

SMD Increase in disease burden

September 2, 2022

```
[1]: #import necessary packages
import matplotlib.pyplot as plt
import numpy as np
import sympy
from IPython.display import Image
from tqdm import trange

#Set up sympy to display outputs after a latex conversion.
from sympy.interactive import printing
printing.init_printing(use_latex=True)

# Import custom module
import SMB_Code_models_equilibria as models_equil
```

1 1 Where does an increase in ϵ cause a discontinuous increase in disease burden and what is the increase in disease burden.

```
[2]: param_values = {'N':1, 'epsilon':0.4, 'beta_W': 0.04 , 'beta_Z': 0.015, 'gamma': 0.
    ↪01, 'gamma_T': 0.1}
```

```
[3]: epsilon_vals = np. arange (0, 1.001, 0.001)
S_endem = []
I_W_endem = []
I_Z_endem = []

for i in trange(len(epsilon_vals)):
    param_values['epsilon']=epsilon_vals[i]
    prevs = models_equil.replace_inf_end_equil(param_values)
    S_endem.append(prevs[0]['S'])
    I_W_endem.append(prevs[0]['I_W'])
    I_Z_endem.append(prevs[0]['I_Z'])

fig = plt.figure(figsize=(15,5))

fig.suptitle('Proportion over Time (Days)',
            fontsize=20)
```

```

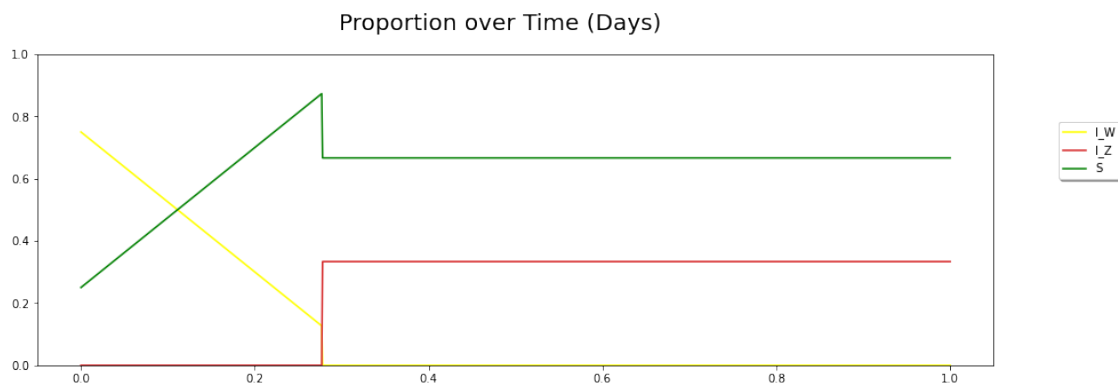
ax = plt.subplot(111)
axes = plt.gca()
axes.set_ylim([0,1])

ax.plot(epsilon_vals,I_W_endem,color='yellow',label='I_W')
ax.plot(epsilon_vals,I_Z_endem,color='tab:red',label='I_Z')
ax.plot(epsilon_vals,S_endem,color='green',label='S')
chartBox = ax.get_position()
ax.legend(loc='upper center', bbox_to_anchor=(1.1, 0.8), shadow=True, ncol=1)
plt.show()

```

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The jump in disease burden occurs when resistant strain endemic equilibrium becomes stable. So what is the first element of `I_Z_endem` to be >0 .

```

[4]: I_Z_endem = np.array(I_Z_endem)
I_Z_endem

np.where(I_Z_endem>0)

```

```

[4]: (array([ 278,  279,  280,  281,  282,  283,  284,  285,  286,  287,  288,
            289,  290,  291,  292,  293,  294,  295,  296,  297,  298,  299,
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982, 983, 984, 985, 986, 987, 988, 989, 990, 991, 992,
993, 994, 995, 996, 997, 998, 999, 1000], dtype=int64),)

```

The values of ϵ , S , I_W and I_Z at that point are equal to:

```
[5]: display(epsilon_vals[278],S_endem[278],I_W_endem[278],I_Z_endem[278])
```

0.278

0.6666666666666667

0

0.3333333333333333

Just before that point the values of ϵ , S , I_W and I_Z are equal to:

```
[6]: display(epsilon_vals[277],S_endem[277],I_W_endem[277],I_Z_endem[277])
```

0.277

0.87325

0.12675

0

Meaning the jump in disease burden is:

```
[7]: S_endem[277]-S_endem[278]
```

```
[7]: 0.2065833333333333
```

1.1 2 Deriving equations for ϵ at the discontinuous increase of disease burden and the increase in Disease burden.

Lets look at the disease equalibria, assocaited Jacobian Matrix and Eigen values.

```
[8]: #Setup Symbols for Sympy
N, S, I_W, I_Z, beta_W, beta_Z, gamma, gamma_T, epsilon = sympy.symbols('N S_
↪I_W I_Z beta_W beta_Z gamma gamma_T epsilon')

Eqn_S = -beta_W/N*I_W*S-beta_Z/
↪N*I_Z*S+gamma*(1-epsilon)*I_W+gamma_T*epsilon*I_W+gamma*I_Z
Eqn_I_W = beta_W/N*I_W*S-gamma*(1-epsilon)*I_W-gamma_T*epsilon*I_W+(beta_W/
↪N-beta_Z/N)*I_W*I_Z
Eqn_I_Z = beta_Z/N*I_Z*S-gamma*I_Z+(beta_Z/N-beta_W/N)*I_W*I_Z

```

```
[9]: ODEs = sympy.Matrix([Eqn_S,Eqn_I_W,Eqn_I_Z])
ODEs
```

```
[9]: 
$$\begin{bmatrix} I_W \epsilon \gamma_T + I_W \gamma (1 - \epsilon) - \frac{I_W S \beta_W}{N} + I_Z \gamma - \frac{I_Z S \beta_Z}{N} \\ I_W I_Z \left( \frac{\beta_W}{N} - \frac{\beta_Z}{N} \right) - I_W \epsilon \gamma_T - I_W \gamma (1 - \epsilon) + \frac{I_W S \beta_W}{N} \\ I_W I_Z \left( -\frac{\beta_W}{N} + \frac{\beta_Z}{N} \right) - I_Z \gamma + \frac{I_Z S \beta_Z}{N} \end{bmatrix}$$

```

```
[10]: equilibria = sympy.solve(ODEs,[S, I_W, I_Z])
equilibria
```

```
[10]: 
$$\left( (S, 0, 0), \left( \frac{I_W \beta_W - I_W \beta_Z + N \gamma}{\beta_Z}, I_W, \frac{-I_W \beta_W^2 + I_W \beta_W \beta_Z - N \beta_W \gamma - N \beta_Z \epsilon \gamma + N \beta_Z \epsilon \gamma_T + N \beta_Z \gamma}{\beta_Z (\beta_W - \beta_Z)} \right), \left( \frac{N (-\epsilon \gamma + \epsilon \gamma_T + \gamma)}{\beta_W}, I_W, 0 \right), \left( \frac{N \gamma}{\beta_Z}, 0, I_Z \right) \right)$$

```

```
[11]: endem_equil = equilibria[-2:]
endem_equil
```

```
[11]: 
$$\left( \left( \frac{N (-\epsilon \gamma + \epsilon \gamma_T + \gamma)}{\beta_W}, I_W, 0 \right), \left( \frac{N \gamma}{\beta_Z}, 0, I_Z \right) \right)$$

```

```
[12]: I_W_equil = N-endem_equil[0][0]
I_Z_equil = N-endem_equil[1][0]
display(I_W_equil,I_Z_equil)
```

$$N - \frac{N (-\epsilon \gamma + \epsilon \gamma_T + \gamma)}{\beta_W}$$

$$N - \frac{N \gamma}{\beta_Z}$$

```
[13]: J_of_ODEs = ODEs.jacobian(X=[S,I_W,I_Z])
J_of_ODEs
```

```
[13]: 
$$\begin{bmatrix} -\frac{I_W \beta_W}{N} - \frac{I_Z \beta_Z}{N} & \epsilon \gamma_T + \gamma (1 - \epsilon) - \frac{S \beta_W}{N} & \gamma - \frac{S \beta_Z}{N} \\ \frac{I_W \beta_W}{N} & I_Z \left( \frac{\beta_W}{N} - \frac{\beta_Z}{N} \right) - \epsilon \gamma_T - \gamma (1 - \epsilon) + \frac{S \beta_W}{N} & I_W \left( \frac{\beta_W}{N} - \frac{\beta_Z}{N} \right) \\ \frac{I_Z \beta_Z}{N} & I_Z \left( -\frac{\beta_W}{N} + \frac{\beta_Z}{N} \right) & I_W \left( -\frac{\beta_W}{N} + \frac{\beta_Z}{N} \right) - \gamma + \frac{S \beta_Z}{N} \end{bmatrix}$$

```

Substitute the 2nd non-disease free equilibrium (non-DFE) into the Jacobian matrix and determine Eigen values.

```
[14]: non_DFE_2 = {'S':equilibria[3][0], 'I_W':equilibria[3][1], 'I_Z':equilibria[3][2]}

J_of_ODEs_non_DFE_2 = J_of_ODEs.subs(non_DFE_2)
J_of_ODEs_non_DFE_2

eigs_J_non_DFE_2 = J_of_ODEs_non_DFE_2.eigenvals()
# The above code line enters the Eigen values as keys to a dictionary.
# It would be more useful to have them as elements in a vector.
eigs_J_non_DFE_2 = [k for k in eigs_J_non_DFE_2.keys()]
eigs_J_non_DFE_2
```

```
[14]:
```

$$\left[\frac{I_Z \beta_W \beta_Z - I_Z \beta_Z^2 + N \beta_W \gamma + N \beta_Z \epsilon \gamma - N \beta_Z \epsilon \gamma_T - N \beta_Z \gamma}{N \beta_Z}, -\frac{I_Z \beta_Z}{N}, 0 \right]$$

1.1.1 2.1 Deriving equation for ϵ at the discontinuous increase of disease burden

Model switches over between equilibrium when the 2nd equation in the set of eigen values = 0 so..

```
[15]: change_point_v2 = sympy.Eq(0,eigs_J_non_DFE_2[0])
      display(change_point_v2)
```

$$0 = \frac{I_Z \beta_W \beta_Z - I_Z \beta_Z^2 + N \beta_W \gamma + N \beta_Z \epsilon \gamma - N \beta_Z \epsilon \gamma_T - N \beta_Z \gamma}{N \beta_Z}$$

```
[16]: epsilon_at_change_v2 = sympy.solve(change_point_v2,epsilon)
      epsilon_at_change_v2
```

$$\left[\frac{-I_Z \beta_W \beta_Z + I_Z \beta_Z^2 - N \beta_W \gamma + N \beta_Z \gamma}{N \beta_Z (\gamma - \gamma_T)} \right]$$

```
[17]: epsilon_at_change_v2=epsilon_at_change_v2[0]
      epsilon_at_change_v2 = epsilon_at_change_v2.subs(I_Z,I_Z_equil)
      epsilon_at_change_v2
```

$$\frac{-N \beta_W \gamma + N \beta_Z \gamma - \beta_W \beta_Z \left(N - \frac{N \gamma}{\beta_Z} \right) + \beta_Z^2 \left(N - \frac{N \gamma}{\beta_Z} \right)}{N \beta_Z (\gamma - \gamma_T)}$$

```
[18]: epsilon_at_change_v2.subs(param_values)
```

```
[18]: 0.2777777777777778
```

Lets check this is the correct value

```
[19]: epsilon_vals[278]
```

```
[19]: 0.278
```

```
[20]: param_values['epsilon']=epsilon_at_change_v2.subs(param_values)
      param_values
```

```
[20]: {'N': 1,
      'epsilon': 0.2777777777777778,
      'beta_W': 0.04,
      'beta_Z': 0.015,
      'gamma': 0.01,
      'gamma_T': 0.1}
```

Increase in disease burden in replacement model is:

```
[21]: models_equil.replace_inf_end_equil(param_values)
```

```
[21]: [{'S': 0.8750000000000000, 'I_W': 0.1250000000000000, 'I_Z': 0}]
```

This is indeed the correct value of ϵ .

1.2 2.2 Deriving Equation for the Increase in Disease burden.

```
[22]: inc_burd = I_Z_equil - I_W_equil.subs(epsilon,epsilon_at_change_v2)
      inc_burd
```

$$[22]: -\frac{N\gamma}{\beta_Z} + \frac{N \left(\gamma - \frac{\gamma(-N\beta_W\gamma + N\beta_Z\gamma - \beta_W\beta_Z(N - \frac{N\gamma}{\beta_Z}) + \beta_Z^2(N - \frac{N\gamma}{\beta_Z}))}{N\beta_Z(\gamma - \gamma_T)} + \frac{\gamma_T(-N\beta_W\gamma + N\beta_Z\gamma - \beta_W\beta_Z(N - \frac{N\gamma}{\beta_Z}) + \beta_Z^2(N - \frac{N\gamma}{\beta_Z}))}{N\beta_Z(\gamma - \gamma_T)} \right)}{\beta_W}$$

```
[23]: inc_burd=inc_burd.simplify()
      inc_burd
```

$$[23]: N - \frac{N\gamma}{\beta_Z} - \frac{N\beta_Z}{\beta_W} + \frac{N\gamma}{\beta_W}$$

```
[24]: inc_burd.subs(param_values)
```

```
[24]: 0.2083333333333333
```

Lets double check.

```
[25]: S_endem[277]-S_endem[278]
```

```
[25]: 0.2065833333333333
```

2 3 Checking working with different set of parameters.

```
[26]: param_values = {'N':1,'epsilon':0.4,'beta_W': 0.04 , 'beta_Z': 0.03,'gamma': 0.
      ↪01,'gamma_T': 0.1}

epsilon_vals = np. arange (0, 1.001, 0.001)
S_endem = []
I_W_endem = []
I_Z_endem = []

for i in trange(len(epsilon_vals)):
    param_values['epsilon']=epsilon_vals[i]
    prevs = models_equil.replace_inf_end_equil(param_values)
    S_endem.append(prevs[0]['S'])
    I_W_endem.append(prevs[0]['I_W'])
    I_Z_endem.append(prevs[0]['I_Z'])

fig = plt.figure(figsize=(15,5))

fig.suptitle('Proportion over Time (Days)',
            fontsize=20)

ax = plt.subplot(111)
axes = plt.gca()
```

```

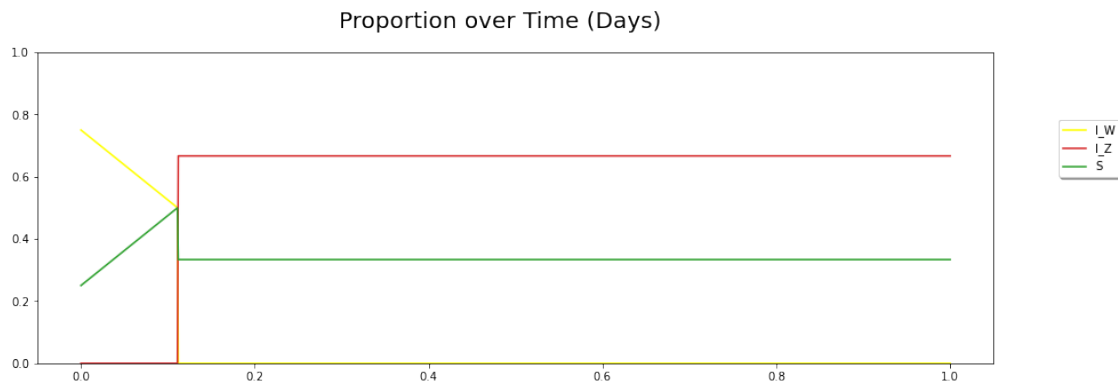
axes.set_ylim([0,1])

ax.plot(epsilon_vals,I_W_endem,color='yellow',label='I_W')
ax.plot(epsilon_vals,I_Z_endem,color='tab:red',label='I_Z')
ax.plot(epsilon_vals,S_endem,color='tab:green',label='S')
chartBox = ax.get_position()
ax.legend(loc='upper center', bbox_to_anchor=(1.1, 0.8), shadow=True, ncol=1)
plt.show()

```

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The jump in disease burden occurs when resistant strain endemic equilibrium becomes stable. So what is the first element of `I_Z_endem` to be `>0`.

```

[27]: I_Z_endem = np.array(I_Z_endem)
      I_Z_endem

      np.where(I_Z_endem>0)

```

```

[27]: (array([ 112,  113,  114,  115,  116,  117,  118,  119,  120,  121,  122,
              123,  124,  125,  126,  127,  128,  129,  130,  131,  132,  133,
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684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694,
695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705,
706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716,
717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727,
728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738,
739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749,
750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760,
761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771,
772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782,

```

783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793,
794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804,
805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815,
816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826,
827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837,
838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 848,
849, 850, 851, 852, 853, 854, 855, 856, 857, 858, 859,
860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870,
871, 872, 873, 874, 875, 876, 877, 878, 879, 880, 881,
882, 883, 884, 885, 886, 887, 888, 889, 890, 891, 892,
893, 894, 895, 896, 897, 898, 899, 900, 901, 902, 903,
904, 905, 906, 907, 908, 909, 910, 911, 912, 913, 914,
915, 916, 917, 918, 919, 920, 921, 922, 923, 924, 925,
926, 927, 928, 929, 930, 931, 932, 933, 934, 935, 936,
937, 938, 939, 940, 941, 942, 943, 944, 945, 946, 947,
948, 949, 950, 951, 952, 953, 954, 955, 956, 957, 958,
959, 960, 961, 962, 963, 964, 965, 966, 967, 968, 969,
970, 971, 972, 973, 974, 975, 976, 977, 978, 979, 980,
981, 982, 983, 984, 985, 986, 987, 988, 989, 990, 991,
992, 993, 994, 995, 996, 997, 998, 999, 1000], dtype=int64),)

```

The values of ϵ , S , I_W and I_Z at that point are equal to:

```
[28]: display(epsilon_vals[112],S_endem[112],I_W_endem[112],I_Z_endem[112])
```

```
0.112
```

```
0.3333333333333333
```

```
0
```

```
0.6666666666666667
```

Just before that point the values of ϵ , S , I_W and I_Z are equal to:

```
[29]: display(epsilon_vals[111],S_endem[111],I_W_endem[111],I_Z_endem[111])
```

```
0.111
```

```
0.49975
```

```
0.50025
```

```
0
```

Meaning the jump in disease burden is:

```
[30]: S_endem[111]-S_endem[112]
```

```
[30]: 0.1664166666666667
```

By derived calculation the the jump in deisease burden should occur when $\epsilon =$

```
[31]: epsilon_at_change_v2.subs(param_values)
```

[31]: 0.1111111111111111

The increase in disease burden should be:

```
[32]: inc_burd.subs(param_values)
```

[32]: 0.1666666666666667

All seems correct, minor differences can be put down to rounding errors and that epsilon was altered in increments of 0.001 when plotting graphs of stable endemic equilibria.

3 4 Plots of cost of antimicrobial resistance (reduction in transmission $1 - \frac{\beta_Z}{\beta_W}$) against discontinuous increase in disease burden as a proportion of the population. (Figure 3)

```
[33]: param_values = {'N':1, 'beta_W': 0.04 , 'beta_Z': 0.015, 'gamma': 0.01, 'gamma_T': 0.1}
      dpi = 96 # dpi for this screen is according to: https://www.infobyip.com/detectmonitordpi.php
```

Remember the I_W strain's $R_0 = \frac{\beta_Z}{\gamma}$. When $\beta_Z = 0.25\beta_W = 0.01$ and I_W strain's $R_0 = 1$, therefore we will not plot below $\beta_Z = 0.25\beta_W = 0.01$.

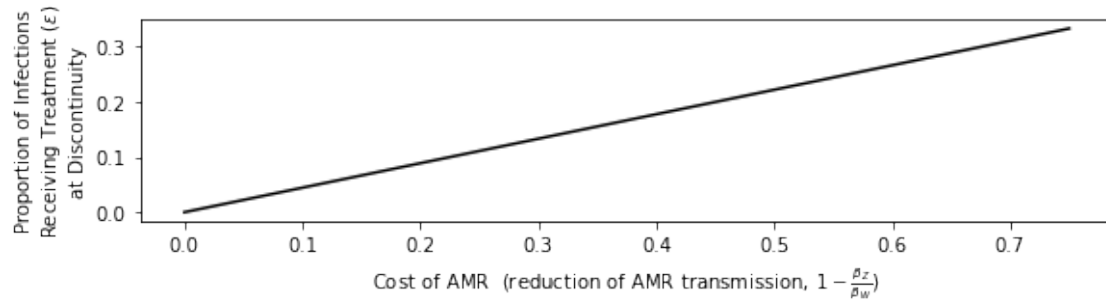
```
[34]: beta_Z_props = np. arange (int(25), int(101), int(1))
      beta_Z_props = np.divide(beta_Z_props,100)
      level_of_treatment = []

      for prop in beta_Z_props:
          param_values['beta_Z'] = param_values['beta_W']*prop
          epsilon = epsilon_at_change_v2.subs(param_values)
          level_of_treatment.append(epsilon)

      fig_epsilon = plt.figure(figsize=(870/dpi, 185/dpi))

      ax = plt.subplot(111)
      axes = plt.gca()

      ax.plot(np.subtract(1,beta_Z_props),level_of_treatment,color='black')
      ax.set_xlabel(r'Cost of AMR (reduction of AMR transmission,  $1 - \frac{\beta_Z}{\beta_W}$ )')
      ax.set_ylabel('Proportion of Infections Receiving Treatment ( $\epsilon$ )\nat Discontinuity')
      plt.show()
```



```
[35]: fig_epsilon.savefig('Epsilon at disease jump v AMR to AMS transmission.png',
    ↳bbox_inches='tight')
```

```
[36]: param_values = {'N':1, 'beta_W': 0.04 , 'beta_Z': 0.015, 'gamma': 0.01}
```

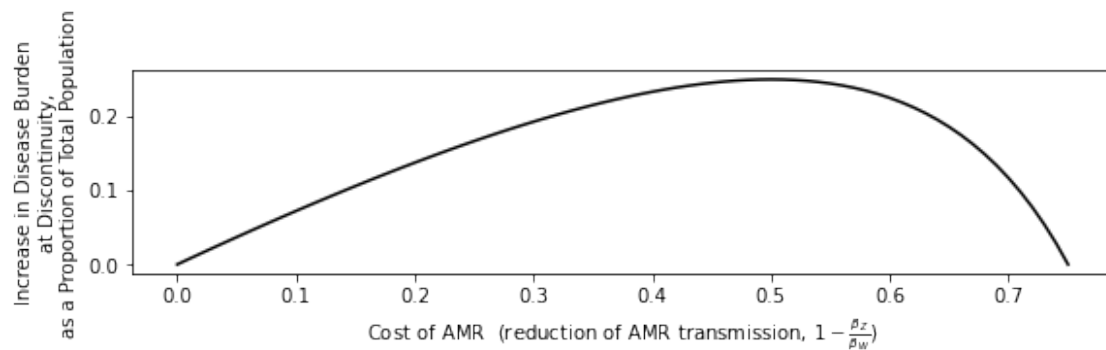
```
[37]: increases_in_burden = []

for prop in beta_Z_props:
    param_values['beta_Z'] = param_values['beta_W']*prop
    increase = inc_burd.subs(param_values)
    increases_in_burden.append(increase)

fig_increase_burden = plt.figure(figsize=(870/dpi, 185/dpi))

ax = plt.subplot(111)
axes = plt.gca()

ax.plot(np.subtract(1, beta_Z_props), increases_in_burden, color='black')
ax.set_xlabel(r'Cost of AMR (reduction of AMR transmission,
    ↳ $1 - \frac{\beta_Z}{\beta_W}$ )')
ax.set_ylabel('Increase in Disease Burden\nat Discontinuity,\nas a Proportion\n↳of Total Population')
plt.show()
```



```
[38]: fig_increase_burden.savefig('Increase in disease burden v AMR to AMS_
↳transmission.png', bbox_inches='tight')
```

```
[39]: np.where(beta_Z_props==0.9)[0][0]
```

```
[39]: 65
```

```
[40]: display(increases_in_burden[np.where(beta_Z_props==0.
↳9)[0][0]],level_of_treatment[np.where(beta_Z_props==0.9)[0][0]])
```

```
0.0722222222222221
```

```
0.04444444444444444
```

```
[41]: display(increases_in_burden[np.where(beta_Z_props==0.
↳5)[0][0]],level_of_treatment[np.where(beta_Z_props==0.5)[0][0]])
```

```
0.25
```

```
0.2222222222222222
```

```
[ ]:
```