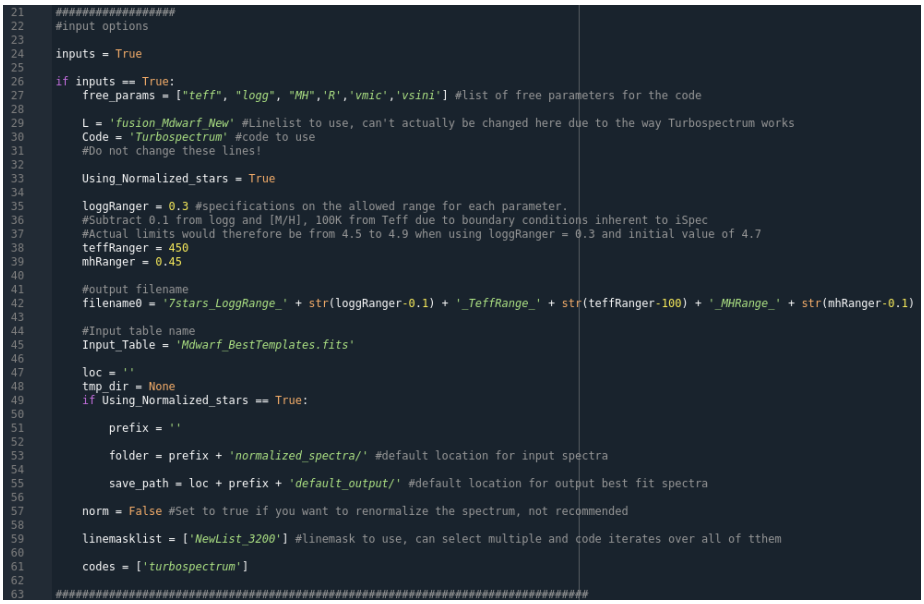
2.7 BestTemplateCalc.py

This simple routine works as the second half of the previous one, as it simply scans through the full table "Mdwarf_ChiSq_Table.fits" generated by ChiSq-Calc.py and provides as the output a smaller table "Mdwarf_BestTemplates.fits" containing only the best templates found for each star. It does not look into the available spectra, but rather only filters the input table and selects the best templates for each star.

This routine can be used to find not only the template with the lowest χ^2 for each star, but every other template within a given error margin as well. This margin can be customized by changing the variable "margin" in line 28 - see Figure 2.8. The output will be saved to the fits table "Mdwarf_BestTemplates.fits", but that can be customized as well.

2.8 ispec_ParameterFinder.py

This final, more complex routine, is designed to actually determine the stellar parameters for its selected stars. It is based on the function "determine_astrophysical_parameters_using_synth_ available in the file example.py in the original iSpec distribution.



```
#################
#input options

inputs = True

if inputs == True:
    free_params = ["teff", "logg", "MH",'R','vmic','vsini'] #list of free parameters for the code

    L = 'fusion_Mdwarf_New' #Linelist to use, can't actually be changed here due to the way Turbospectrum works
    Code = 'Turbospectrum' #code to use
    #Do not change these lines!

    Using_Normalized_stars = True

    loggRanger = 0.3 #specifications on the allowed range for each parameter.
    #Subtract 0.1 from logg and [M/H], 100K from Teff due to boundary conditions inherent to iSpec
    #Actual limits would therefore be from 4.5 to 4.9 when using loggRanger = 0.3 and initial value of 4.7
    teffRanger = 450
    mhRanger = 0.45

    #output filename
    filename0 = '7stars_LoggRange_' + str(loggRanger-0.1) + '_TeffRange_' + str(teffRanger-100) + '_MHRange_' + str(mhRanger-0.1)

    #Input table name
    Input_Table = 'Mdwarf_BestTemplates.fits'

    loc = ''
    tmp_dir = None
    if Using_Normalized_stars == True:

        prefix = ''

        folder = prefix + 'normalized_spectra/' #default location for input spectra

        save_path = loc + prefix + 'default_output/' #default location for output best fit spectra

    norm = False #Set to true if you want to renormalize the spectrum, not recommended

    linemasklist = ['NewList_3200'] #linemask to use, can select multiple and code iterates over all of tthem

    codes = ['turbospectrum']

#################################################################################
```

Figure 2.9: Code for the routine ispec_ParameterFinder.py - input section

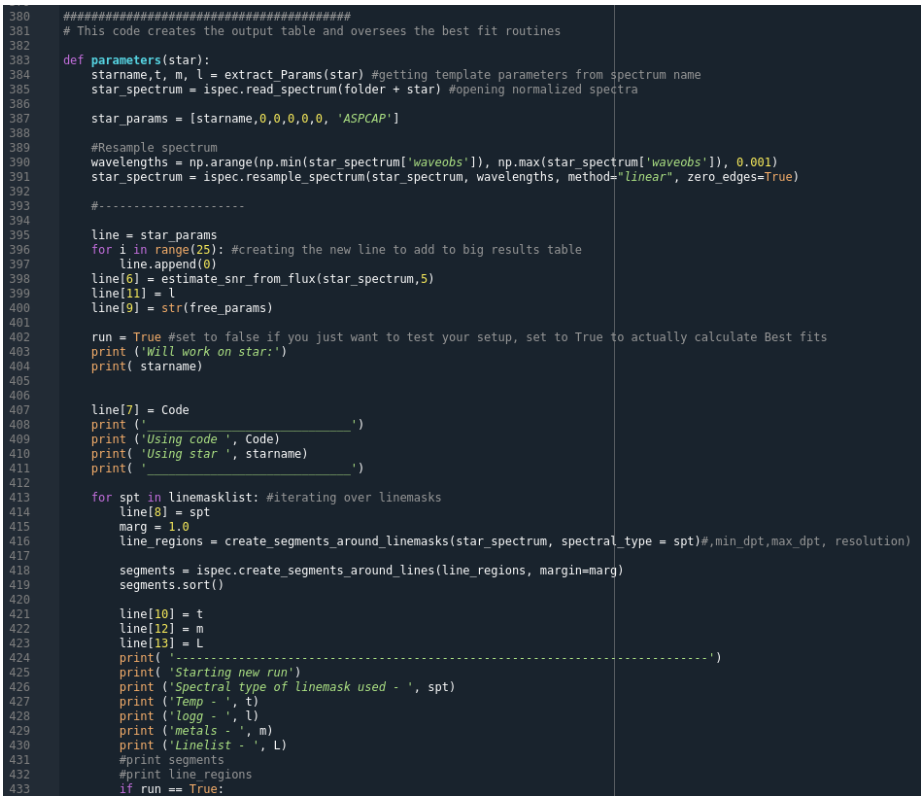
The code will run, by default, on every star + template combination listed in the input table Mdwarf_BestTemplates.fits - created by the previous routine BestTemplateCalc.py. In order for the code to run properly, each of the normalized spectra must be available at the folder "/normalized_spectra/". The code will output a best fit synthetic spectrum for each in the fits file, saving them to "/default_output/", as well as a master table summarizing the templates used and parameters derived for each star in the list, together with the χ^2 values measured for each combination.

Many things in this routine can be customized, such as the parameters left as free as iSpec runs, the radiative transfer code, the limits in the freedom of the three main parameters ($T_{\rm eff}$, $\log g$ and $[M/H]$) - see Figure 2.9. The linelist used is acutally defined inside "/ispec/spectrum.py", as due to the complicated way the interaction between Turbospectrum and iSpec is set up, it could not be changed in this location, and the variable "L" simply denotes the name of the linelist to present in the output table.

Another important thing to note about the boundary conditions for $T_{\rm eff}$, $\log g$ and $[M/H]$ is that iSpec will include an additional safety margin inside its code, so the margins written here are 0.1 dex above the desired boundaries for $\log g$ and $[M/H]$, and 100 K for $T_{\rm eff}$.

The output spectra is, by default, saved to "/default_output/", but this destination can be customized as well.

The body of the routine has many important parts, including a vacuum to air wavelength conversion, a function to generate the linemask segments, functions designed to create the structure of the final output table, and functions designed to find the names and parameters of the studied spectra from their file names. The user is advised not to edit any of these functions unless they know exactly what they are doing.



```
#####################################
# This code creates the output table and oversees the best fit routines

def parameters(star):
    starname,t, m, l = extract_Params(star) #getting template parameters from spectrum name
    star_spectrum = ispec.read_spectrum(folder + star) #opening normalized spectra

    star_params = [starname,0,0,0,0,0, 'ASPCAP']

    #Resample spectrum
    wavelengths = np.arange(np.min(star_spectrum['waveobs']), np.max(star_spectrum['waveobs']), 0.001)
    star_spectrum = ispec.resample_spectrum(star_spectrum, wavelengths, method="linear", zero_edges=True)

    #--------------------

    line = star_params
    for i in range(25): #creating the new line to add to big results table
        line.append(0)
    line[6] = estimate_snr_from_flux(star_spectrum,5)
    line[11] = l
    line[9] = str(free_params)

    run = True #set to false if you just want to test your setup, set to True to actually calculate Best fits
    print ('Will work on star:')
    print( starname)


    line[7] = Code
    print ('_____')
    print ('Using code ', Code)
    print( 'Using star ', starname)
    print( '_____')

    for spt in linemasklist: #iterating over linemasks
        line[8] = spt
        marg = 1.0
        line_regions = create_segments_around_linemasks(star_spectrum, spectral_type = spt)#,min_dpt,max_dpt, resolution)

        segments = ispec.create_segments_around_lines(line_regions, margin=marg)
        segments.sort()

        line[10] = t
        line[12] = m
        line[13] = L
        print( '--------------------------------------------------------------------------------')
        print( 'Starting new run')
        print ('Spectral type of linemask used - ', spt)
        print ('Temp - ', t)
        print ('logg - ', l)
        print ('metals - ', m)
        print ('Linelist - ', L)
        #print segments
        #print line_regions
        if run == True:
```

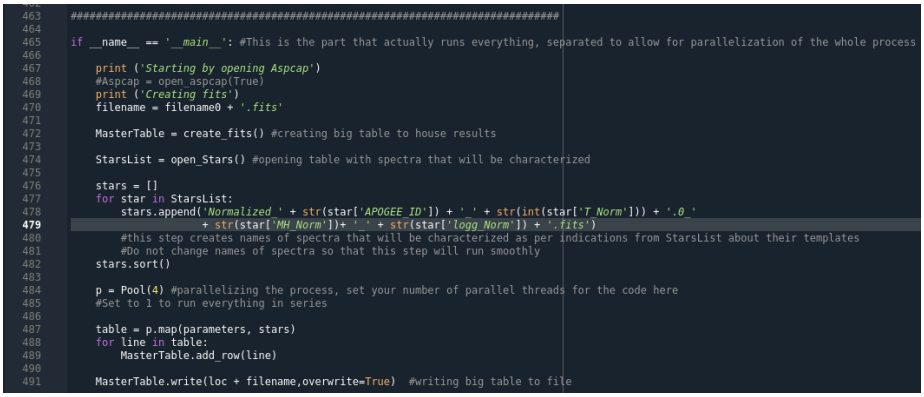
Figure 2.10: Code for the routine ispec_ParameterFinder.py - control section

The main function that controls the inputs and outputs and aggregates the actual results from the synthetic spectra is “parameters(star)” - see Figure 2.10. This function will operate the “determine_astrophysical_parameters_using_synth_spectra()” function with the desired inputs and combine them into the output table.

The main code is included at the end of the routine and it has parallelization utilities built within. To create multiple threads and run the synthesis of multiple stars at the same time, the user simply has to edit the number at line 481 -

```
p = Pool(4)
```

to their desired number of threads.



```
463  ######################################################################
464
465  if __name__ == '__main__': #This is the part that actually runs everything, separated to allow for parallelization of the whole process
466
467      print ('Starting by opening Aspcap')
468      #Aspcap = open_aspcap(True)
469      print ('Creating fits')
470      filename = filename0 + '.fits'
471
472      MasterTable = create_fits() #creating big table to house results
473
474      StarsList = open_Stars() #opening table with spectra that will be characterized
475
476      stars = []
477      for star in StarsList:
478          stars.append('Normalized_' + str(star['APOGEE_ID']) + '_' + str(int(star['T_Norm'])) + '.0_'
479                       + str(star['MH_Norm'])+ '_' + str(star['logg_Norm']) + '.fits')
480          #this step creates names of spectra that will be characterized as per indications from StarsList about their templates
481          #Do not change names of spectra so that this step will run smoothly
482      stars.sort()
483
484      p = Pool(4) #parallelizing the process, set your number of parallel threads for the code here
485      #Set to 1 to run everything in series
486
487      table = p.map(parameters, stars)
488      for line in table:
489          MasterTable.add_row(line)
490
491      MasterTable.write(loc + filename,overwrite=True)  #writing big table to file
```

Figure 2.11: Code for the routine ispec_ParameterFinder.py - main section

Chapter 3

Important warnings

Many of the routines will default their outputs to "/default_output/", and the files must then be moved so the next routines can be run. This is done so the user can run each routine individually while learning how to operate the code, but it can easily be customized by changing the output locations in the input sections of each code.

In addition, the names of the output spectra by a given routine are very important to the following routines, as they contain information about the stars being analyzed, the templates used for the normalization, or the output parameters given by the code. The names of the output files of intermediate routines such as normalized_Mdwarfs_grid.py should not be changed unless the user knows exactly what they are doing.

Finally, the routines included are a complement to the papers Sarmento et al. ((2020)) and Sarmento et al. ((2021)), and a complete read of those papers is suggested for a full understanding of them.

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