**Evolution on graphs and the transition to cancer**

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*Multi-stage mathematical models have contributed a great deal to our understanding of*

*cancer, from Armitage and Doll’s original work in the 1950s, to Knudson’s studies of*

*retinoblastoma in the 1970s. My ongoing research extends these models using evolutionary*

*graph theory, with edges on the graph representing distinct molecular mechanisms. This*

*approach will let us connect epidemiology to genomics.*

*My latest advance is a new semi-analytical numerical method to compute hazard curves,*

*which is a much more efficient way to compute probabilities and likelihoods than either random*

*sampling, or approximate Bayesian computation. By combining this method with maximum*

*likelihood estimation, we can make new, precise estimates of mutation rates from data on*

*age and copy number alterations. In particular, when applied to vestibular schwannoma, this*

*approach enables new estimates of mutation rates in Schwann precursor cells.*

**References**

[1] A.U. Thor and S. Author, Title of book, publisher, year.

[2] A.U. Thor and S. Author, Title of article, journal, volume (number): pages, year.