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*In silico*chromosome staining

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The chromosomal bands observed upon Giemsa staining are thought to correspond generally to regions that are GC-poor (Giemsa-dark, G bands) and GC-rich (Giemsa-light, R bands). The exact relationship between sequence base composition and cytogentic banding is still unclear, however. In the January 22 Proceedings of the National Academy of Sciences, Niimura and Gojobori describe a computational method to explore the association between the Giemsa banding pattern and local GC content (*Proc Natl Acad Sci USA* 2002, **99:**797-802). They began with human chromosomes 21 and 22 and developed a 'two-window analysis' method to investigate GC content compared to flanking regions. Using a local window of 2.5 Mb and a regional window of 9.3 Mb, they were able to create an *in silico* banding pattern that resembled Giemsa staining. They extended their *in silico*staining method to the whole human genome and demonstrate impressive accuracy in predicting Giemsa-dark bands.

References

1. *Proceedings of the National Academy of Sciences*, [http://www.pnas.org]