Preface

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A rigid origami crease pattern generates a manifold whose true low-dimensional structure is known exactly, in closed form. Rigid folding bends the sheet along creases only; the facets stay flat. The folded surface is therefore isometric to the flat sheet, and geodesic distances measured along the surface are unchanged by folding. The flat crease pattern is not an approximation of the correct two-dimensional embedding. It *is* the correct embedding — the answer key.

That single property is what this book is built on.

Standard benchmarks for dimension reduction — the Swiss roll, the S-curve, the severed sphere — give one fixed geometry and a visual impression of success. A crease pattern gives an exact reconstruction error and a parameterised family of test problems. The fold angle θ runs continuously from a flat sheet to a fully compressed one, so every method's performance becomes a curve rather than a single number, and no configuration can be cherry-picked.

Chari and Pachter have argued that two-dimensional embeddings of high-dimensional biological data are systematically misleading. The usual rebuttal is anecdotal. On a manifold where the truth is known exactly, the distortion can be *measured* instead of argued about — and, more usefully, the evaluation metrics themselves can be checked against truth. That is the reason this book exists.

What this book is not

It is not a treatment of rigidity theory, computational origami design, or deep generative modelling. It is not a tutorial on `bookdown`, `make`, or project tooling. Where a section could not be tied back to the ground-truth claim above, it was cut rather than kept for completeness.

Companion package

The companion R package foldbenchR is publicly available. This book renders with the helper scripts versioned alongside its chapters, so the package is not required to build the book or inspect its recorded benchmarks.