MilAMin in the browser: a million unknowns a minute in TypeScript and WebAssembly

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Abstract In 2008 MILAMIN showed that a finite element code written in native MATLAB, a language then held to be too slow for large problems, could set up, solve and post-process one million unknowns per minute on a desktop, provided every stage of the pipeline gets equal care. This note brings the same pipeline to the web browser: Triangle meshing, 7-node Crouzeix-Raviart elements, supernodal Cholesky with fill-reducing ordering and Powell-Hestenes pressure iterations, in TypeScript and WebAssembly. Nothing is installed. Stokes models of inclusions, layers and grain swarms with up to two million unknowns are written in a few lines of JavaScript, and the folding and boudinage of layered rock is stepped through time. On a 2025 phone a million-unknown Stokes problem is meshed, assembled, factorized, iterated and rendered in nine seconds. Its assembly and solution alone take five to six times less than the 49 s the 2008 desktop needed for the same stages, and even a 2013 desktop lies below the 2008 curve at every size up to the four-gigabyte limit of WebAssembly. The largest gain came from the supernodal factorization, not from threads; the thread scaling on all devices is consistent with a memory-bandwidth limit. The solution is verified against the analytical circular-inclusion solution on a sequence of refined meshes. MilAMin, the browser version, runs at milamin.org; the code is public, under the GPL except for Triangle, which keeps its own terms, and the benchmark, the convergence study and the model presets have command-line twins that run the same code.

Keywords finite element method, Stokes flow, WebAssembly, sparse Cholesky, MILAMIN, verification
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1 Introduction

The MILAMIN paper (Dabrowski et al., 2008) made one claim in its title and backed it with a design principle. The claim: a finite element code written in native MATLAB, with unstructured triangular meshes and no compiled extensions, handles one million unknowns per minute on a 2008 desktop, setup, solution and post-processing included. The principle: every stage of the pipeline gets equal care. Meshing, element matrices and assembly, the sparse factorization with a fill-reducing ordering and the pressure iterations all have to scale, because the moment one of them is neglected it dominates the total. The paper was cited by more than 260 publications, and the package remained a reference for what a small, readable finite element code can do.

Eighteen years later the platform with the widest reach is not MATLAB but the web browser. It runs on every desktop and phone and needs no installation. Since WebAssembly (Haas et al., 2017) became a compilation target for C and C++ (Zakai, 2011), it also executes numerical code at a speed comparable to native binaries. Threads and SIMD, single instruction on multiple data, are available where the page is served with the right headers.

This note asks the 2008 question again in the browser. Does the MILAMIN pipeline, ported stage by stage to TypeScript and WebAssembly, still reach a million unknowns a minute? The answer is yes, with a margin, on a phone included. The browser version is written MilAMin, Million A Minute, and the 2008 code MILAMIN throughout this note; the two names differ in case only, so the year is added where the distinction matters. Section 2 shows what the site offers, Section 3 describes the browser pipeline and what was kept and changed from 2008, Section 4 reports the measured performance and what determines it, Section 5 the verification against an analytical solution and Section 6 how the numbers can be reproduced. The site is at https://milamin.org; the code is at https://github.com/dwschmid/milamin-web.

2 Models in the browser

Nothing on the site is downloaded or installed. Opening a page starts a Web Worker that loads the solver's WebAssembly modules, and from then on every model is meshed, solved and drawn on the device in hand.

The playground is the browser answer to downloading MILAMIN and editing the MATLAB. A model is a JavaScript function body of a few lines returning a geometry, as closed polylines or as a point-and-segment list, region seeds with a material attribute and a local mesh size, a viscosity per material and a Dirichlet or free-slip velocity per boundary marker. Inclusions of any shape and viscosity ratio, layered stacks and swarms of grains solve at up to two million unknowns, share as a link and save as figures. Figure 1 shows one of the presets: sixteen stiff ellipses, a thousand times more viscous than the matrix, drawn at random sizes and orientations into a box under simple shear, 64 thousand unknowns meshed, solved and rendered in under two seconds on the desktop of Section 4. In 2008 this took a MATLAB installation, the

MILAMIN sources and a set of input files for the geometry and the meshing; now it takes a page load, on any device, with nothing installed.

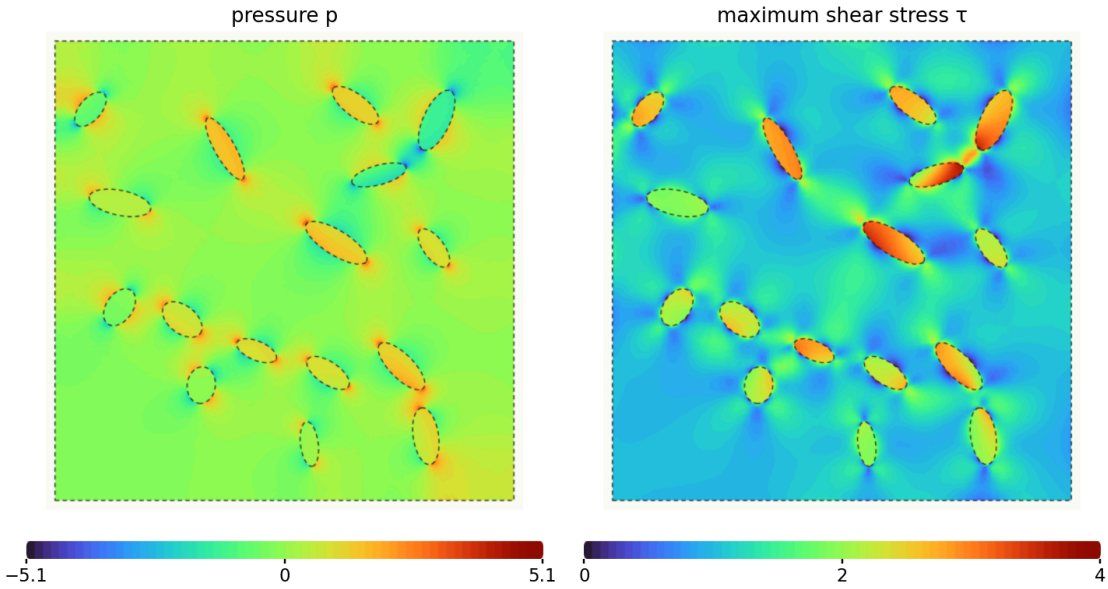

Figure 1. The ellipse-swarm preset of the playground: sixteen stiff ellipses (viscosity ratio 1000) in a box under simple shear, 64,026 unknowns, pressure (left) and maximum shear stress (right), with the automatic colour ranges of the page.

Folder is the browser version of the 2016 tool for folding and boudinage of layered rock (Adamuszek et al., 2016). A layered box is stepped through shortening or extension: at every step it is remeshed, the Stokes problem is solved, with Picard iterations for power-law materials, and the interfaces are advected. The growth rate the solver measures in its first velocity field is compared on the page with the analytical small-amplitude theory, and the later steps trace how that rate falls once the fold amplitude is finite. The default model, a single layer a hundred times more viscous than its matrix with a sine perturbation at sixteen layer thicknesses, reaches 50 percent shortening in twenty steps of about 42 thousand unknowns each in 25 s on the same desktop.

The million page makes the 2008 claim as one click and the **benchmark page** measures it on whatever device opens it, stage by stage. The **convergence lab** runs the verification of Section 5 live, on five meshes.

3 The pipeline in the browser

MilAMin keeps the 2008 discretization: the Stokes equations for an incompressible viscous fluid on unstructured triangles, with the 7-node Crouzeix-Raviart element (Crouzeix & Raviart, 1973), quadratic velocities enriched with a cubic bubble and a discontinuous linear pressure, an augmented-Lagrangian penalty in the element matrices and Powell-Hestenes iterations to recover the pressure (Cuvelier et al., 1986). Unknowns are counted as in 2008: two velocity components at each of the seven nodes of every element, the bubble node included. With N the corner and mid-side nodes Triangle produces and E the elements, each of which adds its own centre node, that is $2N + 2E$. The pressure is eliminated element by element and never enters the global system.

The whole pipeline runs in a Web Worker so that the page stays responsive. Its stages are explained below.

Meshing. Shewchuk's Triangle (Shewchuk, 1996), the mesher MILAMIN used, in our own WebAssembly build whose memory grows to what the browser allows. Triangle's exact geometric predicates need strict IEEE arithmetic, so it is compiled without fast-math or SIMD.

Element matrices and assembly. One fused stage, as in the blocked MILAMIN loop: the 7-point quadrature, the penalty term and the bubble condensation for each element, scattered straight into the lower triangle of the sparse matrix. This stage is plain TypeScript over typed arrays, single-threaded.

Factorization. CHOLMOD's supernodal Cholesky (Chen et al., 2008) with the approximate minimum degree ordering (Amestoy et al., 1996), from SuiteSparse 5.13, compiled to WebAssembly with Emscripten. CHOLMOD's dense kernels are served by a small BLAS layer written on Eigen (Guennebaud & Jacob, 2010) with WebAssembly SIMD. Where the page is cross-origin isolated, which gives the browser shared memory, the dense kernels are split across worker threads with OpenMP. Two builds ship, one without a threading runtime and one with; the page picks the build from the thread count the user selects.

Pressure recovery. Powell-Hestenes iterations: factor once, back-substitute per iteration, until all pressure coefficients stop changing.

Post-processing. The fields are evaluated per pixel from the element solution and drawn with a quantized colormap. Pan and zoom re-evaluate; they do not upscale an image.

The stage times shown on the site's pages add up to the quoted totals. Outside them are the one-off start of the worker and its WebAssembly modules and a few milliseconds of bookkeeping. A run with a million unknowns needs about 2.5 gigabytes of memory, of which the Cholesky factor takes about 1.2 gigabytes.

"Port" does not mean identical behaviour in every detail. Table 1 separates what MilAMin preserves from the 2008 code from what it deliberately changes.

Table 1. What MilAMin keeps from MILAMIN 2008 and what it changes.

	MILAMIN 2008	MilAMin
element, penalty, pressure iterations	7-node Crouzeix-Raviart, augmented Lagrangian, Powell-Hestenes	the same
mesher	Triangle, called from MATLAB	Triangle, own WebAssembly build with growable memory
ordering and factorization	AMD and CHOLMOD through MATLAB's `chol`	AMD and CHOLMOD supernodal, compiled to WebAssembly, own BLAS layer
bubble	in the global system (2N + 2E unknowns)	condensed before assembly; the factorized system has 2N unknowns, the pages report 2N + 2E
assembly	blocked, vectorized MATLAB into `sparse2`	one loop over the elements, each matrix scattered straight into the sparse matrix, single-threaded
threads	none	OpenMP in the dense kernels of the factorization, when the page is cross-origin isolated
arithmetic	IEEE double	the same, WebAssembly guarantees it
memory ceiling	the machine	4 GB per WebAssembly instance, about three million unknowns

4 Performance

4.1 The million

The million-unknown case is the site's version of the inclusion benchmark: a circular inclusion a thousand times more viscous than the matrix, in simple shear, on a disc of radius 2.5 (inclusion radius 1) with the analytical far-field velocity prescribed on its rim, at a mesh size that gives 1,000,158 unknowns (166,263 elements). Table 2 lists the stage times on a 2025 phone. The 2008 reference is Table 2 of the paper: 15 s for matrix computation and assembly and 34 s for the solution of one million unknowns, 49 s in all, on an AMD Opteron with MATLAB 2007a, for a different problem, a box with a circular hole and an inclusion ten times more viscous than the matrix under pure shear. The like-for-like comparison is therefore the sum of the browser's element matrices and assembly, factorization and pressure iterations against those 49 s; meshing and rendering, which the 2008 figure excluded, are listed separately and included in the five-stage total.

Table 2. The million-unknown inclusion problem on a Google Pixel 10 (Tensor, eight heterogeneous cores), Chrome for Android, 1,000,158 unknowns. One run per configuration with the phone cool; three repeats of the same size on the benchmark page gave factorizations of 5.5 to 6.3 s and a sweep 4.4 s, so run-to-run variance on this phone is up to twenty percent and the site quotes nine seconds. The speed-up is the 2008 time for matrix computation, assembly and solution, 49 s from Table 2 of the paper, divided by the browser time for the same three stages; the problems and the hardware differ.

stage	2 threads	1 thread
mesh	0.19 s	0.26 s
element matrices and assembly	1.5 s	1.5 s
factorization	5.7 s	5.3 s
Powell-Hestenes iterations	1.8 s	1.7 s
rendering	0.19 s	0.19 s
five stages	**9.3 s**	**9.0 s**
assembly, factorization and iterations	9.0 s	8.5 s
the same three stages, MILAMIN 2008	49 s	49 s
speed-up	5.4	5.8

4.2 Across sizes and devices

Figure 2 places the browser in the context of the 2008 curve. The dashed line is the total time of the mechanical test problem against problem size as read off Figure 5 of the 2008 paper, seven points from 64 thousand to 3.9 million unknowns, with the million-unknown point at 49 s. Its scope is slightly wider than Table 2′s assembly and solution, the paper calls the boundary conditions and the post-processing minor, and it is the only reference that shows how the 2008 time grew with size. The green curve is MilAMin's own sweep on the desktop, an Intel i7-4930K from 2013, run under Node in WSL2 with the same code the page uses and twelve solver threads: meshing, assembly, factorization and pressure iterations from seven thousand to 2.8 million unknowns, the last within a few hundred megabytes of the WebAssembly limit. The red curve is the same sweep on the phone, a Google Pixel 10 in Chrome for Android with two solver threads, from twelve thousand to 2.5 million unknowns, the last in 26 s. The blue point is the processor of the green curve in Chrome with four threads at 1.44 million unknowns. The desktop is simply the machine at hand; that a 2013 processor clears the 2008 curve in a browser is part of the point. Every configuration on every device we measured lies below the 2008 curve at every size, the phone by the widest margin. The peak rate, on the phone between 150 and 300 thousand unknowns, is eleven million unknowns per minute.

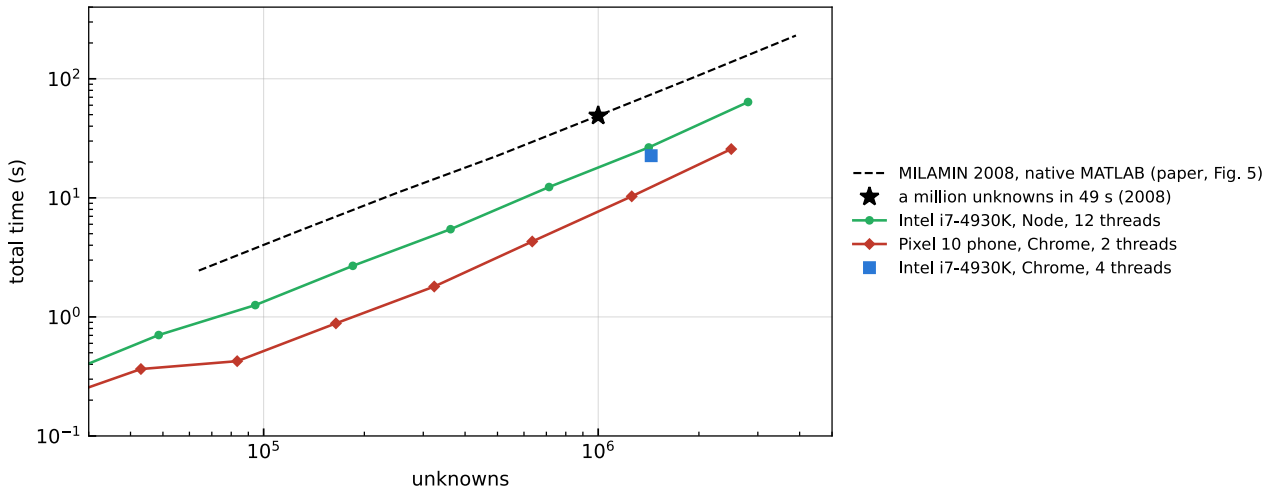

Figure 2. Total pipeline time against unknowns. Dashed: MILAMIN 2008 in native MATLAB, digitized from Figure 5 of the paper, with its million-unknown point. Green: MilAMin under Node on an Intel i7-4930K, the Node twin of the benchmark page, twelve threads. Red: the benchmark page on a Pixel 10 phone in Chrome for Android, two threads. Blue: the benchmark page on the i7-4930K in Chrome, four threads, at 1.44 million unknowns. The problems differ, see the text.

The controlled measurements behind the device points are in Table 3. Both sweeps were run back to back in one browser session with the benchmark page's option to mesh the refinement ladder and solve only the final size, three repeats per configuration; the factorization time is the median of the three and the total the best of the three. A size run on its own is slower than the same size at the top of a ladder, in the factorization only: on the phone 2.5 million unknowns took 33.5 s alone and 25.7 s at the end of the ladder of Figure 2, 22.7 s against 17.7 s for the factorization. Each run starts a

fresh worker, so the run on its own also pays for growing the WebAssembly memory to what the factor needs and for the engine's optimizing compilation of the wasm code, which the ladder has behind it by the time it reaches the top. The curves of Figure 2 are ladders on both machines; the sweeps of Table 3 and the million of Table 2 are runs on their own, the conservative numbers. The phone's runs went in the order one, two, eight threads; its third eight-thread run throttled visibly, every stage inflated, which is why the table quotes medians and why the million in Table 2 was taken with the phone cool.

Table 3. Thread sweeps at 1.44 million unknowns (2008 counting), meshing, assembly, factorization and pressure iterations. The desktop is an Intel i7-4930K, six cores with hyperthreading, quad-channel DDR3; the phone a Google Pixel 10 with the Tensor chip, eight heterogeneous cores, LPDDR5X. One thread means the plain single-threaded WebAssembly build without a threading runtime. Operating system versions were not recorded; the site's benchmark log holds the raw numbers and the protocol.

device	threads	factorization, median of 3	total, best of 3
i7-4930K desktop, 2013, desktop Chromium	1	23.6 s	34.2 s
	2	15.7 s	25.8 s
	4	12.3 s	22.6 s
	6	12.1 s	22.5 s
	12	15.2 s	24.7 s
Pixel 10 phone, 2025, Chrome for Android	1	9.9 s	14.4 s
	2	8.6 s	13.3 s
	8	10.2 s	15.0 s

4.3 What determines the speed

Six observations from the benchmark log, made on the two machines at hand, the 2013 desktop and the 2025 phone, with the caveat that they are inferred from timings, not from hardware counters.

The supernodal algorithm was the main win, not threads. The first browser backend was a simplicial LDL^T factorization. Replacing it with CHOLMOD's supernodal Cholesky cut the single-threaded factorization of the 1.44-million-unknown case on the desktop under Node from 106 s to 28 s: the floating-point work moves into dense level-3 kernels that WebAssembly SIMD can vectorize.

Thread scaling is modest and plateaus early. On the desktop, four threads give 1.9 times on the factorization and 1.5 times on the total; the last two physical cores add nothing, and using all twelve hardware threads regresses about twenty percent below the four-to-six-thread plateau. This is the behaviour of a memory-bandwidth-limited kernel with the small supernodal fronts that two-dimensional problems produce, and it follows the isoefficiency relation the original MILAMIN technical notes documented for their parallel solver (Krotkiewski & Dabrowski, 2010). We have not measured bandwidth directly, so we state it as consistent with, not established.

Heterogeneous mobile cores break static work splits. With one block per thread and static OpenMP scheduling, eight threads on the phone were 1.7 times slower than one thread: every parallel region waited for a small core to finish the same-sized block as the prime core. Splitting into four times more blocks than threads with dynamic scheduling fixed it without changing the desktop timings.

One phone core does most of what its eight can do. The phone's optimum is two threads at every size, and the second thread buys ten to fifteen percent on the factorization. A single phone core factors as fast as twelve threads of the 2013 desktop, and the phone's single-threaded stages, assembly, pressure iterations and meshing, run about three times faster than on the desktop. That is the measurement; why one 2025 core keeps up with a 2013 desktop is a question of memory systems we did not instrument.

Phones throttle across consecutive runs. Factorization times in one phone session drifted from 7.6 s to 15.9 s over four runs of equal or easier configurations. Quotable numbers need cool-down pauses or first-run values, and the site says so. Desktop variance comes from background load instead.

The factorization is no longer the whole story. In the best configurations of Table 3 it takes 54 percent of the total on the desktop and 65 percent on the phone; meshing, assembly and the pressure iterations, all on one thread, take the rest. More threads can therefore only shrink the smaller part, which is why the pages start at four threads on a desktop and two on a phone and leave the choice to the user. On the desktop the next stage to speed up is the assembly in plain TypeScript, not the solver.

5 Verification

Speed is worthless if the answer is wrong. For the circular-inclusion problem the exact solution is known analytically (Schmid & Podladchikov, 2003), which allows the one test numerics cannot argue with: solve on finer and finer meshes and watch the true error fall at the rate theory predicts. The site's convergence lab runs this study live, five meshes each halving the element size; the numbers below are from its Node twin.

Errors are relative L_2 norms integrated over the mesh with the element quadrature rule, for the velocity and for the maximum shear stress $\tau = 2\mu\sqrt{e_{xx}^2 + e_{xy}^2}$, the scalar invariant the pages draw, not the stress tensor. The mesh approximates the circular interface by straight edges, so between the polygon and the circle lies a sliver of area $O(h^2)$ in which the mesh has the wrong material. Element quadrature never samples it, the sliver being a thousand times thinner than an element, so the study evaluates the exact solution in each element with the branch of its own material continued smoothly across the circle and then integrates the sliver with a polar Gauss rule, subtracting the continued matrix-side contribution and adding the true inclusion-side one. The domain is thus covered exactly once. Table 4 and Figure 3 give the result: the velocity converges at second order, the stress at first.

Table 4. Convergence on the circular-inclusion problem (viscosity ratio 1000, simple shear, inclusion radius 1, disc of radius 2.5 with the analytical velocity on its rim). Relative L_2 errors against the analytical solution, observed orders between consecutive levels and the share of the squared stress error that comes from the sliver between the polygonal mesh boundary and the circle. Fitted over the finest three levels: velocity $O(h^{1.98})$, stress $O(h^{1.04})$.

h	unknowns	velocity error	order	stress error	order	sliver share
0.283	2,762	1.18e-3		3.76e-2		49%
0.141	10,070	2.47e-4	2.26	1.48e-2	1.34	73%
0.071	36,998	6.40e-5	1.95	6.51e-3	1.19	90%
0.035	142,490	1.63e-5	1.97	3.13e-3	1.06	96%
0.018	561,878	4.11e-6	1.99	1.54e-3	1.02	98%

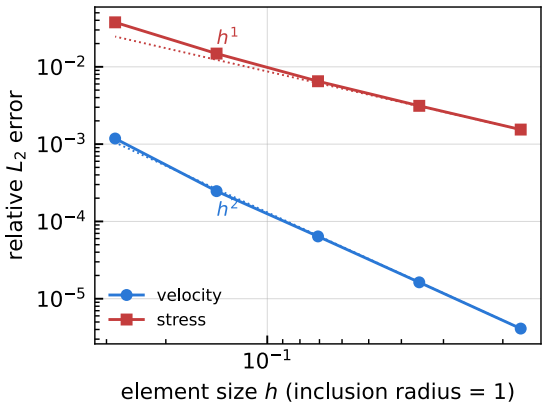

Figure 3. Relative L_2 errors against element size. Dotted lines are the h^2 and h^1 slopes through the finest level.

Both orders are below what the element promises on a smooth problem, and the reason is the geometry, not the element. For the velocity the polygonal interface is an $O(h^2)$ geometric error that caps the element's theoretical $O(h^3)$: on a square domain, where the geometry is exact, the same element measures $O(h^{3.0})$ for the velocity and $O(h^{2.0})$ for the stress against manufactured solutions with constant and with rotational pressure. For the stress the sliver carries an $O(1)$ error over an $O(h^2)$ area, which is $O(h)$ in the L_2 norm, and from the third level on it makes up more than ninety percent of the squared stress error. An error norm that misses the sliver, sampled on a grid or taken with the element quadrature alone, reports an apparent stress order near two.

Beyond the convergence study, the repository's verification suites, run before every release, hold 46 checks of the solver against the analytical circular-inclusion and rigid-polygon solutions and between the two independent factorization paths, the supernodal and a banded Cholesky kept as a reference, plus 26 checks of Folder's growth rates against the analytical small-amplitude theory and accuracy checks of its time stepping and interface resampling.

6 Reproducing the numbers

The benchmark sweep, the convergence study and the playground presets have command-line twins under Node that run the same code as the pages, so the pipeline timings of Figure 2, every number of Table 4 and the presets' solutions can be regenerated without a browser. Device timings are browser measurements and reproduce only on the device: the benchmark log in the repository records them with the protocol that produced them, and the benchmark page runs the sweep on whatever device opens it. The figures of this note are built by a script from the committed sweep results and the convergence twin's output; the script stops with an error if either input is missing.

The WebAssembly binaries are committed, so the site builds without a C++ toolchain; the C++ sources, the build scripts and the exact upstream tarballs they were built from are part of the repository or ship with the site, as the GPL requires. Our own code is licensed under the GPL-2.0-or-later, which the supernodal module of CHOLMOD requires of anything linked with it; the other components keep their licenses, BSD for AMD and COLAMD, MPL-2.0 for Eigen, MIT and OFL for the page libraries and fonts, and Triangle its own non-commercial terms, so the repository as a whole is public but not uniformly GPL. The site lists every component with its license.

7 Conclusion

The 2008 principle survived the change of platform intact: give every stage equal care and a general unstructured finite element code reaches a million unknowns a minute, in the browser as it did in MATLAB. What changed is what it takes to run one. MilAMin needs no MATLAB license, no compiler, no installation and no particular computer; it runs on the phone in your pocket, faster than it ran on the desktops of 2008, and it can be checked against an analytical solution by anyone who opens the page. The barriers that once kept such a code inside a few specialized groups are gone. What remains is the part no platform can supply: knowing what to ask of a model and how to read its answer.

Acknowledgements

Marcin Dabrowski reviewed the site before its release, and his comments improved the benchmark page, the playground and the convergence lab. Marcin Dabrowski and Marcin Krotkiewski are the co-authors of MILAMIN, without which there would be nothing to port. Jonathan Shewchuk's Triangle and Tim Davis's SuiteSparse do the meshing and the factorization.

Data and code availability

The site is at https://milamin.org. The source code of the site, the solver and the applications and the benchmark log with all measurements are at https://github.com/dwschmid/milamin-web, our code under the GPL-2.0-or-later and the bundled components under their own licenses, Triangle among them under non-commercial terms. Release v1.0.0 of the software, the code this note describes, is archived on Zenodo (Schmid, 2026).

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