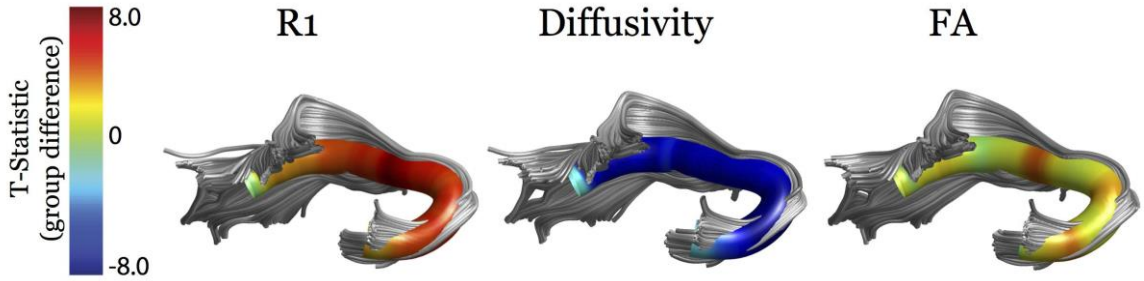
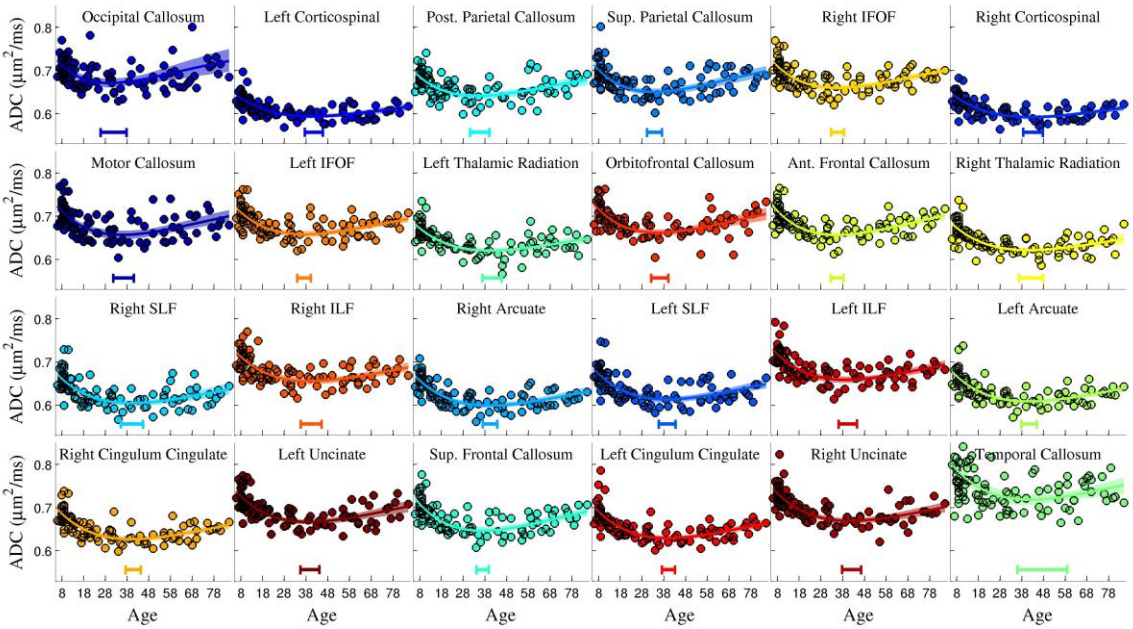
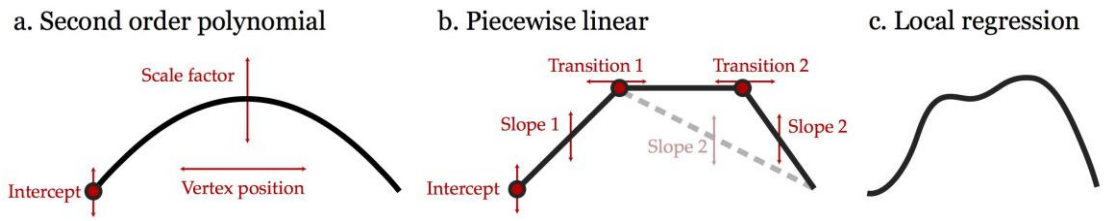


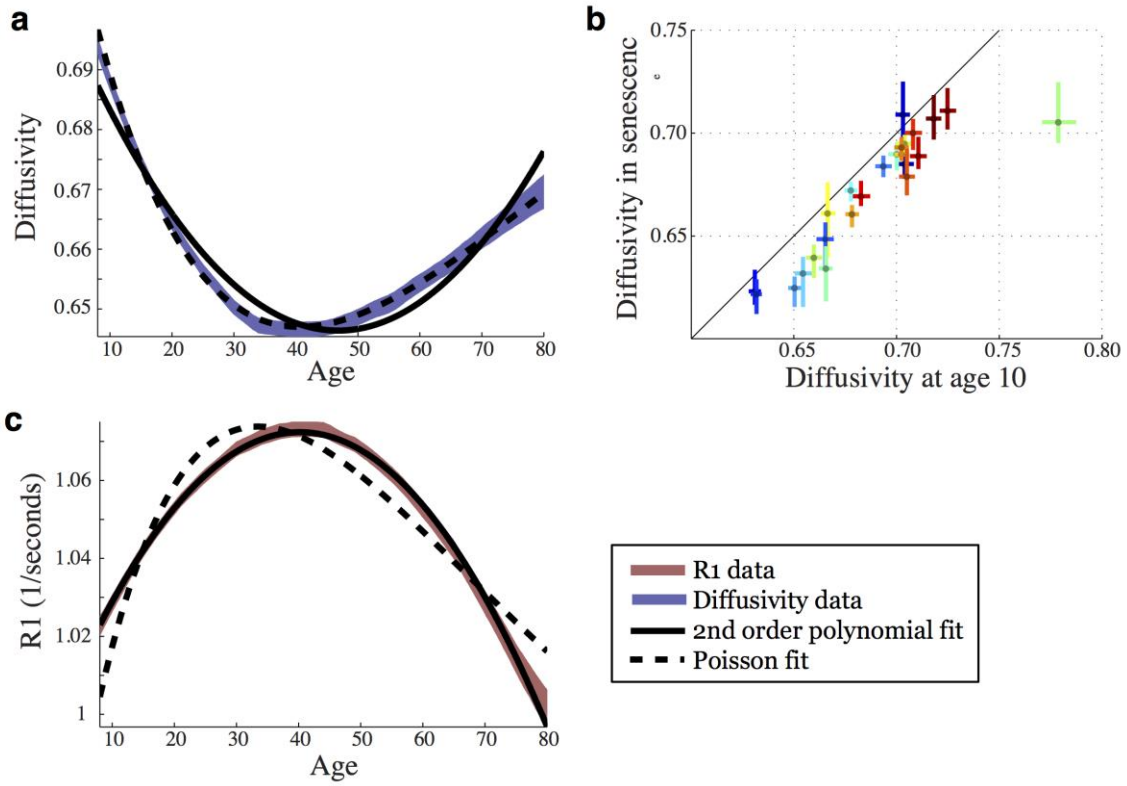
Supplementary Figure 1. R1 and diffusivity development rates, but not FA, are close to constant along the tract length. An independent samples T-test comparing children and adults computed at each point along the Tract Profile for each quantitative MRI parameter. The tract is color-coded based on the amount of developmental change at each point along the tract. While FA development only occurs at specific locations along the fascicle, diffusivity and R1 development is relatively consistent along the tract length. Both R1 and diffusivity show a substantial and consistent (~8 standard errors of the mean) difference between children and adults. For FA, there is a smaller but highly significant effect localized at a few locations along the tract while there are also other locations where the distribution of FA values is completely overlapping for children and adults. Examining all the tracts, on average, there is five times more variability in FA development rates along a tract than there is variability in diffusivity and R1 development rates. Hence, the mean FA development rate for a fascicle is not representative of that fascicle's development. Therefore, we focus the manuscript analyses on tract mean R1 and diffusivity values, as these measures directly relate to the biological composition of the tissue.



Supplementary Figure 2. Diffusivity lifespan curves are well fit by a Poisson curve. Diffusivity lifespan growth curves for each of the 24 tracts ordered based on the amount of change in diffusivity over the lifespan. Colors are the same as in Figure 1 and demonstrate that the tracts that show the largest change in R1 (red) don't necessarily show a large change in diffusivity (e.g. Orbitofrontal callosum). The width of the line denotes the 95% confidence interval Poisson curve model fit which captures the asymmetry of diffusivity development and aging. The age of minimum diffusivity (+/- 95% confidence interval) is shown at the bottom of each plot.



Supplementary Figure 3. Lifespan models of white matter changes. Three classes of models were fit to predict tissue properties as a function of age. (a) The second order polynomial model has 3 parameters. The intercept and vertex position adjust the central position of the parabola with respect to the x and y axis. The scale factor adjusts the magnitude of change, which is mirror-symmetric around the peak. The second order polynomial predicts that greater growth during development is associated with greater decline during aging. (b) The piecewise linear model has either 4 parameters (2 segments) or 5 parameters (3 segments). The intercept and first slope fit a line to summarize the rate of development. The first transition point fits the age at which linear development ends and the tissue property has reached its mature level. The second transition fits the age at which the tissue property begins to show aging related changes and the second slope fits the rate of change in the tissue property during aging. Note that the piecewise linear model can be seen as a more flexible version of the second order polynomial where the slope of development and aging are independent and there can be variable amounts of time between the end of development and the beginning of aging. The last-in-first-our hypothesis predicts that there should be a negative correlation between transition 1 and transition 2: Tracts that reach maturity earlier should begin ageing later. The piecewise linear model can also be simplified by removing the second transition point and fitting the data with two segments that meet at a hinge (shown in gray). (c) The local regression model can assume any smooth shape to fit the data. Hence it does not impose the predictions of any *a priori* hypothesis about the shape of the lifespan curve.



Supplementary Figure 4. Diffusivity changes are asymmetric across the lifespan. (a) The diffusivity measurements differ from the prediction of a symmetric model such as a parabola and are better fit by a Poisson curve. The predictions of the Poisson curve are within 1 standard error of the diffusivity measurements (average along all tracts) across the lifespan. (b) Diffusivity values are not equal on either side (senescence) of the diffusivity peak. Each tracts diffusivity values are shown at ten years of age and at a symmetric distance past the peak estimated from the Poisson curve. The values consistently fall below the identity line: Unlike R1, in senescence diffusivity values do not return to their childhood levels. (c) The R1 data (average along all tracts) are well fit by a symmetric function like a parabola but are not well fit by an asymmetric function like a Poisson curve.