

# Resource Summary Report

Generated by [NIF](#) on Aug 18, 2026

## NOCOM

RRID:SCR\_009310

Type: Tool

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### Proper Citation

NOCOM (RRID:SCR\_009310)

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### 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:** 20260818T043340+0000

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### Ratings and Alerts

No rating or validation information has been found for NOCOM.

No alerts have been found for NOCOM.

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### 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 [NIF](#) .

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.

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.

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.

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.