DNA ‘origami’ helps genes function how they’re supposed to

The GLP aggregated and excerpted this blog/article to reflect the diversity of news, opinion and analysis.

The human genome is longer than the average human. It consists of around two meters of DNA, which must somehow fit into cells, whose nuclei are about 200,000 times narrower.

So it folds. And it folds in such a way that any given stretch can be easily *unfolded*, so the genes within it can be read and used. Knots are verboten, and anyone who has ever shoved headphones into their pockets will know how hard it is to scrunch an extremely long thread into a ball without knotting anything.

In the 1970s, biochemists showed that this feat of extreme origami begins when DNA is wrapped around proteins called histones, creating what looks like a string of beads. This reduces the packing problem, but doesn’t come close to solving it. The wrapped DNA must be folded and twisted in ever more complicated (and as yet unknown) ways. Eventually, it forms large loops.

The loops aren’t just a packing solution. They also bring genes into close contact with distant sequences that turn them on or off. So, the 3-D form of the genome also dictates its function. And to really understand how genes are used (and how they are misused in cases of disease), we need to appreciate the genome as a looping, twisting, physical entity, rather than just a string of letters.

In 2014, a team led by Erez Lieberman Aiden at Baylor College of Medicine took important steps towards this goal by creating an unprecedentedly detailed 3-D map of the human genome. These genetic cartographers used a technique called Hi-C to embalm the genome and identify regions that interact with one another.

Read full, original post: There’s a Mystery Machine That Sculpts the Human Genome