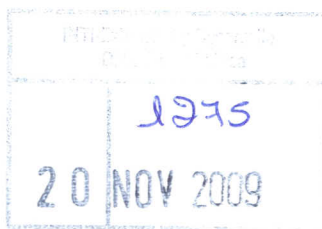
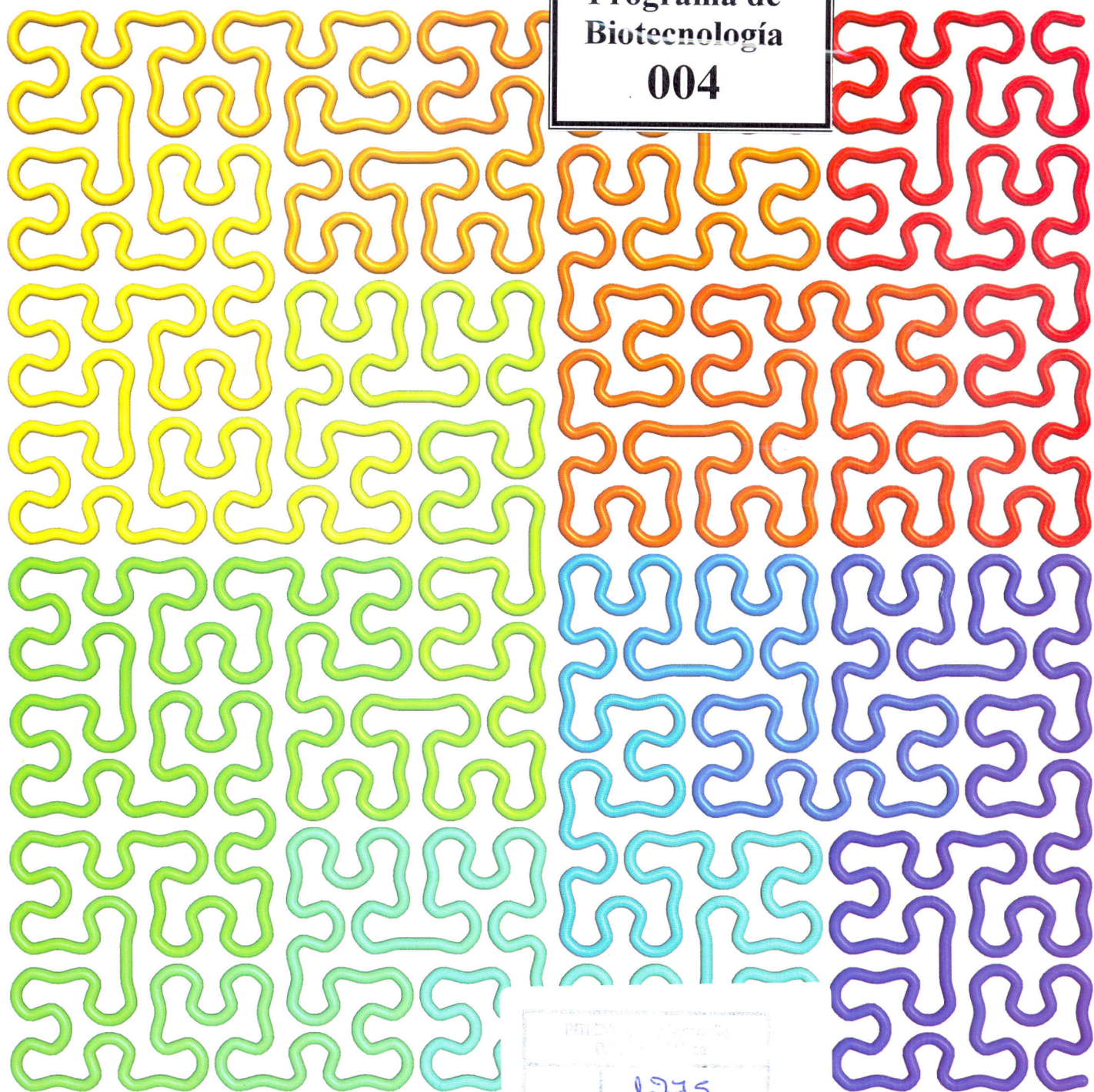


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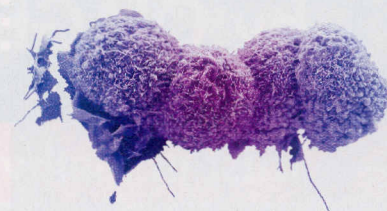
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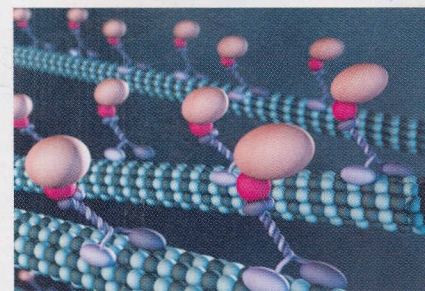
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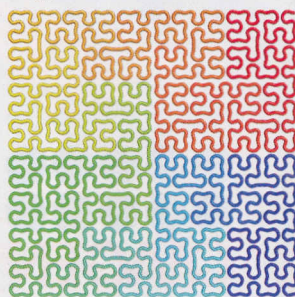


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COVER

First described by David Hilbert in 1891, the Hilbert curve is a one-dimensional fractal trajectory that densely fills higher-dimensional space without crossing itself. A new method for reconstructing the three-dimensional architecture of the human genome, described on page 289, reveals a polymer analog of Hilbert's curve at the megabase scale.

Image: Leonid A. Mirny and Erez Lieberman-Aiden

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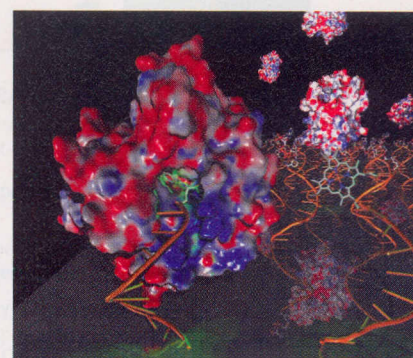
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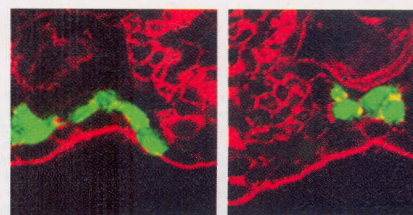
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