

Changes in pattern of epigenetic tags accurately predicts gestational age

Researchers have developed a method for estimating developmental maturity of newborns. It is based on tracking DNA methylation, a structural modification of DNA, whose patterns change as development progresses before birth.

The new method could help doctors assess developmental maturity in [preterm newborns](#) and make decisions about their care, or estimate the time since conception for a woman who does not receive prenatal care during pregnancy. As a research tool, the method could help scientists study connections between the prenatal environment and health in early childhood and adulthood.

The study, led by Alicia Smith and Karen Conneely [at Emory University,] used blood samples from more than 1,200 newborns in 15 cohorts from around the world.

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The researchers also found that the difference between a newborn's age predicted by DNA methylation and by an obstetrician may be another indicator of developmental maturity, and is correlated with birthweight, commonly used as an indicator of perinatal health.

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"This association supports the hypothesis that prenatal adversity associates with changes in neonatal methylation consistent with a delayed developmental age, which may have consequences later in life," the authors write.

The GLP aggregated and excerpted this blog/article to reflect the diversity of news, opinion, and analysis. Read full, original post: [Gestational age estimated through DNA methylation](#)