--------------------------------------------------------------------------------------

The model fitting

--------------------------------------------------------------------------------------

/scratch/borgqvist/Dropbox/Work/Projects/symmetry\_based\_model\_selsection\_carcinogenesis/Code/fit\_to\_data.py:36: RuntimeWarning: overflow encountered in power

return A\*(t\*\*gamma)

/scratch/borgqvist/Dropbox/Work/Projects/symmetry\_based\_model\_selsection\_carcinogenesis/Code/fit\_to\_data.py:36: RuntimeWarning: overflow encountered in power

return A\*(t\*\*gamma)

/scratch/borgqvist/Dropbox/Work/Projects/symmetry\_based\_model\_selsection\_carcinogenesis/Code/fit\_to\_data.py:49: RuntimeWarning: overflow encountered in exp

return ((A)/(np.exp(np.exp(-alpha\*(t-tau)))-C))

/scratch/borgqvist/Dropbox/Work/Projects/symmetry\_based\_model\_selsection\_carcinogenesis/Code/fit\_to\_data.py:49: RuntimeWarning: overflow encountered in exp

return ((A)/(np.exp(np.exp(-alpha\*(t-tau)))-C))

/scratch/borgqvist/Dropbox/Work/Projects/symmetry\_based\_model\_selsection\_carcinogenesis/Code/fit\_to\_data.py:49: RuntimeWarning: overflow encountered in exp

return ((A)/(np.exp(np.exp(-alpha\*(t-tau)))-C))

/scratch/borgqvist/Dropbox/Work/Projects/symmetry\_based\_model\_selsection\_carcinogenesis/Code/symmetry\_toolbox.py:185: RuntimeWarning: overflow encountered in exp

return ((A)/(np.exp(np.exp(-alpha\*(t-tau)))-C))

Fitting is done!

--------------------------------------------------------------------------------------

The transformation scales increasing the age from 80 years to 160 years

--------------------------------------------------------------------------------------

The PLM: epsilon\_PLM = 1.386294361120

The IM-III myeloma: epsilon\_IM\_III\_myeloma = 0.767368329872

The IM-III colon: epsilon\_IM\_III\_colon = 0.650429833712

The IM-III CML: epsilon\_IM\_III\_CML = 0.554786599426

--------------------------------------------------------------------------------------

The symmetry based framework for model selection

--------------------------------------------------------------------------------------

The scales for the framework are the following:

PLM All datasets: epsilon\_scale = 1.386294361120

IM-III myeloma: epsilon\_scale = 0.767368329872

IM-III colon: epsilon\_scale = 0.650429833712

IM-III CML: epsilon\_scale = 0.554786599426

The output:

Myeloma:

Colon cancer:

CML:

Symmetry framework is done!

Illustrate framework!

PLM

PLM epsilon scale: 0.690

IM-III

IM-III epsilon scale: 0.650

--------------------------------------------------------------------------------------

Action of symmetries!

--------------------------------------------------------------------------------------

Epsilon scales for illustrations (i.e. the value that the transformations are pushed with twice)

PLM, 0.3465736

IM-III, 0.3836842

--------------------------------------------------------------------------------------

Calculations are done!