Python On Resonance (PyOR)

Everybody can simulate NMR

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Tutorial 14: Avoided Crossing Part 2

Example: Spin-Lock Induced Crossing (SLIC) - 2 spin half system

In previous tutorial we had plotted avoided crossing for two spin half system. In this tutorial we look into population "oscillation" between singlet and triplet states, when B1 amplitude (Spin Lock) equals J coupling (the SLIC condition).

Reference: PhD Thesis, Stephen J. DeVience, Harward University, 2014.

Load Python packages and define path to the source file "PythonOnResonance.py"

```
In [1]: pathSource = '/media/HD2/Vineeth/PostDoc_Simulations/Github/PyOR_G/Source'

In [2]: from IPython.display import display, HTML
    display(HTML("<style>.container { width:100% !important; }</style>"))
    import sys
    sys.path.append(pathSource)
    import PythonOnResonance as PyOR
    import time
    import numpy as np
    import matplotlib.pyplot as plt
    from matplotlib import rc
    %matplotlib notebook
    import sympy as sp
    from sympy import *
```

Generating Spin System

```
In [3]:
    Define Spin quantum numbers of your spins in "Slist1".
    Slist1[0] is spin of first particle and Slist1[1] is spin of second particle.
    """;
    Slist1 = [1/2,1/2]
```

```
In [4]: """

Define Planck constant equals 1.

Because NMR spectroscopists are more interested to write Energy in frequency units.
```

```
hbarEQ1 = True

In [5]:

"""
Generate Spin Operators
""";

System = PyOR.Numerical_MR(Slist1, hbarEQ1)

"""
Sx, Sy and Sz Operators
""";
Sx, Sy, Sz = System.SpinOperator()
"""
S+ and S- Operators
""";
Sp,Sm = System.PMoperators(Sx,Sy)
```

Zeeman Hamiltonian in Lab Frame

if False then hbarEQ1 = hbar

```
In [6]:
    """
    Gyromagnetic Ratio
    Gamma = [Gyromagnetic Ratio spin 1, Gyromagnetic Ratio spin 1, ...]
    """;
    Gamma = [System.gammaH1, System.gammaH1]
    """
    Define the field of the spectromter, B0 in Tesla.
    """
    Define the chemical Shift of individual spins
    Offset = [chemical Shift spin 1, chemical Shift spin 1, ..]
    """
    Offset = [0,2.8] # Offset frequency in Hz
    deltaV = Offset[1] - Offset[0] # Frequency difference between Spin 1 and 2
    """
    Function "LarmorF" give the list Larmor frequencies of individual spins in lab frame
    LarmorF = System.LarmorFrequency(Gamma, B0, Offset)
    Hz = System.Zeeman(LarmorF, Sz)
```

Larmor Frequency in MHz: [-200.11400882 -200.11401162]

Initialize Density Matrix

```
if Thermal_DensMatrix:
    Hz_EnUnit = System.Convert_FreqUnitsT0Energy(Hz)
    HT_approx = False # High Temperature Approximation is False
    T = 300 # Temperature in Kelvin
    rho_in = System.EqulibriumDensityMatrix(Hz_EnUnit,T,HT_approx)
    rhoeq = rho_in.copy()

else:
    rho_in = np.sum(Sz,axis=0) # Initial Density Matrix
    rhoeq = np.sum(Sz,axis=0) # Equlibrium Density Matrix
    print("Trace of density metrix = ", np.trace(rho_in))
```

Trace of density metrix = 0j

Zeeman Halitonian in Rotating Frame

```
In [8]: off = -2*np.pi*deltaV/2
OmegaRF = [-System.gammaH1*B0 + off ,-System.gammaH1*B0 + off] # RF iradiation in the midd
Hzr = System.Zeeman_RotFrame(LarmorF, Sz, OmegaRF)
```

J Coupling Hamiltonian

```
In [9]:
    Define J couplings between individual spins
    """

Jlist = np.zeros((len(Slist1),len(Slist1)))
    Jlist[0][1] = 17.4
    Hj = System.Jcoupling(Jlist,Sx,Sy,Sz)
```

B1 Hamiltonian (Spin Lock)

```
In [10]: Omega1 = [Jlist[0][1], Jlist[0][1]] # SLIC condition: B1 amplitude equals J coupling betwee
Omega1Phase = [0,0]
Hrf = System.Zeeman_B1(Sx,Sy,Omega1,Omega1Phase)
```

Total Hamiltonian

```
In [11]: Hslic = Hzr + Hj + Hrf # Hamiltonina duirng Spin Lock
```

We will work with 4 Spin-Lock Eigenstates

1. Spin-Lock Eigenstates (when B1 amplitude of RF >> Chemical shift difference)

$$|\phi_{+}> = rac{1}{2}(|lphalpha>+|lphaeta>+|etalpha>+|etaeta>) = rac{1}{\sqrt{2}}|T_{0}>+rac{1}{2}(|T_{-}>+|T_{+}>)$$
 $|\phi_{0}> = rac{1}{\sqrt{2}}(|lphalpha>-|etaeta>) = rac{1}{\sqrt{2}}(|T_{-}>-|T_{+}>)$
 $|\phi_{S}> = rac{1}{\sqrt{2}}(|lphaeta>-|etalpha>) = |S_{0}>$

$$|\phi_{-}> = rac{1}{2}(-|lphalpha>+|lphaeta>+|etalpha>-|etaeta>) = rac{1}{\sqrt{2}}|T_{0}>-rac{1}{2}(|T_{-}>+|T_{+}>)$$

2. Zeeman Eigenstates

$$|\alpha \alpha>, |\alpha \beta>, |\beta \alpha>, |\beta \beta>$$

3. Singlet-Triplet States

-0.707106781186548

In [15]:

0.5

```
|T_{+}>, |T_{0}>, |T_{0}>, |S_{0}>
```

```
In [12]:
           Zeeman eigen states
           B_Z = System.ZBasis_H(Hz)
           Matrix(B_Z[0])
          |1/2,1/2\rangle|1/2,1/2\rangle, |1/2,1/2\rangle|1/2,-1/2\rangle, |1/2,-1/2\rangle|1/2,1/2\rangle, |1/2,-1/2\rangle|1/2,-1/2\rangle
Out[12]:
In [13]:
           Lets make Spin-Lock Eigenstates from Zeeman eigen states
           Phi_p = 0.5 * (B_Z[0] + B_Z[1] + B_Z[2] + B_Z[3]) # linear combination of triplet states
           Phi_0 = (1/sqrt(2)) * (B_Z[0] - B_Z[3]) # linear combination of triplet states
           Phi\_S = (1/sqrt(2)) * (B\_Z[1] - B\_Z[2]) # Singlet State
           Phi_m = 0.5 * (B_Z[1] + B_Z[2] - B_Z[0] - B_Z[3]) # linear combination of triplet states
           Matrix(Phi_p)
Out[13]:
            0.5
In [14]:
           0.00
           Let make a basis transformation operator, U
           Inorder to transform all operators from Zeeman basis to Spin-Lock Eigenstates
           """;
           U = np.zeros((System.Vdim, System.Vdim))
           U[:,0] = Phi_m.T
           U[:,1] = Phi_0.T
           U[:,2] = Phi_p.T
           U[:,3] = Phi_S.T
           Matrix(U)
                                                           0
Out[14]:
                    0.707106781186548
                                           0.5
             0.5
                             0
                                           0.5
                                                  0.707106781186548
                             0
                                           0.5
                                                 -0.707106781186548
```

0

```
Lets make the population operators from Spin-Lock Eigenstates
          pop_P population of Phi_p # linear combination of triplet states
          pop_0 population of Phi_0 # linear combination of triplet states
          pop_S population of Phi_S # Singlet states
          pop_M population of Phi_m # linear combination of triplet states
          pop_P = Phi_p @ Phi_p.T
          pop_0 = Phi_0 @ Phi_0.T
          pop_S = Phi_S @ Phi_S.T
          pop_M = Phi_m @ Phi_m.T
In [16]:
          The population operators are in Zeeman basis
          Matrix(pop_P)
           0.25
                  0.25
                        0.25
                              0.25^{-}
Out[16]:
           0.25
                  0.25
                        0.25
                              0.25
           0.25
                  0.25
                        0.25
                              0.25
           0.25
                        0.25
                              0.25
                  0.25
In [17]:
          0.00
          Convert the operators into Spin-Lock basis
          pop_P_SL = np.linalg.inv(U) @ pop_P @ U
          pop_0_SL = np.linalg.inv(U) @ pop_0 @ U
          pop_S_SL = np.linalg.inv(U) @ pop_S @ U
          pop_M_SL = np.linalg.inv(U) @ pop_M @ U
          Hslic_SL = np.linalg.inv(U) @ Hslic @ U # Changing the basis of Hamiltonian to Spin-Lock
In [18]:
          Matrix(pop_M)
                           -0.25
                                     0.25 7
            0.25
                    -0.25
Out[18]:
            -0.25
                    0.25
                            0.25
                                    -0.25
            -0.25
                    0.25
                            0.25
                                    -0.25
            0.25
                    -0.25
                           -0.25
                                     0.25
In [19]:
          Matrix(pop_0)
            0.5
                      0
                         -0.5\,
Out[19]:
             0
                      0
                  0
                           0
             0
                  0
                      0
                           0
                  0
                          0.5
                      0
In [20]:
          Matrix(pop_P)
                  0.25
                        0.25
                              0.25^{-1}
           \lceil 0.25 \rceil
Out[20]:
           0.25
                  0.25
                        0.25
                              0.25
                  0.25
           0.25
                        0.25
                              0.25
           0.25
                  0.25
                        0.25
                              0.25
In [21]:
          Matrix(pop_S) # Singlet
```

```
Out[21]: \begin{bmatrix} 0 & 0 & 0 & 0 \\ 0 & 0.5 & -0.5 & 0 \\ 0 & -0.5 & 0.5 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}
```

Pulse

```
In [22]:
    Rotate the magnetization about Y-axis, by an angle theta.
    """;
    pulse_angle = 90.0
    rho = System.Rotate_H(rho_in,pulse_angle,np.sum(Sy,axis=0))
    rho_SL = np.linalg.inv(U) @ rho @ U # Changing the basis of density matrix to Spin-Lock be
```

Relaxation Constant

```
In [23]:
    R1 = 1.0
    R2 = 2.0
    System.Relaxation_Constants(R1,R2)

    Rprocess = "No Relaxation"
```

Evolution of Density Matrix under first Spin Lock

```
In [24]:
    dt = 1.0e-4
    Spin_Lock_Time = 1
    Npoints1 = int(Spin_Lock_Time/dt)
    print("Number of points in the simulation", Npoints1)

"""
    option for solver, "method": "Unitary Propagator" or "ODE Solver"
"""
    method = "Unitary Propagator"

    start_time = time.time()
    t1, rho_t1 = System.Evolution_H(rhoeq,rho_SL,Sx,Sy,Sz,Sp,Sm,Hslic_SL,dt,Npoints1,method,Rg end_time = time.time()
    timetaken = end_time - start_time
    print("Total time = %s seconds " % (timetaken))
```

Number of points in the simulation 10000 Total time = 0.05933833122253418 seconds

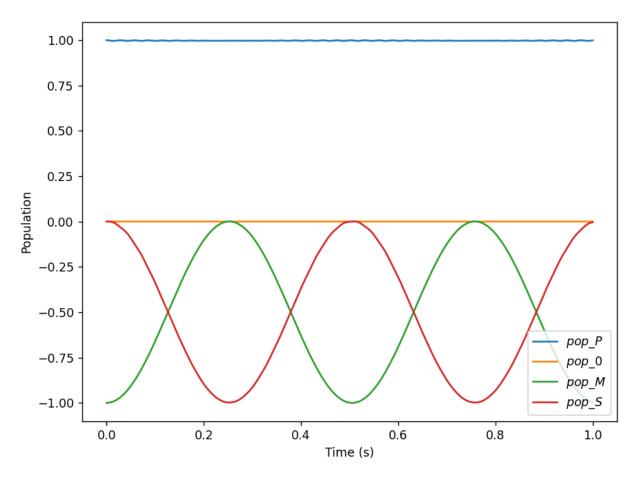
Expetation Value - Population

```
In [25]:
    start_time = time.time()
    t, population_P = System.Expectation_H(rho_t1,pop_P_SL,dt,Npoints1)
    t, population_0 = System.Expectation_H(rho_t1,pop_0_SL,dt,Npoints1)
    t, population_M = System.Expectation_H(rho_t1,pop_M_SL,dt,Npoints1)
    t, population_S = System.Expectation_H(rho_t1,pop_S_SL,dt,Npoints1)
    end_time = time.time()
    timetaken = end_time - start_time
    print("Total time = %s seconds " % (timetaken))
```

Total time = 111.60574984550476 seconds

Plotting the Population

```
In [26]:
    plt.figure(1)
    plt.plot(t,population_P,"-",label=r"$pop\_P$")
    plt.plot(t,population_0,"-",label=r"$pop\_0$")
    plt.plot(t,population_M,"-",label=r"$pop\_M$")
    plt.plot(t,population_S,"-",label=r"$pop\_S$")
    plt.xlabel("Time (s)")
    plt.ylabel("Population")
    plt.legend()
```



```
/opt/anaconda3/lib/python3.9/site-packages/numpy/core/_asarray.py:102: ComplexWarning: Cas ting complex values to real discards the imaginary part return array(a, dtype, copy=False, order=order)
/opt/anaconda3/lib/python3.9/site-packages/numpy/core/_asarray.py:102: ComplexWarning: Cas ting complex values to real discards the imaginary part return array(a, dtype, copy=False, order=order)
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```

Conclusion:

Out[26]:

So we can see the population between pop_M and pop_S oscillates. So if we wait $t_{SLIC,max}=\frac{0.707}{\Delta\nu}$, in this case is it 0.2525 seconds, $\Delta\nu$ is the chemical shift difference, we can populate the singlet state.

Plotting the Eigen Values

Any suggestion? write to me

If you see something is wrong please write to me, so that the PyOR can be error free.

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In []:			