

Resource Summary Report

Generated by [PRECISE-TBI](#) on Aug 2, 2026

NOCOM

RRID:SCR_009310

Type: Tool

Proper Citation

NOCOM (RRID:SCR_009310)

Resource Information

URL: <http://gaow.github.io/genetic-analysis-software/n-1.html#nocom>

Proper Citation: NOCOM (RRID:SCR_009310)

Description: Software application to estimate parameters for mixture of normal distributions (entry from Genetic Analysis Software)

Abbreviations: NOCOM

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, fortran, ms-dos, os2

Resource Name: NOCOM

Resource ID: SCR_009310

Alternate IDs: nlx_154500

Record Creation Time: 20220129T080252+0000

Record Last Update: 20260801T191048+0000

Ratings and Alerts

No rating or validation information has been found for NOCOM.

No alerts have been found for NOCOM.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Tamagawa K, et al. (2017) The Effects of CpG Densities around Transcription Start Sites on Sex-Biased Gene Expression in *Poecilia reticulata*. *Genome biology and evolution*, 9(5), 1204.

Hayashi Y, et al. (2013) Construction and characterization of normalized cDNA libraries by 454 pyrosequencing and estimation of DNA methylation levels in three distantly related termite species. *PloS one*, 8(9), e76678.

Robinson KL, et al. (2011) Evidence for widespread genomic methylation in the migratory locust, *Locusta migratoria* (Orthoptera: Acrididae). *PloS one*, 6(12), e28167.

Ortiz A, et al. (2011) An admixture analysis of the age at index episodes in bipolar disorder. *Psychiatry research*, 188(1), 34.

Okamura K, et al. (2010) Gradual transition from mosaic to global DNA methylation patterns during deuterostome evolution. *BMC bioinformatics*, 11 Suppl 7(Suppl 7), S2.

Tang CS, et al. (2010) Adaptive Evolution Hotspots at the GC-Extremes of the Human Genome: Evidence for Two Functionally Distinct Pathways of Positive Selection. *Advances in bioinformatics*, 2010, 856825.

Hunt BG, et al. (2010) Functional conservation of DNA methylation in the pea aphid and the honeybee. *Genome biology and evolution*, 2, 719.

Tang CS, et al. (2007) A structural split in the human genome. *PloS one*, 2(7), e603.