




MultiMin: Mixture-of-Gaussians fitting and visualization for multivariate data and single-valued functions

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Summary

MultiMin is a Python package for fitting and analyzing *Mixtures of Gaussians* (MoGs, also known as Gaussian mixture models) in one or many dimensions. The package provides (i) a compact parameterization of multivariate Gaussian mixtures, (ii) numerical maximum-likelihood fitting tools for data samples (including partially truncated domains), and (iii) publication-ready visualizations through a unified corner-plot-like interface. In addition, MultiMin includes an experimental workflow to fit *single-valued functions* (e.g., time-series, spectra, or model curves) using MoG basis functions, returning interpretable diagnostics such as R^2 and goodness-of-fit measures.

Statement of need

Gaussian mixture models are a standard and versatile tool for density estimation, clustering, and probabilistic modeling because they can approximate complex continuous distributions through weighted sums of multivariate Gaussians (Bishop, 2006; McLachlan & Peel, 2000). In research workflows, however, practitioners often need more than a black-box mixture estimator: they need a parameterization that is convenient for scientific interpretation, explicit control over covariance structure, support for bounded (truncated) variables, and a visualization layer that can compare samples and fitted models consistently across dimensions.

MultiMin addresses these needs by providing a research-oriented API centered on three core components:

- `MixtureOfGaussians`: definition, sampling, evaluation, and serialization of MoGs.
- `FitMoG` / `FitFunctionMoG`: numerical fitting tools for (i) multivariate samples via maximum-likelihood minimization and (ii) single-valued functions (e.g., spectra) via nonlinear least squares, both exposed through a consistent, data-first interface with many optional controls (domains, bounds, optimizer options, diagnostics).
- `MultiPlot`: a consistent grid visualization system for samples, PDFs, histograms, contours, and optional marginals (i.e., a unified alternative to piecemeal corner plotting).

The package is implemented in Python and integrates with the scientific Python ecosystem (NumPy (Harris et al., 2020), SciPy (Virtanen et al., 2020), and Matplotlib (Hunter, 2007)). It is distributed as open source under the AGPLv3 license and includes extensive example notebooks that can be executed end-to-end.

37 State of the field

38 Several mature libraries provide Gaussian mixture models, most prominently scikit-learn's
 39 GaussianMixture estimator (Pedregosa et al., 2011). Such tools are excellent general-
 40 purpose solutions for machine learning pipelines, but they typically emphasize predictive
 41 usage and integration rather than scientific interpretability and publication-centric workflows.
 42 In practice, many research users still need to build a layer around these estimators to (i) express
 43 domain-specific constraints (e.g., partially bounded variables), (ii) extract explicit parametric
 44 representations for reporting, and (iii) generate consistent multivariate diagnostic figures that
 45 combine samples and fitted densities.

46 MultiMin complements this landscape by focusing on scientific workflows:

- 47 ■ **Interpretability-first parameterization:** MoG components can be accessed and reported
 48 as weights, means, standard deviations, correlations, and full covariance matrices.
- 49 ■ **Partially truncated domains:** fitting can be performed while enforcing bounded support
 50 for selected variables (common in physical quantities constrained to intervals), with the
 51 truncation explicitly represented in the fitted model.
- 52 ■ **Unified diagnostic plotting:** the same high-level plotting interface can overlay data,
 53 mixture PDFs, contours, histograms, and marginals across dimensions, facilitating
 54 reproducible figures for papers.

55 Theoretical background

56 **Mixture representation.** A MoG with M components in k dimensions is represented as

$$f(\tilde{x}) = \sum_{i=1}^M w_i \mathcal{N}_k(\tilde{x}; \tilde{\mu}_i, \Sigma_i),$$

57 with weights $\sum_i w_i = 1$. The package provides helpers to construct covariance matrices from
 58 more interpretable quantities (e.g., per-dimension standard deviations and correlation/rotation
 59 parameterizations), which is useful in scientific settings where covariances are rarely specified
 60 directly.

61 **Partially truncated multivariate Gaussians.** Many scientific variables are naturally bounded (e.g.,
 62 ratios, angles, physical parameters constrained to an interval). MultiMin supports *partially*
 63 *truncated* multivariate Gaussians by explicitly representing the truncation domain and using it
 64 consistently in evaluation, sampling, and fitting. Starting from the unbounded multivariate
 65 normal,

$$\mathcal{N}_k(\tilde{x}; \tilde{\mu}, \Sigma) = \frac{1}{\sqrt{(2\pi)^k \det \Sigma}} \exp \left[-\frac{1}{2} (\tilde{x} - \tilde{\mu})^\top \Sigma^{-1} (\tilde{x} - \tilde{\mu}) \right],$$

66 let $T = \{l, \dots, m\} \in \{1, \dots, k\}$ be the set of truncated coordinates and let $a_i < b_i$ be the
 67 bounds for each $i \in T$. The truncation region is

$$A_T = \{\tilde{x} \in \mathbb{R}^k : a_i \leq \tilde{x}_i \leq b_i \quad \forall i \in T\},$$

68 with the remaining coordinates $i \notin T$ unbounded. The partially truncated multivariate normal
 69 is then defined as

$$\mathcal{T}\mathcal{N}_T(\tilde{x}; \tilde{\mu}, \Sigma, \mathbf{a}_T, \mathbf{b}_T) = \frac{\mathcal{N}_k(\tilde{x}; \tilde{\mu}, \Sigma) \mathbf{1}_{A_T}(\tilde{x})}{Z_T(\tilde{\mu}, \Sigma, \mathbf{a}_T, \mathbf{b}_T)},$$

70 where $\mathbf{1}_{A_T}$ is the indicator function of A_T and the normalization constant is

$$Z_T(\tilde{\mu}, \Sigma, \mathbf{a}_T, \mathbf{b}_T) = \int_{A_T} \mathcal{N}_k(\tilde{\mathbf{V}}; \tilde{\mu}, \Sigma) d\tilde{\mathbf{V}} = \mathbb{P}_{\tilde{x} \sim \mathcal{N}_k(\tilde{\mu}, \Sigma)}(\tilde{x} \in A_T).$$

MultiMin encodes bounds through a per-dimension domain argument (e.g., `domain=[[a_1,b_1], ..., [a_k,b_k]]`, with `None` for unbounded coordinates). A *truncated MoG* is obtained by mixing truncated components with the same truncation region,

$$f_T(\tilde{x}) = \sum_{i=1}^M w_i \mathcal{T} \mathcal{N}_T(\tilde{x}; \tilde{\mu}_i, \mathbf{a}_T, \mathbf{b}_T).$$

Maximum-likelihood fitting. For a dataset $\{\tilde{x}_n\}_{n=1}^N$ and a parametric MoG density $f(\tilde{x} | \theta)$ (where θ is a serialized list of parameters containing the components of $\tilde{\mu}_i, \Sigma_i$), MultiMin estimates parameters by classical maximum-likelihood. The likelihood and (negative) log-likelihood objectives are

$$\mathcal{L}(\theta) = \prod_{n=1}^N f(\tilde{x}_n | \theta),$$

$$\text{NLL}(\theta) = - \sum_{n=1}^N \log f(\tilde{x}_n | \theta),$$

and the package minimizes NLL (or its normalized variant) with `scipy.optimize.minimize` (Virtanen et al., 2020). We do not use an expectation–maximization (EM) clustering formulation as a primary strategy because the typical use case here is not unsupervised cluster discovery: instead, users select a predetermined number of components (e.g., for a controlled parametric approximation or a physically motivated mixture), and the goal is a direct parametric fit under constraints such as partial truncation.

Software design

MultiMin is organized as a compact, research-oriented library where the main public objects are imported from the top-level namespace (`import multim as mn`). Internally, functionality is split into a few focused modules that mirror the conceptual workflow “define model → fit → diagnose/visualize → export”:

- **Modeling (mog):** `MixtureOfGaussians` implements parameterized multivariate mixtures, including partially truncated domains via a per-dimension domain specification. The class supports sampling, evaluation (PDF/log-PDF), parameter transformations convenient for scientific reporting (e.g., standard-deviation/correlation forms and covariance constructors in `Stats`), and serialization of a fitted model.
- **Fitting (fitting):** `FitMoG` performs classical maximum-likelihood estimation by minimizing the negative log-likelihood with `scipy.optimize.minimize`, using a flattened parameter vector that is mapped to physical parameters (weights, means, covariance structure) and optionally constrained through bounds. Truncated variables are handled consistently through the same domain definition used by `MixtureOfGaussians`. For single-valued functions, `FitFunctionMoG` fits a MoG basis to $(X, F(X))$ pairs via nonlinear least squares, using an analytically updated global normalization at each objective evaluation and offering higher-level modes (e.g., adaptive routines guided by peak finding and smoothing utilities from `SciPy`).
- **Visualization (plotting):** `MultiPlot` provides a consistent grid layout for scatter/histogram/PDF/contour overlays, with a single “properties” specification controlling labels and ranges across panels. The plotting API is intentionally “thin” and Pythonic: most methods accept standard Matplotlib-style keyword arguments (plus structured dictionaries such as `sargs`, `hargs`, `dargs`, and `margs`) so users can tune aesthetics without rewriting plotting logic. Optional marginal panels can be enabled when needed.
- **Utilities (util, base):** small helpers provide robust I/O (e.g., `Util.get_data` for packaged example datasets), numerical/statistical helpers (`Stats`), and lightweight base functionality shared by the main classes.

114 ▪ **Optional acceleration (cmog):** when the compiled library is available, MultiMin generates
 115 callables that route evaluation through ctypes wrappers around optimized batch
 116 evaluators, enabling fast likelihood/PDF evaluation on large grids without changing the
 117 high-level user code.

118 Across the API, defaults are chosen to keep common workflows short (a few lines from raw arrays
 119 to a fitted model and a figure), while exposing many optional parameters to support controlled
 120 scientific use cases (fixed domains, constrained covariances, custom initialization and bounds,
 121 detailed optimizer options, and fully customizable plotting). A complete documentation site with
 122 narrative examples and the full API reference is provided at <https://multimin.readthedocs.io>.

123 Code examples

124 **Visualization as a first-class feature.** Multivariate visual diagnostics are handled by MultiPlot,
 125 which uses a consistent grid layout to render scatter plots, histograms, PDF heatmaps, and
 126 contour overlays. This design is conceptually similar to corner-plot workflows ([Foreman-Mackey, 2016](#)), but MultiMin couples the visualization directly to MoG objects and fitted
 127 results, ensuring that “data vs model” comparisons reuse the same ranges, labels, and aesthetics.
 128 The typical end-to-end workflow (data generation, visualization, fitting, and plotting) is a few

129 lines of code, mirroring the tutorial notebooks shipped with the project:

```
import numpy as np
import multimin as mn

deg = np.pi / 180

# Synthetic sample from a 3D, 2-component MoG
weights = [0.5, 0.5]
mus = [[1.0, 0.5, -0.5], [1.0, -0.5, +0.5]]
sigmas = [[1, 1.2, 2.3], [0.8, 0.2, 3.3]]
angles = [[10 * deg, 30 * deg, 20 * deg], [-20 * deg, 0.0, 30 * deg]]
Sigmas = mn.Stats.calc_covariance_from_rotation(sigmas, angles)
mog_true = mn.MixtureOfGaussians(mus=mus, weights=weights, Sigmas=Sigmas)

np.random.seed(1)
data = mog_true.rvs(5000)

# Fit and plot
F = mn.FitMoG(data=data, ngauss=2)
F.fit_data()
G=F.plot_fit(
    properties=["x", "y", "z"],
    pargs=dict(cmap='Spectral_r'),
    sargs=dict(s=0.2, edgecolor='None', color='w', nbins=30),
    cargs=dict(levels=50, zorder=+300, alpha=0.3),
    figsize=3,
    marginals=True
)
```

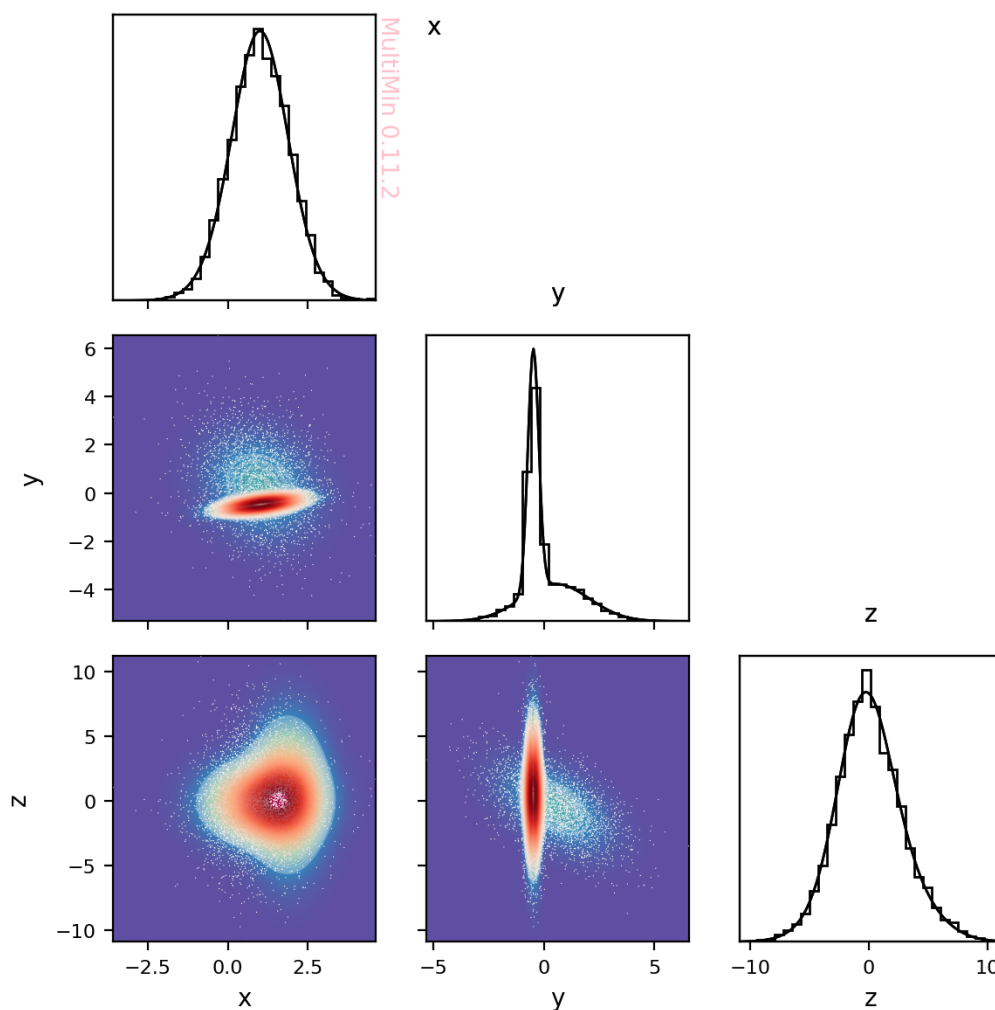


Figure 1: Example of a fitted multivariate MoG visualized with MultiPlot.

131 Fit quality diagnostics for multivariate fits are available via a Kolmogorov–Smirnov (K–S)
132 distance computed on $S = -2 \log \mathcal{L}(\tilde{x})$ (observed vs. synthetic samples) and an optional Q–Q
133 plot:

```
stats = F.quality_of_fit(data=data, n_sim=5000, plot_qq=True, figsize=5)
ks_dist = stats["ks_dist"]
r2_identity = stats["r2_identity"]
```

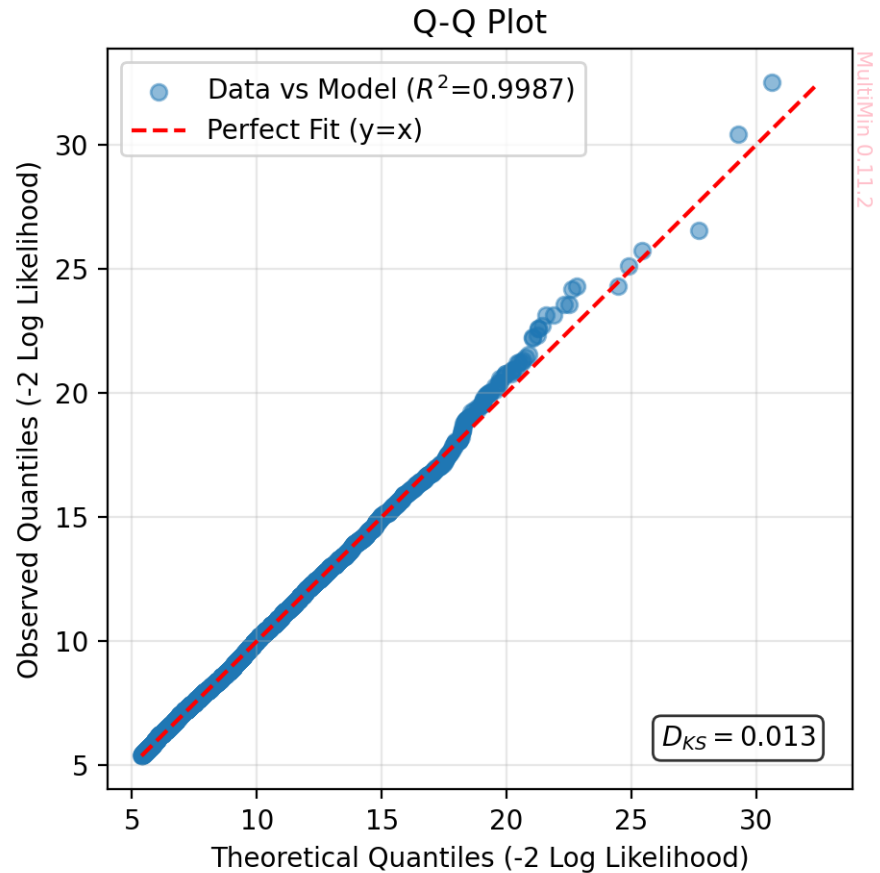


Figure 2: Q-Q plot and K-S distance for a multivariate MoG fit.

Univariate mix-of-gaussian fitting

In addition to fitting samples, MultiMin includes an experimental workflow to fit *single-valued functions* (univariate or multivariate) by matching a MoG-based model to $(X, F(X))$ pairs. In the univariate function-fitting setting this is formulated as a nonlinear least-squares problem (minimizing squared residuals between the observed function values and the model prediction on the mesh), and the package reports diagnostics such as R^2 that are useful for model selection and automated fitting loops.

A practical example of the function-fitting workflow is the decomposition of a complex univariate spectral line profile into a small number of Gaussian components. The spectrum used in this example is shipped with MultiMin (`complex-line.txt`) and is based on the multi-component synthetic spectra used in the context of GaussPy+ (Riener et al., 2019). It can be loaded via `mn.Util.get_data` and `numpy.loadtxt` and then fitted as:

```
import numpy as np
import multimn as mn

path = mn.Util.get_data("complex-line.txt")
chan, spectrum = np.loadtxt(path, unpack=True, comments="#")

Ff = mn.FitFunctionMoG(data=(chan, spectrum), ngauss=3)
Ff.fit_data(mode="adaptive", advance=10)
fig = Ff.plot_fit(dargs=dict())
```

```
stats_f = Ff.quality_of_fit()
```

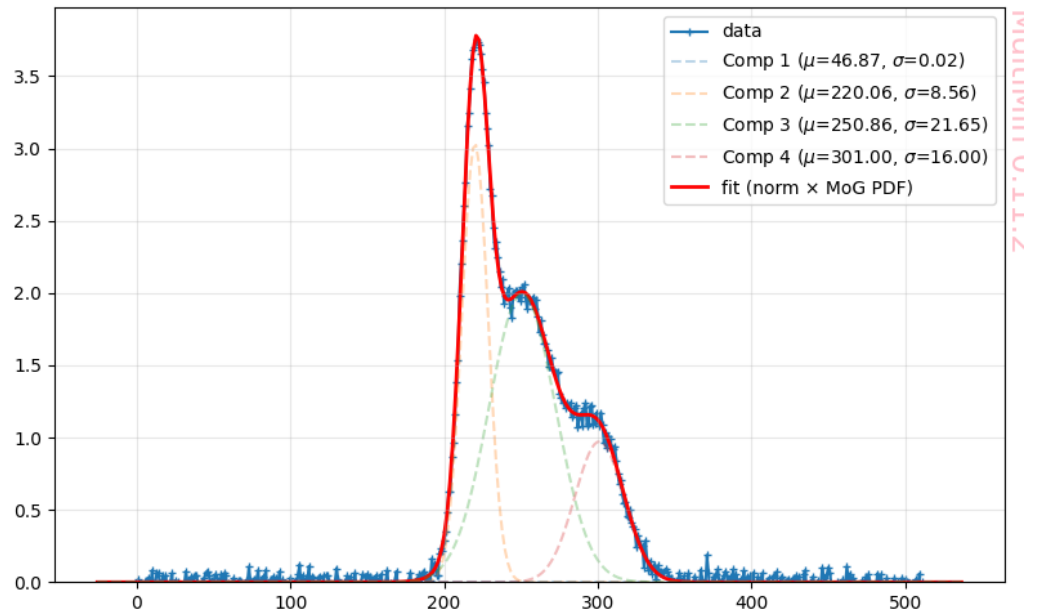


Figure 3: Example of a complex spectral line and a MoG-based fit using FitFunctionMoG.

146 Semi-analytical descriptions and accelerated evaluators

147 Beyond fitting and plotting, MultiMin can export fitted distributions as semi-analytical artifacts
148 suitable for papers and high-throughput evaluation. In particular, fitted MoGs can be rendered
149 as LaTeX (explicit parameters and matrices) and as self-contained Python callables. For
150 example, the LaTeX export can be generated as follows:

```
latex_str, _ = F.mog.get_function(type="latex", print_code=False, decimals=4)
print(latex_str)
```

151 The latex_str output is formatted as follows:

$$f(\mathbf{x}) = w_1 \mathcal{N}(\mathbf{x}; \boldsymbol{\mu}_1, \Sigma_1) + w_2 \mathcal{N}(\mathbf{x}; \boldsymbol{\mu}_2, \Sigma_2)$$

152 where

$$w_1 = 0.4909$$

$$\boldsymbol{\mu}_1 = \begin{pmatrix} 0.9577 \\ 0.5176 \\ -0.4634 \end{pmatrix}$$

$$\Sigma_1 = \begin{pmatrix} 1.0805 & -0.3353 & 0.2666 \\ -0.3353 & 2.3655 & -1.716 \\ 0.2666 & -1.716 & 4.4798 \end{pmatrix}$$

$$w_2 = 0.5091$$

$$\boldsymbol{\mu}_2 = \begin{pmatrix} 1.0192 \\ -0.481 \\ 0.6188 \end{pmatrix}$$

156

$$_2 = \begin{pmatrix} 0.6319 & 0.1054 & -0.0236 \\ 0.1054 & 0.0604 & -0.0145 \\ -0.0236 & -0.0145 & 11.0725 \end{pmatrix}$$

157 Here the normal distribution is defined as:

$$\mathcal{N}(\mathbf{x}; \boldsymbol{\mu},) = \frac{1}{\sqrt{(2\pi)^k \det}} \exp \left[-\frac{1}{2}(\mathbf{x} - \boldsymbol{\mu})^\top{}^{-1}(\mathbf{x} - \boldsymbol{\mu}) \right]$$

158 These expressions can be incorporated into scientific publications to provide a semi-analytical
159 representation of the fitted distribution.

160 Accelerated evaluators

161 Optionally, the generated Python code can target C-optimized batch evaluators exposed
162 through ctypes for fast evaluation on large grids:

```
code_str_c, f_fast_c = F.mog.get_function(
    type="python",
    cmog=True,
    print_code=False
)
```

163 When the optional C backend is available, `cmog=True` routes evaluation through ctypes
164 wrappers around compiled batch evaluators. In `examples/multimin_cmog.ipynb`, a
165 representative micro-benchmark shows a speedup for point-wise evaluation (same fitted MoG,
166 same machine/kernel):

- 167 ▪ **Single point:** Python callable $\sim 60 \mu\text{s}$ per loop vs `cmog=True` $12 \mu\text{s}$ per loop. Speed-up
168 $\sim \times 5$.
- 169 ▪ **Batch (10,000 points):** Python callable $445 \mu\text{s}$ per loop vs `cmog=True` $280 \mu\text{s}$ per loop.
170 Speed-up $\sim \times 2$.

171 Comparison with other similar tools

172 MultiMin overlaps with existing Gaussian-mixture tooling, but targets a different point in
173 the design space: it prioritizes scientific interpretability, bounded (truncated) domains, and
174 reproducible diagnostics/figures as first-class outputs.

175 **Comparison with scikit-learn.** `scikit-learn` provides a widely used `GaussianMixture`
176 implementation oriented toward machine-learning workflows (e.g., clustering and density
177 estimation pipelines) (Pedregosa et al., 2011). MultiMin can be used for similar density-
178 estimation tasks, but emphasizes an explicit, report-friendly parameterization (weights, means,
179 standard deviations/correlations/covariances), publication-ready multivariate visualization via
180 MultiPlot, and domain-aware (partially truncated) likelihoods. The repository includes a
181 notebook-level comparison between MultiMin and `scikit-learn` GMM (see Figure 4).

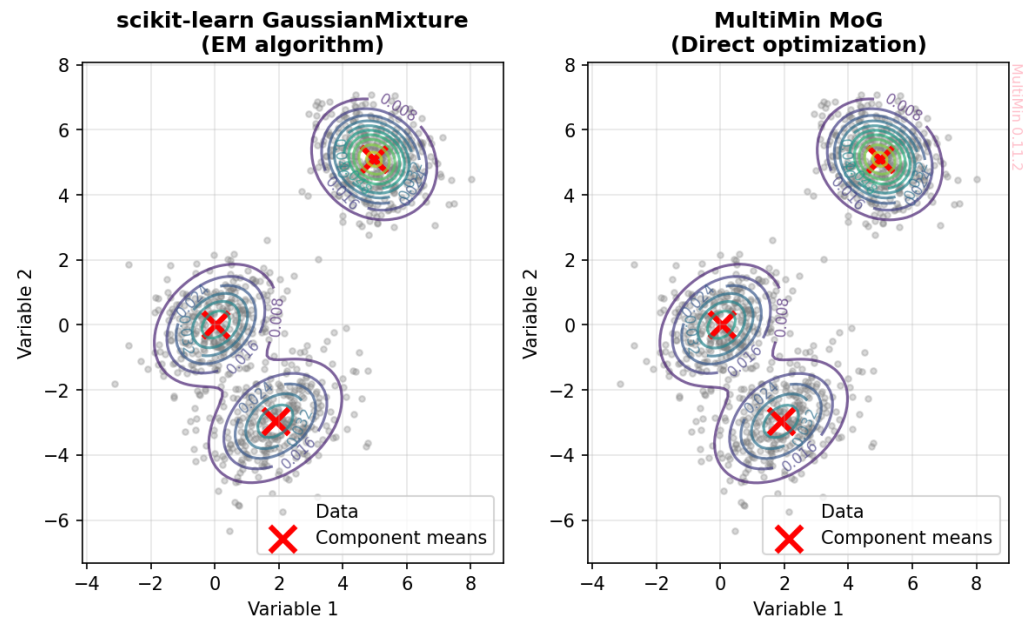


Figure 4: Comparison figure produced by the MultiMin notebooks, contrasting mixture-model workflows.

Comparison with GaussPy+. GaussPy+ is a specialized automated Gaussian decomposition package for emission-line spectra, with substantial algorithmic machinery for noise estimation, quality control, and (optionally) spatially coherent refitting in large surveys (Riener et al., 2019). MultiMin is not a drop-in replacement for that end-to-end pipeline; however, for the core task of fitting a spectrum with multiple Gaussian components, the FitFunctionMoG workflow produces comparable decompositions in representative cases (e.g., the complex-line example included with this package and shown in Figure 3), while providing a unified API that also extends to multivariate MoG fitting with shared diagnostics (e.g., K-S / Q-Q tests).

Research impact statement

MultiMin was developed to support research workflows where multivariate distributions must be fitted, interpreted, and communicated with consistent diagnostics. The repository includes reproducible notebooks demonstrating applications such as Near-Earth asteroid datasets and controlled comparisons against scikit-learn's GMM implementation, along with gallery figures that can be directly reused in publications and reports. By integrating fitting, diagnostics, and visualization in a single package, MultiMin reduces the glue code typically required to turn a fitted mixture model into reproducible, publication-quality results.

AI usage disclosure

Generative AI tools were used during the development and documentation of MultiMin, including the preparation of this manuscript. Specifically, AI assistance was used for drafting text, refactoring portions of code, and scaffolding tests and examples. All AI-assisted outputs were reviewed, edited, and validated by the human author(s), who made the core technical and design decisions and verified correctness via automated tests and executable notebooks.

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