

Numerical Methods for Partial Differential Equations - Notes - v0.4.0

260236

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Preface

Every theory section in these notes has been taken from the sources:

- Course slides. [\[1\]](#)

About:

 [GitHub repository](#)

These notes are an unofficial resource and shouldn't replace the course material or any other book on numerical methods for partial differential equations. It is not made for commercial purposes. I've made the following notes to help me improve my knowledge and maybe it can be helpful for everyone.

As I have highlighted, a student should choose the teacher's material or a book on the topic. These notes can only be a helpful material.

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1 Basic Concepts

In this course, we introduce numerical methods for the solution of **Partial Differential Equations** (PDEs), with focus on the **Finite Element** (FE) **method**¹ and the use of the computer for the construction of the PDEs numerical solution.

We will consider the numerical approximation of elliptic and parabolic PDEs by considering their variational formulation, Galérkin and FE approximations in 1D/2D/3D, the theoretical properties and practical use of the methods, algorithmic aspects, and interpretation of the numerical results.

Advanced topics include the approximation of saddle-point PDEs (Stokes equations), vectorial, nonlinear, and multiphysics differential problems, domain decomposition methods exploiting the properties of the PDEs, and the introduction to parallel computing for the FE method, i.e., in the *High Performance Computing* (HPC) framework.

Finally, the course will feature the use of the [deal.II software library](#), a C++ open source FE library, and [ParaView](#) for the visualization of numerical solution and scientific computing data.

¹The **Finite Element Method (FEM)** is a popular method for numerically solving differential equations arising in engineering and mathematical modeling. Typical problem areas of interest include the traditional fields of structural analysis, heat transfer, fluid flow, mass transport, and electromagnetic potential. Computers are usually used to perform the calculations required. With high-speed supercomputers, better solutions can be achieved, and are often required to solve the largest and most complex problems. ([source](#))

1.1 Mathematical Models and Scientific Computing

Definition 1: Mathematical Model

A **Mathematical Model** is a set of (algebraic or differential) equations that is able to represent the features of a complex system or process.

❓ Why do they exist?

Models are **developed** to:

- Describe
- Forecast
- Control

The **behavior or evolution of such systems**.

We are interested in the physics models. **Physics-based models** are those **mathematical models that are derived from physical principles** (like conservation laws of mass, momentum, energy, etc.) **and that encode natural laws of leading to (differential) equations whose solutions are often represented in the form of functions**. However, the analytical solution of such models is rarely available in closed form, for which numerical approximation methods are instead employed.

Definition 2: Numerical Modelling

Numerical Modelling indicates sets of numerical methods that **determine an approximate solution of the original** (often infinite-dimensional) **mathematical model**, by turing it into a *discrete problem* (algebraic, finite-dimensional), whose dimension (size) is typically very large.

Definition 3: Scientific Computing

Scientific Computing is a branch of Mathematics that **numerically solves (differential) mathematical models by building approximate solutions though the use of a calculator**.

For numerical models of large size, parallel architectures for calculators and the HPC framework are typically used.

❓ Why did we introduce mathematical models and physical models?

Because they are connected and used together. Mathematical models are conventionally used altogether with theoretical (mathematical) models and experimental tests. Unfortunately, in several cases theoretical models are not available (like in Computational Medicine) or experimental tests are not meaningful or cannot be performed (for example, for nuclear testing). Physics-based models have witnessed an increasing role in the modern society in virtue of the massive developments of Scientific Computing and computational tools.

Since a large amount of data is becoming available from multiple sources nowadays, data-driven models are fundamentals. **Data-driven models** are those mathematical models built from meaningful data that do not rely on physical principles, because the latter are not available or are not reliable, and whose construction calls for statistical learning methods.

Physics-based mathematical models (**mathematical problems**) are a fundamental pillar in the understanding and prediction of several physical phenomena and processes (**physical problems**). However, these mathematical models lead to problems that can rarely be solved analytically, or in an exact way (**exact solution**), especially for PDEs: with only a few exceptions, it is not possible to write their solution explicitly.

Numerical methods and numerical approximation techniques (**numerical problems**) serve the purpose to determine an **approximate solution** of a mathematical model. When the calculator is used to determine such approximate solution, the latter is called **numerical solution** (see the Figure 1).



Figure 1: Scientific Computing.

1.2 Differential Models and PDEs

Definition 4: Partial Differential Equation (PDE)

A **differential equation** (model) is an equation that involves **one or more derivatives of an unknown function**. In an **Ordinary Differential Equation (ODE)**, every derivative of the unknown solution is with respect to a single independent variable. If instead, derivatives are partial, then we have a **Partial Differential Equation (PDE)**.

In other words, it is a differential equation where its derivatives are partial.

There are different types of PDEs, and their nature depends on the conditions and their type. Mathematically, we can represent a **differential model** (equation) as follows:

$$\mathcal{P}(u; g) = 0 \quad \text{differential equation (mathematical problem)} \quad (1)$$

Where:

- \mathcal{P} indicates the *model*;
- u is the *exact solution*, a function of one or more independent variables (space and/or time variables);
- g indicates the *data*.

1.2.1 ODEs

Ordinary Differential Equation (ODE) is also known as **initial value problem**.

≡ I°ODE - Cauchy problem

A **first order ODE**, a **Cauchy problem**, is a differential problem, whose:

- **Solution** $u = u(t)$ is a function of a single independent variable t , often interpreted as time.
- A **single condition** is assigned on the solution, at a point (usually, the left end of the integration interval).

Its form is the following find $u : I \subset \mathbb{R} \rightarrow \mathbb{R}$ such that:

$$\begin{cases} \frac{du}{dt}(t) = f(t, u(t)) & t \in I \\ u(t_0) = u_0 \end{cases} \quad (2)$$

Where:

- $I = (t_0, t_f] \subset \mathbb{R}$ is a **time interval**;
- u_0 is the **initial value** assigned at $t = t_0$;
- $f : I \times \mathbb{R} \rightarrow \mathbb{R}$

🔍 **Meaning.** The equation describes the **evolution of a scalar quantity** u over time t , **without distribution in space**.

🔍 **Vectorial problems.** In vectorial problems, the **unknown is a vector-valued function** $\mathbf{u} = \mathbf{u}(t)$, where $\mathbf{u} = (u_1, \dots, u_m) \in \mathbb{R}^m$, with $m \geq 1$. The first order Cauchy problem reads: find $\mathbf{u} : I \subset \mathbb{R} \rightarrow \mathbb{R}^m$ such that:

$$\begin{cases} \frac{d\mathbf{u}}{dt}(t) = \mathbf{f}(t, \mathbf{u}(t)) & t \in I \\ \mathbf{u}(t_0) = \mathbf{u}_0 \end{cases}$$

Where $\mathbf{u}_0 \in \mathbb{R}^m$ is the initial datum and $\mathbf{f} : I \times \mathbb{R}^m \rightarrow \mathbb{R}^m$.

≡ II°ODE - Cauchy problem

A **second order Cauchy problem** sees second order time derivatives and two initial conditions. It reads as: find $u : I \subset \mathbb{R} \rightarrow \mathbb{R}$ such that:

$$\begin{cases} \frac{d^2u}{dt^2}(t) = f\left(t, u(t), \frac{du}{dt}(t)\right) & t \in I \\ \frac{du}{dt}(t_0) = v_0 \\ u(t_0) = u_0 \end{cases} \quad (3)$$

Where the initial data are u_0 and v_0 , while $f : I \times \mathbb{R} \times \mathbb{R} \rightarrow \mathbb{R}$.

1.2.2 PDE, boundary value problem in 1D

The **Boundary value problem in 1D** is characterized by a **single independent variable** x , which represents the **space coordinate in an interval** $\Omega = (a, b) \in \mathbb{R}$ (1D).

The problem involves **second order derivatives of the unknown solution** $u = u(x)$ with respect to x . The value of u , or the **value of its first derivate**, is a **set at the two boundaries of the domain** (interval) Ω , that is at $x = a$ and $x = b$ (the domain boundary is $\partial\Omega = \{a, b\}$).

Let us consider the following **Poisson problem** with (homogeneous) Dirichlet boundary conditions: find $u : \Omega \subset \mathbb{R} \rightarrow \mathbb{R}$ such that:

$$\begin{cases} -\frac{d^2u}{dx^2}(x) = f(x) & x \in \Omega = (a, b) \\ u(a) = u(b) = 0 \end{cases} \quad (4)$$

This equation models a **stationary phenomenon** (the time variable doesn't appear in fact) and represent a **diffusion model**.

Example 1

For example, the diffusion model models the diffusion of a pollutant along a 1D channel $\Omega = (a, b)$ or the vertical displacement of an *elastic thread* fixed at its ends. In the first case, $f = f(x)$ indicates the source of the pollutant along the flow, while in the second case, f is the traverse force acting on the elastic thread, in the hypothesis of negligible mass and small displacements of the thread.

Boundary value problem in 1D vs ODE

We remark that the **boundary value problem in 1D is a particular case of PDEs**, even if it involves only derivatives with respect to a single independent variable x . Indeed, even if apparently similar to a second order ODE, the boundary value problem is in reality substantially **different** from an ODE:

- In ODE, two conditions are set at $t = t_0$;
- In the boundary value problem in 1D, one condition is set at $x = a$ and the other one at $x = b$.

The conditions in the boundary value problem determine to the so-called global nature of the model.

1.2.3 PDE, initial and boundary value problem in 1D

Initial and boundary value problem in 1D is a type of problems that concern equations that **depend on space and time**:

- The **unknown solution** $u = u(x, t)$ both depends on the space coordinate $x \in \Omega \subset \mathbb{R}$ in 1D;
- The **time variable** $t \in I \subset \mathbb{R}$.

In this case, the initial conditions at $t = 0$ must be prescribed, as well as the boundary conditions at the ends of the interval in 1D.

The **Heat equation**, also known as **Diffusion equation**, with Dirichlet boundary conditions assumes the following form: find $u : \Omega \times I \rightarrow \mathbb{R}$ such that:

$$\begin{cases} \frac{\partial u}{\partial t}(x, t) - \mu \frac{\partial^2 u}{\partial x^2}(x, t) = f(x, t) & x \in \Omega = (a, b), t \in I \\ u(a, t) = u(b, t) = 0 & t \in I \\ u(x, t_0) = u_0(x) & x \in \Omega = (a, b) \end{cases} \quad (5)$$

Example 2

For example, the unknown function $u(x, t)$ describes the temperature in a point $x \in \Omega = (a, b)$ and time $t \in I$ of a metallic bar covering the space interval Ω . The diffusion coefficient μ represents the thermal response of the material and it is related to its thermal conductivity. The Dirichlet boundary conditions express the fact that the ends of the bar are kept at a reference temperature (zero degrees in this case), while at time $t = t_0$ the temperature is assigned in each point $x \in \Omega$ through the initial function $u_0(x)$. Finally, the bar is subject to a heat source of linear density $f(x, t)$.

1.2.4 PDE, boundary value problem in multidimensional domains

The Poisson problem (equation 4, page 9) can be **extended in multidimensional domains** $\Omega \subset \mathbb{R}^d$, with $d = 2, 3$; the solution is $u = u(\mathbf{x})$, where $\mathbf{x} = (x_1, \dots, x_d)^T \in \mathbb{R}^d$. This leads to the following Poisson problem with (homogeneous) Dirichlet boundary conditions: find $u : \Omega \subset \mathbb{R}^d \rightarrow \mathbb{R}$ such that:

$$\begin{cases} -\Delta u = f & \text{in } \Omega \text{ (i.e. } \mathbf{x} \in \Omega) \\ u = 0 & \text{on } \partial\Omega \text{ (i.e. } \mathbf{x} \in \partial\Omega) \end{cases} \quad (6)$$

Where:

- The **Laplace operator**:

$$\Delta u(\mathbf{x}) := \sum_{i=1}^d \frac{\partial^2 u}{\partial x_i^2}(\mathbf{x})$$

- The **domain** $\Omega \subset \mathbb{R}^d$ is endowed with boundary $\partial\Omega$;
- $f = f(x)$ is the **external forcing term**.

This equation is used **for example** to **model the vertical displacement of an elastic membrane fixed at the boundaries**.

1.2.5 PDE, initial and boundary value problem in multidimensional domains

The **multidimensional** counterpart of the **heat equation** (5, page 10) reads: find $u : \Omega \times I \rightarrow \mathbb{R}$ such that:

$$\begin{cases} \frac{\partial u}{\partial t} - \mu \Delta u = f & \mathbf{x} \in \Omega, t \in I \\ u(\mathbf{x}, t) = 0 & \mathbf{x} \in \partial\Omega, t \in I \\ u(\mathbf{x}, t_0) = u_0(\mathbf{x}) & \mathbf{x} \in \Omega \end{cases} \quad (7)$$

Where u_0 is the **initial datum**. The **solution** is $u = u(\mathbf{x}, t)$.

1.2.6 Classification of PDEs

A PDE is a relationship among:

- The partial derivatives of a function $u = u(\mathbf{u}, t)$, that is the PDE **solution**;
- **Spatial coordinates** $\mathbf{x} = (x_1, \dots, x_d)^T \in \mathbb{R}^d$ on which the solution depends (if the problem is defined in a spatial domain $\Omega \subset \mathbb{R}^d$).
- **Time variable** t .

Therefore, a PDE can be written as:

$$\mathcal{P}\left(u, \frac{\partial u}{\partial t}, \frac{\partial u}{\partial x_1}, \dots, \frac{\partial u}{\partial x_d}, \dots, \frac{\partial^{p_1+\dots+p_d+p_t} u}{\partial x_1^{p_1} \dots \partial x_d^{p_d} \partial t^{p_t}}, \mathbf{x}, t; g\right) = 0 \quad (8)$$

Where $p_1, \dots, p_d, p_t \in \mathbb{N}$ and g are the data.

Definition 5: PDE order

The **PDE order** is the **maximum order of derivation** that appears in \mathcal{P} , that is:

$$q = p_1 + \dots + p_d + p_t \quad (9)$$

Definition 6: PDE is linear

The **PDE is linear** if \mathcal{P} **linearly depends** on u and its **derivatives**.

√ Classification

Let us focus on linear PDEs of order $q = 2$ with constant coefficients, so that the general PDE formulation is:

$$\mathcal{L}u = g$$

Where \mathcal{L} is a second order, **linear differential operator**. When only two independent variables (our case) x_1 and x_2 are considered, the operator \mathcal{L} applied to the function u reads:

$$\mathcal{L}u = A \cdot \frac{\partial^2 u}{\partial x_1^2} + B \cdot \frac{\partial^2 u}{\partial x_1 \partial x_2} + C \cdot \frac{\partial^2 u}{\partial x_2^2} + D \cdot \frac{\partial u}{\partial x_1} + E \cdot \frac{\partial u}{\partial x_2} + F \cdot u$$

For some constant coefficients $A, B, C, D, E, F, G \in \mathbb{R}$. If $d = 2$ (our case), the **independent variables** can represent the *space coordinates*:

- $x_1 = x$
- $x_2 = y$

After introducing the **PDE discriminant** (a quantity that helps determine the type of PDE):

$$\Delta := B^2 - 4AC \quad (10)$$

The PDE can be classified as:

- **Elliptic PDE** if $\Delta < 0$
- **Parabolic PDE** if $\Delta = 0$
- **Hyperbolic PDE** if $\Delta > 0$

🔍 What are the implications of PDE classification?

The different nature of the PDE impacts on:

- **Type and amount of data to prescribe as boundary;**
- **Initial conditions** to ensure the well-posedness of the problem (existence and uniqueness of the solution);
- The **phenomena that can be described** by the PDE;
- The **information that encapsulates**.

In general:

- **Elliptic PDE** typically describes **stationary phenomena**, without time evolution of quantities.
- **Parabolic PDE** describes **wave propagation phenomena** with infinite velocity of propagation.
- **Hyperbolic PDE** describes **wave propagation phenomena** but with finite velocity of propagation.

1.3 Numerical Methods

Since in most cases of practical interest we **cannot solve a PDE analytically**, we need to use **numerical methods** that allow us to construct an *approximation* u_h of the *exact solution* u , for which the corresponding *error* $(u - u_h)$ can be quantified and/or estimated.

$$\begin{array}{ccc}
 \mathcal{P}(u; g) = 0 & & \text{PDE (mathematical problem)} \\
 \downarrow & & \text{numerical method} \\
 \mathcal{P}_h(u_h; g_h) = 0 & & \text{approximate PDE (numerical problem)}
 \end{array}$$

Where:

- g_h is an approximation of the data g ;
- \mathcal{P}_h is a characterization of the approximate problem.

The subscript h indicates a **discretization parameter** that characterizes the numerical approximation. Conventionally, the smaller is h , the better is the approximation of u made by u_h . Furthermore, the error $(u - u_h)$ tends to zero as h gets smaller and smaller. In this course, we will specifically introduce the FE method (page 4) to build the numerical approximation of PDEs.

■ Summary Notation

| Notation | Description |
|-------------------------------|--|
| $\mathcal{P}(u; g) = 0$ | PDE (mathematical problem) |
| u | <i>exact solution</i> of a PDE |
| u_h | <i>approximate solution</i> of a PDE |
| $(u - u_h)$ | <i>error</i> (quantified and/or estimated; tends to zero if h is smaller) |
| h | <i>discretization parameter</i> (\downarrow smaller h , better approximation; \uparrow higher h , poor approximation) |
| $\mathcal{P}_h(u_h; g_h) = 0$ | approximate PDE (numerical problem) |
| g_h | <i>approximation</i> of the <i>data</i> g |
| \mathcal{P}_h | <i>characterization</i> of the approximate problem. |

Table 1: Notation used to approximate the PDE with numerical methods.

1.4 From Mathematical to Numerical Problem

1.4.1 The Mathematical Problem (MP)

Let us consider a **Physical Problem (PP)** endowed with a **physical solution**, let say u_{ph} , and **dependent on data** indicated with g .

The **Mathematical Problem (MP)** is represented by the **mathematical formulation of the PP** and has **mathematical solution** u . Therefore, we indicate the MP as:

$$\mathcal{P}(u; g) = 0 \quad (11)$$

Where:

- $u \in \mathcal{U}$
- $g \in \mathcal{G}$, and \mathcal{G} is the set or space of **admissible data**.

Where \mathcal{U} and \mathcal{G} are suitable sets or spaces.

Definition 7: Model Error

The error between the physical and mathematical solutions is called **Model Error**:

$$e_m := u_{ph} - u \quad (12)$$

Where:

- u_{ph} is the physical solution;
- u is the mathematical solution.

The model error takes into account all those **characteristics of the PP that are not represented or captured by the MP**.

? When a Mathematical Problem is *well-posed*?

Definition 8: *well-posed* MP

The mathematical problem MP is *well-posed* (**stable**) if and only if there **exists a unique solution** $u \in \mathcal{U}$ **that continuously depend on the data** $g \in \mathcal{G}$.

From the previous definition, we remark that \mathcal{G} is the set of admissible data, i.e., those for which the MP admits a unique solution. Furthermore, *continuously depend on the data* means that **small perturbations on data** $g \in \mathcal{G}$ **lead to small changes on the solution** $u \in \mathcal{U}$ of the MP. However, a measure of this sensitivity is given by the condition number of the MP.

1.4.2 The Numerical Problem (NP)

The **Numerical Problem (NP)** is an **approximation of the Mathematical Problem** (MP, equation 11, page 15). We indicate its **numerical solution** as u_h , where h stands as a suitable **discretization parameter**.

$$\mathcal{P}_h(u_h; g_h) = 0 \quad (13)$$

Where:

- $u_h \in \mathcal{U}_h$
- $g_h \in \mathcal{G}_h$, and g_h is the representation of the **data in the NP**.

Where \mathcal{U}_h and \mathcal{G}_h are suitable sets or spaces.

Definition 9: Truncation Error

The error between the mathematical and numerical solutions is called **Truncation Error**:

$$e_h := u - u_h \quad (14)$$

Where:

- u is the mathematical solution;
- u_h is the numerical solution.

The truncation error can be considered as the error resulting from the **discretization of the MP**.

Numerical solution calculated on the computer

When the numerical solution is computed by running the algorithm on a computer, we need more notations and concepts.

- \hat{u}_h is the **final solution**.
- The final solution is affected by a **Round-Off error** e_r :

$$e_r := u_h - \hat{u}_h \quad (15)$$

Such round-off errors depend on the machine architecture, on the representation of the numbers at the calculator, and on operations made in floating-point arithmetic.

- The truncation error e_h (equation 14, page 16) and the Round-Off error e_r (equation 15) concur to determine the **Computational error** e_c :

$$e_c := e_h + e_r = (u - u_h) + (u_h - \hat{u}_h) = u - \hat{u}_h \quad (16)$$

For some NP, we can have a round-off error less than a truncation error $|e_r| \ll |e_h|$, for which $e_c \approx e_h$.

? When a Numerical Problem is *well-posed*?

Definition 10: *well-posed* NP

The numerical problem NP is *well-posed* (**stable**) if and only if there **exists a unique solution** $u_h \in \mathcal{U}_h$ **that continuously depends on the data** $g_h \in \mathcal{G}_h$.

Consider the numerical solution calculated only on the computer

In practice, numerical solutions are computed on a computer. Therefore, it is reasonable to obtain a computational error that tends to zero as the numerical method improves, namely as the discretization parameter h goes to zero. This concept is encoded in the definition of convergence.

Definition 11: *convergence* NP

The NP is **convergent** when the **computational error tends to zero** for h tending to zero, that is:

$$\lim_{h \rightarrow 0} e_c = 0 \quad (17)$$

A crucial aspect is to qualify the convergence of the NP, that is determining the convergence order of the NP.

Definition 12: *convergence order*

If $|e_c| \leq Ch^p$, with C a positive constant independent of h and p , then the NP is **convergent with order** p .

? How to estimate the convergence order?

The convergence order can be estimated for many reasons (error estimation, method comparison, accuracy verification, etc.). If there exists a constant $\tilde{C} \leq C$ independent of h and p such that $\tilde{C}h^p \leq |e_c| \leq Ch^p$, then we can write $|e_c| \approx Ch^p$ and we can **estimate the convergence order p of the NP by using the known solution u of the MP**. There are two approaches:

1. Algebraic estimation of p .

- (a) We compute the computational errors e_{c1} and e_{c2} for the NP corresponding to two different values of h that are “sufficiently” small, say h_1 and h_2 .
- (b) Then:
 - Writing $|e_{c1}| \approx Ch_1^p$ and $|e_{c2}| \approx Ch_2^p$
 - Noticing that $\frac{|e_{c1}|}{|e_{c2}|} = \left(\frac{h_1}{h_2}\right)^p$

We estimate the order p as:

$$p = \frac{\log\left(\frac{|e_{c1}|}{|e_{c2}|}\right)}{\log\left(\frac{h_1}{h_2}\right)} \quad (18)$$

2. **Graphical estimation of p .** We represent the errors $|e_c|$ and h on a plot in log-log scale. As $\log |e_c| = \log(Ch^p) = \log(C) + p \log(h)$, we have $p = \arctan(\theta)$, where θ is the slope of the curve (h, e_c) , a straight line in log-log scale. Instead of computing θ , it is possible to verify that the curves (h, e_c) and (h, h^p) are parallel in log-log scale.

In other words it involves plotting the error against the step size on a log-log scale and analyzing the resulting graph:

- (a) **Compute Errors:** Perform the numerical method for several step sizes h , such as h_1, h_2, h_3, \dots , and compute the corresponding errors e_1, e_2, e_3, \dots .
- (b) **Log-Log Plot:** Plot the errors e_i against the step sizes h_i on a log-log scale. This means we plot $\log(h_i)$ on the x-axis and $\log(e_i)$ on the y-axis.
- (c) **Linear Relationship:** If the method has a convergence order p , the relationship between the error and the step size should follow $e \approx Ch^p$. Taking the logarithm of both sides gives:

$$\log(e) \approx \log(C) + p \log(h)$$

This indicates that the plot of $\log(e)$ versus $\log(h)$ should be a straight line with a slope equal to p .

- (d) **Determine Slope:** The slope of the line in the log-log plot is the convergence order p . We can estimate this slope by fitting a linear regression line to the data points.

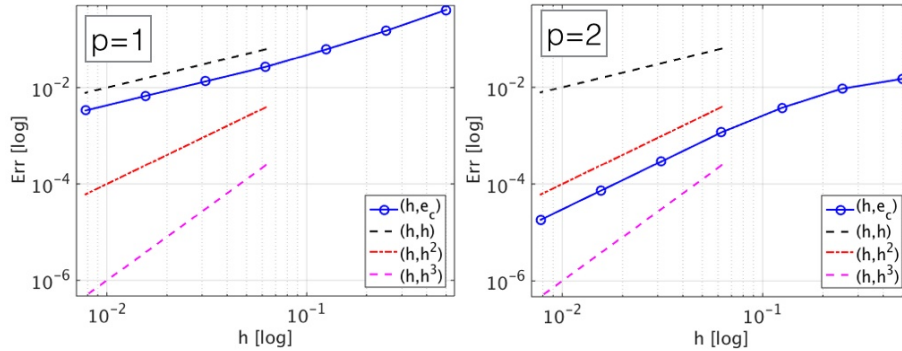


Figure 2: Graphical estimation of the convergence order p of a NP: computational errors $|e_c|$ vs h .

❓ When is convergence guaranteed in NP?

Unfortunately, a *well-posed* NP is not necessarily convergent. To ensure convergence of the NP, this is required to satisfy the consistency property (roughly speaking, the NP must be a “faithful copy” of the original MP).

Definition 13: NP consisten and strongly consistent

The Numerical Problem NP is **consistent** if and only if:

$$\lim_{h \rightarrow 0} \mathcal{P}_h(u; g) = \mathcal{P}(u; g) = 0 \quad g \in \mathcal{G}_h$$

The Numerical Problem NP is **strongly consistent** if and only if:

$$\mathcal{P}_h(u; g) \equiv \mathcal{P}(u; g) = 0 \quad \forall h > 0, g \in \mathcal{G}_h$$

Let highlights the main differences:

- Definition:
 - **Consistent**. Consistency requires that as the discretization parameter h tends to zero $\lim_{h \rightarrow 0}$, the process $\mathcal{P}_h(u; g)$ approaches the exact process $\mathcal{P}(u; g)$ and both become zero. This means that **over time and with finer discretization, the numerical approximation converges to the exact solution**.
 - **Strongly Consistent**. Strong consistency means that for any positive value of h ($\forall h > 0$, no matter how small), the process $\mathcal{P}_h(u; g)$ is exactly equal to the exact process $\mathcal{P}(u; g)$ and both are zero. This implies that the **numerical approximation already matches the exact solution for any step size**.
- Condition of h :
 - **Consistent**. The condition applies in the limit as h approaches zero. The **process gradually converges to the exact solution as the discretization parameter becomes infinitesimally small**.
 - **Strongly Consistent**. The condition applies for all $h > 0$. This is a **stronger requirement** because it demands that the numerical method is **accurate for any discretization parameter**, not just in the limit.

In practice, the *Consistent* indicates that the numerical method improves and approaches the exact solution as the discretization parameter is refined. It guarantees eventual **accuracy, but not necessarily immediate or uniform accuracy for larger h** . On the other hand, *Strongly Consistent* indicates that the numerical method is always accurate, regardless of the discretization parameter. This implies a **higher level of reliability and precision for any h** , making it a stronger and more robust form of consistency.

The **Lax-Richtmyer Equivalence Theorem** is a cornerstone of numerical analysis, linking the concepts of consistency, well-posedness (stability), and convergence. It provides a **rigorous framework for validating numerical methods and ensuring that they produce accurate and reliable solutions**. Furthermore, the following theorem guarantees that if a *numerical problem is well-posed and consistent, then the NP is also convergent*.

Theorem 1 (Lax-Richtmyer, equivalence). *If the Numerical Problem NP:*

$$\mathcal{P}_h(u_h; g_h) = 0 \quad u_h \in \mathcal{U}_h, g_h \in \mathcal{G}_h$$

Is consistent:

$$\lim_{h \rightarrow 0} \mathcal{P}_h(u; g) = \mathcal{P}(u; g) = 0 \quad g \in \mathcal{G}_h$$

Then, it is well-posed if and only if it is also convergent.

It is a fundamental theorem in numerical analysis because **it ensures that stability and consistency are sufficient to guarantee convergence**. Conversely, if we have a proof that the NP is consistent, we “only” need to show that the problem is well-posed to automatically prove convergence (and vice versa).

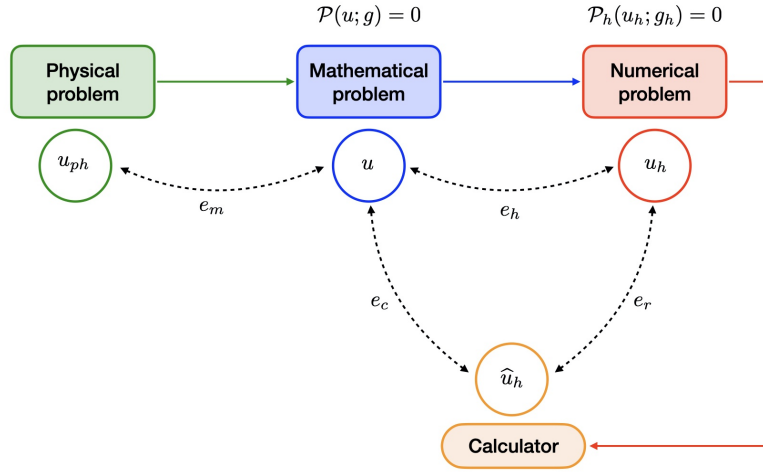


Figure 3: Physical (PP), Mathematical (MP), and Numerical (NP) problems. Corresponding solutions (u_{ph} , u , u_h , and \hat{u}_h) and errors (model $e_m = u_{ph} - u$, truncation $e_h = u - u_h$, round-off $e_r = u_h - \hat{u}_h$, and computational $e_c = e_h + e_r$ errors).

2 Laboratory

2.1 Introduction

The laboratory sessions complement the theoretical course by providing a **hands-on experience** in the numerical approximation of PDEs. The main goal is to bridge the gap between the mathematical formulation of PDEs, their variational and finite element discretizations, and their actual computer implementation.

Throughout the laboratories, we will progressively construct finite element solvers for a variety of model PDEs:

- Starting from the Poisson equation in 1D, moving towards multidimensional diffusion-reaction problems;
- Introducing verification and validation strategies for numerical codes;
- Extending to time-dependent problems such as the heat equation;
- Exploring nonlinear PDEs, elasticity, and saddle-point problems such as Stokes flows.

Each laboratory is designed to emphasize not only the **mathematical correctness** of the discretization, but also the **computational aspects**: efficiency, robustness, and scalability.

Software

The laboratory relies on:

- `deal.II` is an open-source C++ software library for solving partial differential equations (PDEs) using the finite element method (FEM).


The name `deal.II` stands for “Differential Equations Analysis Library, version II”. It is a finite element framework designed to make it easier to implement complex numerical methods for PDEs. It is widely used in both academia and industry for research, education, and simulation.

❓ Why is it used in laboratories? It provides full control over every step of the FEM pipeline: mesh generation, assembly, linear solvers, visualization. It forces us to understand the mathematics and the implementation, instead of just using a black-box solver. Finally, it is well documented and has extensive tutorial programs (step-1, step-2, ...), which the laboratory exercises build upon.

❓ Why do people say that `deal.II` is complicated? It’s a C++ library, not a GUI tool. Unlike COMSOL or ANSYS, we write C++ code that uses `deal.II`’s classes. That means we need to understand:

- FEM theory (variational forms, weak formulations, basis functions);
- The C++ programming model (templates, object-oriented design);
- The linear algebra backend (solvers, preconditioners).

The first labs are deliberately kept simple because even setting up a finite element mesh, assembling the stiffness matrix, and applying boundary conditions requires some work.

 **Why is deal.II respected?** Despite the initial complexity, `deal.II` is **very mature and widely used in scientific computing**. Aerospace, automotive, and energy companies use FEM frameworks like `deal.II`, FEniCS, or proprietary codes to simulate physical systems. Research groups in Europe and the US use `deal.II` on HPC clusters for multi-physics and optimization problems.

- ParaView is an **open-source data analysis and visualization application**. It's designed to handle very large scientific datasets (from MBs to TBs). Our finite element codes produce numerical solutions (vectors of values at mesh nodes, or fields defined in VTK/VTU file formats). These are not human-friendly to interpret. ParaView lets us **load the mesh and solution** files produced by `deal.II`. We can then **plot solutions in 2D/3D**, extract values along a line or surface, animate time-dependent results, compute integrals, etc..
- `gmsh` is an **open-source mesh generator** (also with a built-in post-processor). It allows us to create computational grids for finite element methods. For simple domains (intervals, unit squares, unit cubes), `deal.II` can generate meshes internally. But for **non-trivial geometries** (like irregular domains, or those with boundary partitions), we need an external mesh generator.

In addition, profiling and debugging tools (e.g. `TimerOutput`, `gperftools`) are used to analyze and optimize performance.

Computational Environment

While the course suggests using the MK module system, a more versatile approach is to work with either:

- a **native installation** of the required software stack (`deal.II`, ParaView, `gmsh`, etc.), or
- a **Docker container**, which ensures reproducibility and avoids configuration issues.

These alternatives are recommended for who prefer independence from the university's MK modules and allow seamless experimentation on personal or cloud-based machines.

✂ Environment Setup

Download version 9.5.0 of **deal.II** (which we are using for the course) from their website, following their guide. If we are using WSL or Ubuntu, we can download it more easily using the command:

```
1 sudo apt-get install libdeal.ii-dev
```

Download the **ParaView** visualization software from its original website:



If we're using Ubuntu, the easier command for the latest version is:

```
1 sudo apt install paraview
```

2.2 FEM for Poisson 1D

2.2.1 What is the Poisson Equation?

The **Poisson equation** is one of the most fundamental Partial Differential Equations (PDEs). In general form (in multiple dimensions):

$$-\Delta u(x) = f(x), \quad x \in \Omega \quad (19)$$

With some boundary conditions on $\partial\Omega$. Where:

- $u(x)$ is the **unknown function** (temperature, displacement, potential, etc.).
- Δ is the **Laplacian operator**, i.e. sum of second derivatives.

$$\Delta u = \frac{\partial^2 u}{\partial x_1^2} + \frac{\partial^2 u}{\partial x_2^2} + \dots \quad (20)$$

- $f(x)$ is the **source term** (where heat is produced, where force acts, etc.).

So the Poisson equation says **the curvature of u (second derivate) balances the source f** .

🔍 What does “1D” mean?

Normally the Poisson equation is written in 2D or 3D (for surfaces and volumes).

- In **2D**, it's like heat distribution on a plate.
- In **3D**, it's like heat or potential in a cube.

In **1D**, the domain $\Omega = (0, 1)$ is just a line (an interval). So the Laplacian reduces to an ordinary second derivative:

$$\Delta u(x) = \frac{d^2 u}{dx^2}$$

Therefore, in 1D, the Poisson equation looks like:

$$-u''(x) = f(x) \quad (21)$$

If we allow a variable coefficient $\mu(x)$, it becomes:

$$-(\mu(x)u'(x))' = f(x)$$

Example 1: Physical analogy

Imagine a **metal bar of length 1**. Fix both ends to zero temperature (they're in contact with ice). Apply a **heat source** (or sink, if negative) in some region of the bar. Then the **temperature distribution** inside the bar is described by the 1D Poisson equation.

Another analogy. Think of a **stretched elastic string** fixed at both

ends. Apply a **vertical load** (the forcing f) on some region. The resulting shape of the string $u(x)$ satisfies the Poisson equation.

The core idea

The Poisson equation links:

- The **curvature** of the unknown function $u(x)$ (its second derivate)
- To the **source term** $f(x)$.

Formally:

$$-u''(x) = f(x) \quad (\text{in 1D})$$

That means wherever $f(x)$ is nonzero, it *forces* the function $u(x)$ to bend (curve). If $f(x) = 0$, the equation reduces to:

$$-u''(x) = 0 \quad \implies \quad u''(x) = 0$$

Whose solutions are straight lines. So **no sources, flat solution**.

Physical interpretations

We can understand Poisson in multiple ways, depending on the field:

1. **Heat conduction.** The equation says: “The way temperature curves along the bar is dictated by how much heat we add/remove locally”.
 - $u(x)$: temperature.
 - $f(x)$: heat sources (positive) or sinks (negative).
2. **Electrostatics.** The equation says: “Charges create curvature in the potential”.
 - $u(x)$: electric potential.
 - $f(x)$: charge distribution (density).
3. **Elasticity.** The equation says: “Where we press on the string, it bends”.
 - $u(x)$: displacement of a string or membrane.
 - $f(x)$: applied load (force per unit length).

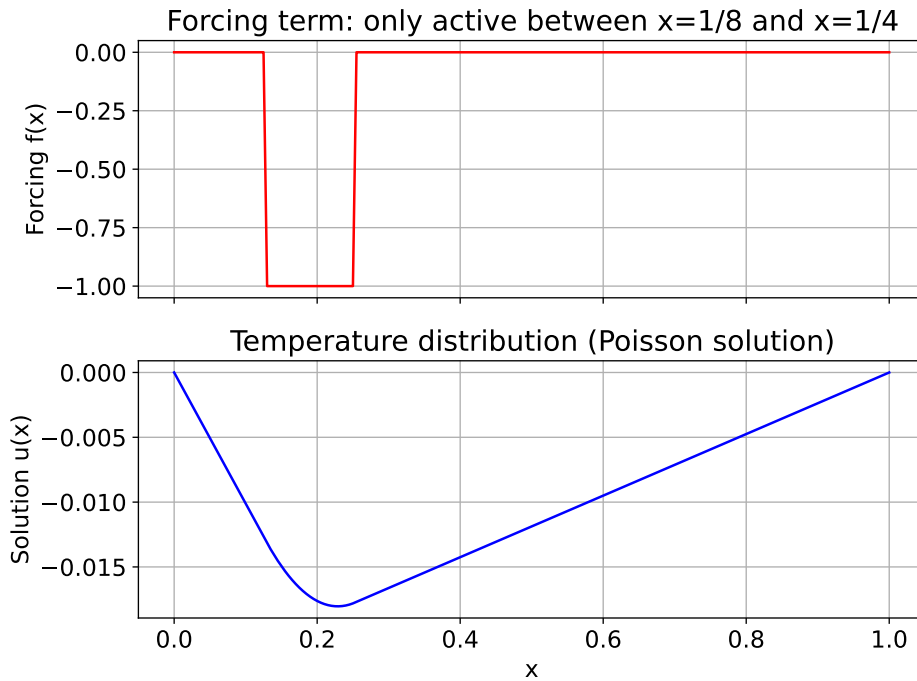


Figure 4: Visual explanation of the 1D Poisson problem. **Top graph (red)** is the forcing term $f(x)$. It is **zero everywhere**, except between $x = \frac{1}{8}$ and $x = \frac{1}{4}$, where it is negative (-1). That means only in that region we have a “sink” of heat. The **bottom graph (blue)** is the solution $u(x)$, i.e. the **temperature profile** along the bar. The ends are fixed at $u(0) = u(1) = 0$. In the middle, the solution bends downward because of the negative forcing. Outside the forcing region, the solution is almost straight (since $f = 0$, then the curvature is 0). So visually, the bar stays at 0 at the ends, but dips in the middle where we apply the negative forcing.

For example, this graph could represent heat conduction in a bar.

- $u(x)$: **temperature** along a thin bar of length 1.
- Boundaries: both ends clamped to 0°C (in contact with ice).
- $f(x) = -1$ between $x = \frac{1}{8}$ and $x = \frac{1}{4}$: this is like a **cooling region** (a heat sink).
- Physical picture: the bar stays cold at the ends and gets even colder in the middle where cooling is applied, producing the “dip”.

❓ What is the purpose of the Poisson equation?

The Poisson equation gives us the **response of the system**, not just the input. Why? Because physical systems are not isolated points:

- Temperature at a point depends on how heat flows along the entire bar.
- Displacement of a string at one point depends on forces applied nearby and the string's stiffness.
- Potential at a point depends on all surrounding charges.

The Poisson equation encodes that **interaction through curvature**:

$$-u''(x) = f(x)$$

- The second derivate u'' measures how much the solution bends.
- The boundary conditions (ends fixed at 0) propagate constraints.
- The combination of f and boundaries gives the actual **shape of the solution**.

For example, consider figure 4 on page 26. In particular, consider our forcing (the red curve in the top graph). It is localized, but the solution (the blue curve in the bottom graph) is **spread out**:

- The dip is not only in the forcing region, it extends beyond, up to the ends.
- This spreading comes from the diffusion mechanism encoded by Poisson.

So if we only look at $f(x)$, we know *where the cause is*. But if we solve Poisson, we know *how the whole system reacts*.

Example 2: Real-world analogy

Imagine putting an ice cube (the sink) in one part of a metal bar. From the forcing alone, we know *where* the cooling happens. But we don't know how the **temperature profile along the whole bar** looks; is the bar uniformly cold? Does the dip propagate? Solving Poisson tells us exactly the **temperature distribution everywhere**, considering both the sink and the fixed-zero boundary conditions.

2.2.2 Problem definition

The Poisson equation itself is a general PDE:

$$-u''(x) = f(x) \quad \text{in some domain}$$

To make it a **mathematical problem** we say:

- *Where* we are solving it: the **domain** $\Omega = (0, 1)$.
- *What constraints* we impose: the **boundary conditions** $u(0) = u(1) = 0$.
- *What data* we have: here $\mu(x) = 1$ and a particular forcing $f(x)$.

Using these definitions, we can formulate the problem as a Boundary Value Problem (BVP). Without these specifications, “the Poisson equation” is too vague: infinitely many situations are possible, and no unique solution can be defined.

Deepening: Boundary Value Problem (BVP)

Before explaining what a BVP is, it is important to understand the difference between a classic ODE and a PDE.

❓ Differential Equations: ODE vs PDE

- An **ODE (Ordinary Differential Equation)** involves derivatives with respect to *one variable* (usually time t).
- A **PDE (Partial Differential Equation)** involves derivatives with respect to *several variables* (like space x , y , z , and maybe time).

Both need some extra information to be **solvable**. That “extra information” comes in two main flavors:

- **Initial conditions** (tell us the state at $t = 0$, then we can evolve forward in time).
- **Boundary conditions** (tell us what happens at the edges of the spatial domain, then we can solve inside).

📖 Boundary Value Problem (BVP)

A **Boundary Value Problem (BVP)** is a differential equation (ODE or PDE) with conditions prescribed **at the boundary of the domain**. Formally:

$$\begin{cases} Lu(x) = f(x), & x \in \Omega, \\ \text{Boundary conditions on } \partial\Omega. \end{cases}$$

- L : differential operator (e.g. $-u''$ in 1D Poisson).
- Ω : = the domain (like the interval $(0, 1)$).
- $\partial\Omega$: the boundary (here just the two points 0 and 1).

❓ Why Dirichlet Boundary Condition (Dirichlet BC)?

In this laboratory, we impose $u = 0$ at both ends. That corresponds physically to the ends of the bar are held at zero temperature. Other choices are possible (Neumann, Robin, etc.), but **Dirichlet** is the simplest starting case.

❓ Why we call it “Problem Definition”?

Because in numerical methods (and PDE theory) the workflow is always:

1. **Continuous problem definition**: PDE + domain + boundary conditions.
2. **Weak formulation**: rewrite it in an integral form suitable for analysis.
3. **Galerkin formulation**: restrict to a finite-dimensional space.
4. **Finite element formulation**: translate into linear algebra.
5. **Implementation**: write the solver in `deal.II`.

So “problem definition” is step 1 of this workflow.

Deepening: Dirichlet Boundary Condition

When we solve a PDE, we don’t just solve “inside” the domain Ω . We must also tell the solver **what happens at the edges** (the boundary $\partial\Omega$).

There are three classical types:

1. **Dirichlet** \rightarrow fix the **value** of the solution at the boundary.
2. **Neumann** \rightarrow fix the **derivative/flux** of the solution at the boundary.
3. **Robin** (mixed) \rightarrow fix a **combination** of value and derivative.

A **Dirichlet condition** prescribes directly the solution value:

$$u(x) = g(x) \quad \text{on } \partial\Omega \quad (22)$$

- If $g(x) = 0$, it’s called a **Homogeneous Dirichlet condition**.
- If $g(x) \neq 0$, it’s **Non-Homogeneous Dirichlet**.

In our case, we impose: $u(0) = u(1) = 0$. At the both ends of the bar, the temperature (or displacement, or potential) is forced to **zero**. That’s a **homogeneous Dirichlet boundary condition**.

Problem Definition: Poisson Equation in 1D

We are working on the interval (domain):

$$\Omega = (0, 1)$$

The **equation** is:

$$\begin{cases} -(\mu(x)u'(x))' = f(x), & x \in \Omega, \\ u(0) = u(1) = 0 \end{cases}$$

The unknown function is $u(x)$, for example the **temperature along a 1D bar**. The coefficient $\mu(x) = 1$ is the **diffusion coefficient** or **conductivity** of the material. If it varied, it would mean the material has regions that conduct more or less. Finally, the forcing term $f(x)$ is a piecewise function:

$$f(x) = \begin{cases} 0, & x \leq \frac{1}{8} \text{ or } x > \frac{1}{4}, \\ -1, & \frac{1}{8} < x \leq \frac{1}{4}. \end{cases}$$

There is a **negative source term** (a “sink” of heat, or a downward force density) only in the interval $\left(\frac{1}{8}, \frac{1}{4}\right]$. Outside, nothing happens ($f = 0$).

We use Dirichlet boundary conditions:

$$u(0) = u(1) = 0$$

- Physically: the ends of the bar are fixed to zero temperature.
- Mathematically: they “anchor” the solution and ensure uniqueness.

The PDE we wrote above (differential equation + boundary conditions) is called the **strong formulation**. It’s “*strong*” because it requires $u(x)$ to be smooth enough so that derivatives exist in the classical sense. Later, we’ll relax this condition with the **weak formulation**.

Deepening: Strong Formulation

The **Strong Formulation** of a PDE is the problem written:

- as a **differential equation** (derivatives explicitly present),
- together with **boundary conditions** (Dirichlet, Neumann, ...),
- requiring the solution $u(x)$ to be smooth enough for the derivatives to make sense pointwise.

So, for this laboratory, the strong formulation is exactly:

$$\begin{cases} -(\mu(x)u'(x))' = f(x), & x \in (0, 1), \\ u(0) = u(1) = 0, \end{cases}$$

With $\mu(x) = 1$, and our piecewise forcing $f(x)$.

❓ Why “strong”?

Because it requires “strong” regularity:

- The solution u must be differentiable enough so that $u'(x)$ and $(\mu u)'(x)$ exist as classical derivatives.
- We must be able to plug $u(x)$ **directly into the PDE** and check if it satisfies the equation *point by point*.

If f is discontinuous (as in our lab, where it jumps at $x = \frac{1}{8}$ and $x = \frac{1}{4}$), the strong formulation becomes tricky because classical derivatives may not exist everywhere. That’s why we move to the **weak formulation**: it relaxes smoothness requirements but still captures the PDE.

≡ Workflow in PDE analysis

1. **Strong formulation**: the PDE as we would write it in physics. Clear, but often too strict mathematically.
2. **Weak formulation**: rewrite as an integral equation using test functions and integration by parts. Because it is more flexible (allows solutions with less regularity, e.g. only square-integrable derivatives). This is the starting point for numerical methods.
3. **Galerkin / Finite Element formulation**: approximate the weak formulation in a finite-dimensional space, leading to a linear algebra system.

2.2.3 Weak formulation

We start from the **strong problem**:

$$\begin{cases} -u''(x) = f(x), & x \in (0, 1), \\ u(0) = u(1) = 0 \end{cases}$$

To obtain the weak formulation, we use test functions.

1. **Introduce test functions.** We don't try to force $u(x)$ to satisfy the equation pointwise. Instead, we “test” it against a set of functions $v(x)$ called **test functions**. They live in the same function space as u , with the same boundary conditions (so $v(0) = v(1) = 0$). This space is called:

$$V = H_0^1(0, 1) = \{v \in L^2(0, 1) \mid v' \in L^2(0, 1), v(0) = v(1) = 0\} \quad (23)$$

Deepening: Test function

A **Test Function** is not the solution itself, but an *arbitrary function* we use to “probe” whether the PDE is satisfied. Formally:

- A test function is usually called $v(x)$.
- It belongs to a certain function space V (often the same as the solution space).
- It must satisfy the **same boundary conditions** as the solution if those are homogeneous (like Dirichlet $u = 0$ on the boundary).

In our case:

$$V = H_0^1(0, 1) = \{v \in L^2(0, 1) \mid v' \in L^2(0, 1), v(0) = v(1) = 0\}$$

❓ Why do we need them?

Because instead of requiring the PDE to hold **pointwise** (strong), we require it to hold **on average against all test functions**:

$$a(u, v) = F(v) \quad \forall v \in V$$

This means:

- If the equality holds for all possible test functions v , then the solution u must encode the correct behavior of the PDE.
- Test functions are like “magnifying glasses”: by choosing different v , we check the equation in different ways.

Example 3: Analogy

Imagine we don't know the exact shape of a curve, but we can test it with different weights.

- Multiplying by $v(x)$ and integrating is like asking: “How does the error of my solution project onto this particular pattern $v(x)$?”
- If the error is orthogonal to *all* test functions, then the solution must be correct.

✂ In practice (Finite Elements)

Later, when we do the **Galerkin method**, we restrict test functions v to be combinations of **basis functions** (hat functions, polynomials, ...). So instead of “all possible test functions”, we only require the PDE to hold for a finite set of them. That's how we get a linear system $AU = f$.

🔗 Summary

A **test function** v is an arbitrary function from a suitable space (here $H_0^1(0,1)$). We multiply the PDE by v and integrate, to weaken the formulation. The condition “for all test functions” ensures the weak solution is equivalent to the strong one (if enough regularity). In finite elements, test functions become the basis functions of the discrete space.

2. **Multiply by a test function and integrate.** Multiply the PDE by $v(x)$ and integrate over $(0,1)$:

$$\int_0^1 (-u''(x)) \cdot v(x) \, dx = \int_0^1 f(x) \cdot v(x) \, dx \quad (24)$$

This is already “weaker”, because we're not asking the PDE to hold point-wise, only **in an averaged sense** against all test functions.

- 🔍 **Why multiply by a test function?** If we just write the residual of the PDE:

$$R(x) = -u''(x) - f(x) \quad (25)$$

Then the strong form requires $R(x) = 0$ **at every point**. That's too strict. Instead, we say:

- “We don't care if $R(x)$ is exactly 0 everywhere,
- We only care that $R(x)$ produces no effect when measured against any admissible test function $v(x)$ ”.

So, multiplying by $v(x)$ is like “projecting the error” onto a shape.

- If for every possible shape v , the projection vanishes, then the error must be zero.

- If the residual had any “component” left, some test function would catch it.

Great Analogy: Imagine we don’t know if a sound is silent. We pass it through every possible frequency filter (test functions). If all filters output 0, then the sound is really zero.

- ❓ **Why integrate?** Because multiplying alone just gives a function $R(x) \cdot v(x)$. To reduce it to a single **number** (a condition we can actually impose), we integrate over the domain:

$$\int_0^1 R(x) \cdot v(x) \, dx = 0$$

Integration turns the **pointwise condition** into a **global/average condition**. It’s like asking: “*what’s the net effect of the residual when weighted by $v(x)$ across the whole domain?*”. If this is 0 for all v , it forces the residual itself to be 0 in the weak sense.

Analogy: If we want to check if water in a pipe is really at 0 pressure, we don’t measure every molecule. We place sensors (test functions) that average pressure over regions. If all averages say 0, the whole pipe is at 0.

3. **Integration by parts.** We move one derivative away from u (so we don’t require u'' to exist, only u'):

$$\int_0^1 -u''(x) \cdot v(x) \, dx = \left[-u'(x) \cdot v(x) \right]_0^1 + \int_0^1 u'(x) \cdot v'(x) \, dx$$

The boundary term $\left[-u'(x)v(x) \right]_0^1$ vanishes, because $v(0) = v(1) = 0$. We are left with:

$$\int_0^1 u'(x) \cdot v'(x) \, dx = \int_0^1 f(x) \cdot v(x) \, dx \quad (26)$$

This is the **core weak formulation equation**.

- ❓ **Why do integration by parts?** Because, before this step, the integral contains the second derivative, $u''(x)$. That means the solution u must be **twice differentiable** (second derivative must exist in the classical sense). But in practice, with discontinuous sources or with finite element approximations, u'' might not exist everywhere.

Integration by parts transfers one derivative from u onto the test function v . That way, we only require u' to exist (so u just needs to be once differentiable) and v is smooth enough so that v' exists too. This relaxes the regularity (that’s the whole point of the weak formulation).

Example 4: Integration by parts - Analogy

Imagine we want to test if someone’s handwriting is smooth:

- Checking **second derivatives** is like asking for very

fine, strict smoothness (hard!).

- By integrating by parts, we only ask them to be “once smooth”, not “twice smooth”.
- That’s much easier to satisfy, and still captures the essence.

So in other words, integration by parts is necessary because it removes the second derivative on u , replacing it with first derivatives on both u and the test function. This reduces the regularity requirement, making the weak problem solvable in larger spaces (like H^1).

4. **Define bilinear and linear forms.** Writing integrals every time is messy. Mathematicians like to give names to these two operations:

- The **left-hand side** looks like a special product between u and v . So we call it a **bilinear form** (because it’s linear in u and in v separately):

$$a(u, v) := \int_0^1 u'(x) \cdot v'(x) \, dx \quad (27)$$

It is like the **energy inner product** between u and v .

- The **right-hand side** is an integral that only depends on v . So we call it a **linear functional** (linear in v):

$$F(v) := \int_0^1 f(x) \cdot v(x) \, dx \quad (28)$$

It is like the **effect of the forcing** f measured against v .

🔍 **Why do this?** Because once we define these two objects, the weak problem looks **super compact**:

$$\text{Find } u \in V \text{ such that } a(u, v) = F(v) \quad \forall v \in V \quad (29)$$

That’s just a clean way of saying:

$$\int_0^1 u'(x) \cdot v'(x) \, dx = \int_0^1 f(x) \cdot v(x) \, dx \quad \forall v \in V$$

In simple terms, the weak problem says: “Find u such that, when tested against all possible v , the internal energy balance $a(u, v)$ equals the external forcing $F(v)$ ”.

2.2.4 Galerkin formulation

Now we move from the **weak formulation** (still infinite-dimensional) to the **Galerkin formulation**, which is the bridge to something a computer can handle.

💡 Galerkin idea

We have a PDE that is too difficult to solve point by point. Therefore, we obtain a weaker form that is more flexible but still **infinite-dimensional** (function space). We use the **Galerkin method**, which is a general approach for **approximating weak problems in finite-dimensional subspaces**.

Take the weak formulation (29, page 35):

$$a(u, v) = F(v) \quad \forall v \in V$$

Restrict to a **finite-dimensional subspace** $V_h \subset V$, or $V_h \subset H_0^1$:

$$a(u_h, v_h) = F(v_h) \quad \forall v_h \in V_h \quad (30)$$

So, instead of “all possible functions in V ”, we only allow functions in V_h . And instead of infinitely many test functions, we only check the condition for test functions in V_h . So the **Galerkin formulation** is:

$$\text{Find } u_h \in V_h \text{ such that } a(u_h, v_h) = F(v_h) \quad \forall v_h \in V_h \quad (31)$$

📖 In theory (mathematical meaning)

This is a **projection**:

- The true solution u might not be in V_h .
- But we find the **closest approximation** u_h in that space, such that the **residual is orthogonal to V_h** .
- That’s why Galerkin works: the error $u - u_h$ is “perpendicular” to all test functions in V_h .

When we require the error $e = u - u_h$ to be orthogonal to the approximation space V_h :

$$a(e, v_h) = 0 \quad \forall v_h \in V_h$$

We are saying: “*the error has no component along any direction inside V_h* ”. That’s the analogue of the vector case, the shortest path from a point to a line is along the perpendicular. So Galerkin says: *take the approximation u_h such that the error is perpendicular to the chosen subspace*.

So in theory, Galerkin is just **orthogonal projection** of the weak problem onto a finite subspace.

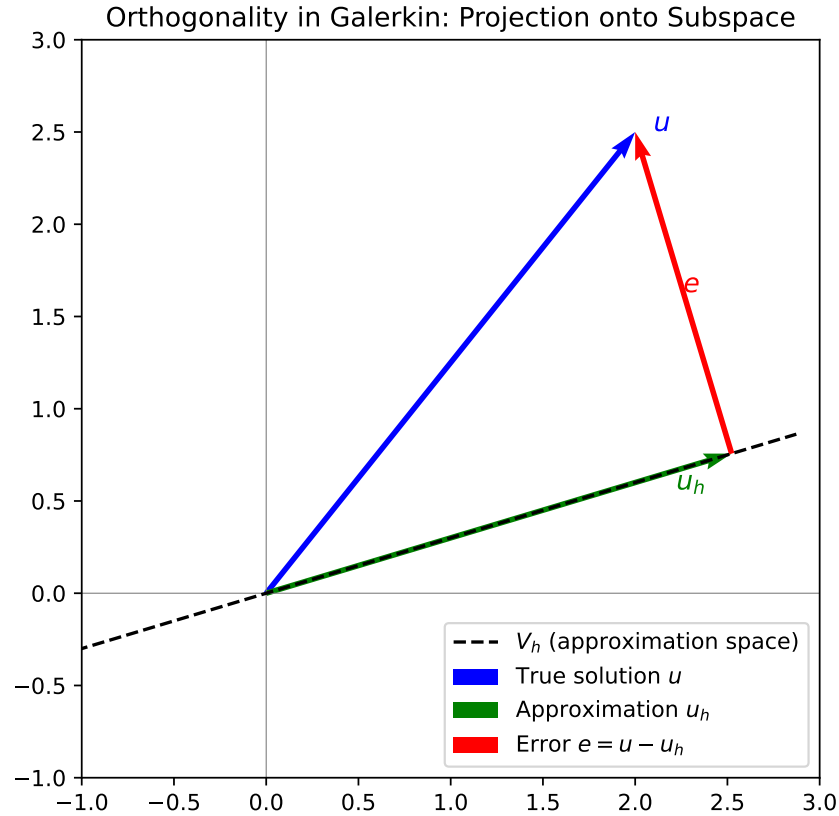


Figure 5: Orthogonality in Galerkin: Projection onto Subspace.

- The dashed line is our **approximation space** V_h (all the functions we can represent).
- The **blue vector** is the true solution u (not in V_h).
- The **green vector** is the Galerkin approximation u_h , which lies in V_h .
- The **red vector** is the error $e = u - u_h$.

Notice: the red error is **perpendicular** to the line V_h . That's exactly what "orthogonality of the residual" means; Galerkin forces the error to be perpendicular to our chosen approximation space, ensuring the *closest possible* approximation.

Remark 1: Orthogonality**✿ Orthogonality in high school math**

In Euclidean space $(\mathbb{R}^2, \mathbb{R}^3)$, two vectors are **Orthogonal** if their dot product is zero:

$$x \cdot y = 0 \quad (32)$$

That means they are “perpendicular”. Here, orthogonality means *the shortest distance from a point to a line is the perpendicular*.

❓ Perpendicular? Take two vectors in the plane:

$$u = (u_1, u_2), \quad v = (v_1, v_2)$$

Their dot product is:

$$u \cdot v = u_1 v_1 + u_2 v_2$$

Now, recall the formula with the angle θ between them:

$$u \cdot v = \|u\| \|v\| \cos(\theta)$$

So:

- If $u \cdot v > 0$, angle $< 90^\circ$.
- If $u \cdot v < 0$, angle $> 90^\circ$.
- If $u \cdot v = 0$, then $\cos \theta = 0$, then $\theta = 90^\circ$.

That’s exactly why “orthogonal” means “perpendicular”: the inner product vanishes when vectors meet at a right angle.

X¹ Orthogonality in function spaces

Now, when we move from vectors to **functions**, the dot product is replaced by an **inner product**. For example, in $L^2(0, 1)$ (square-integrable functions), the inner product is:

$$(u, v) = \int_0^1 u(x) \cdot v(x) \, dx$$

So two functions u, v are **Orthogonal** if:

$$\int_0^1 u(x) \cdot v(x) \, dx = 0$$

This is the function-space version of “perpendicular”. Here, orthogonality means *the Galerkin solution u_h is the closest function in V_h to the true solution u , with distance measured in the PDE’s energy norm*.

That's the **Galerkin formulation**.

- The exact solution u lives in V (infinite world).
- The approximate solution u_h lives in V_h (finite world).
- We require the weak form to hold for all test functions in V_h .

🔍 Choosing V_h

The **true solution** lives in an *infinite-dimensional world* (all possible admissible functions). We cannot compute in infinity. So we **pick a smaller world**, a *finite-dimensional subspace* V_h . That smaller world is where Galerkin will search for the approximate solution u_h .

🔍 **What is V_h really?** Think of V_h as our **toolbox of functions**. It's the set of shapes that our approximation is based on. For example:

- If we choose **straight lines** between mesh points, V_h are piecewise linear functions.
- If we choose **parabolas** on each mesh cell, V_h are piecewise quadratic functions.
- If we choose **sines and cosines**, V_h are trigonometric polynomials (spectral method).

In our laboratory, V_h is always:

$$V_h = \{\text{functions that are continuous and piecewise polynomials on a mesh,} \\ \text{with } u = 0 \text{ at the boundary}\}$$

🔍 **Why do we care about which V_h ?** Because:

- A **bad choice** of V_h : we cannot approximate the solution well.
- A **good choice** of V_h : as we refine (smaller mesh, higher polynomial degree), the approximation converges to the true solution.

So the whole art of finite element is: *how do we design V_h so that it's expressive enough but still computable?*

- Domain: $(0, 1)$.
- Mesh: cut into N intervals.
- (V_h) : functions that are continuous, zero at the ends, and linear on each small interval.
- Approximation space:

$$V_h = \{v \in C^0([0, 1]) : v|_K \in \mathbb{P}_1, \forall K \in \mathcal{T}_h, v(0) = v(1) = 0\}$$

Deepening: Where does V_h come from?

From the previous sections, we had the following:

Find $u \in V = H_0^1(0, 1)$ such that $a(u, v) = F(v) \quad \forall v \in V$

So the exact solution lives in:

$$V = H_0^1(0, 1) = \{v \in L^2(0, 1) : v' \in L^2(0, 1), v(0) = v(1) = 0\}$$

This space is **infinite-dimensional** (all functions with square-integrable derivative, vanishing at endpoints).

We want a **finite-dimensional** subspace $V_h \subset V$. So we must impose two things: (1) **boundary condition** (keep $v(0) = v(1) = 0$, so that $V_h \subset H_0^1$), (2) **finite dimension** (instead of “all functions”, choose a restricted family of functions easy to handle).

1. **Choose a mesh.** Split $[0, 1]$ into small subintervals:

$$\mathcal{T}_h = \{K_1, K_2, \dots, K_N\}, \quad K_i = [x_{i-1}, x_i]$$

Here $h = \max_i |K_i|$ is the **mesh size**.

2. **Choose a polynomial degree.** On each element K , we allow only polynomials of degree $\leq r$.
 - If $r = 1$: linear functions on each element.
 - If $r = 2$: quadratics.
 - And so on.

This is written as $v|_K \in \mathbb{P}_r$.

3. **Impose continuity.** Finite element functions are not just piecewise polynomials: they must be **globally continuous** (otherwise they wouldn't belong to H_0^1). So we require $v \in C^0([0, 1])$.
4. **Impose boundary conditions.** Finally, we enforce $v(0) = v(1) = 0$ to respect the homogeneous Dirichlet boundary conditions.

So the space is:

$$V_h = \{v \in C^0([0, 1]) : v|_K \in \mathbb{P}_r, \forall K \in \mathcal{T}_h, v(0) = v(1) = 0\}$$

If $r = 1$, that's piecewise linear FE functions. If $r = 2$, piecewise quadratic, and so on. In summary, we obtain the formula for V_h by restricting the infinite weak space $V = H_0^1$ in 4 steps: first, we *mesh* the domain. Then, on each mesh cell, we allow only low-degree polynomials. Next, we glue them together with continuity. Finally, we impose boundary conditions. That's exactly the standard definition of a finite element space.

2.2.5 Finite Element formulation

We already derived:

- **Weak formulation** (page 32), find $u \in V$ such that:

$$a(u, v) = F(v) \quad \forall v \in V$$

Where:

- $V = H_0^1(\Omega)$
- $a(u, v) = \int_0^1 u'(x) v'(x) \, dx$
- $F(v) = \int_0^1 f(x) v(x) \, dx$

- **Galerkin formulation** (page 36), restrict to a finite-dimensional space $V_h \subset V$:

$$a(u_h, v_h) = F(v_h) \quad \forall v_h \in V_h$$

So the question is: **how to choose V_h** ?

2.2.5.1 Constructing the finite-element space V_h

We want to approximate the infinite-dimensional space. The weak formulation lives in $V = H_0^1(\Omega)$, which is infinite-dimensional. To make it computable, Galerkin requires a **finite-dimensional subspace** $V_h \subset V$. But how do we describe V_h ? We need a concrete way.

Mesh gives structure. A **Mesh** is a way to divide our domain Ω (here $(0, 1)$) into **smaller, simple pieces** called **elements**.

- In 1D: elements are **intervals**.

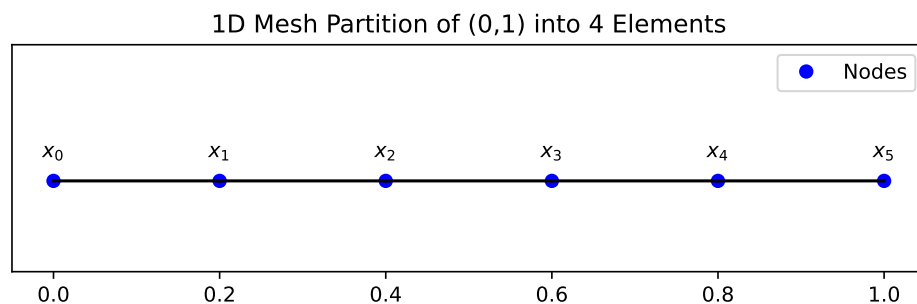


Figure 6: An example of a 1D mesh for $(0, 1)$, partitioned into 4 elements (so 5 internal nodes plus the two boundaries). Each segment is an **element**, and the blue dots are the **nodes** x_0, x_1, \dots, x_5 .

- In 2D: elements are usually **triangles** or **quadrilaterals**.

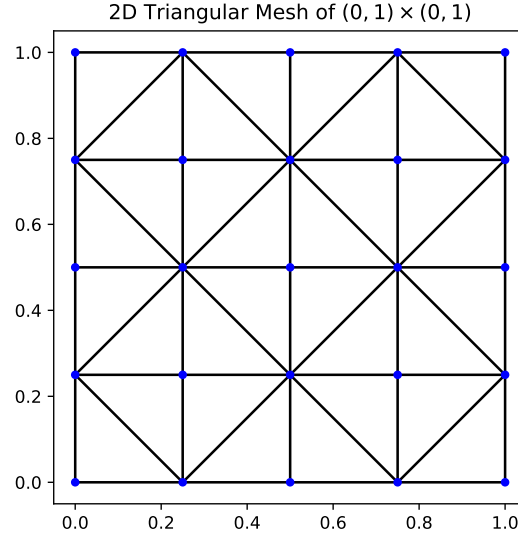


Figure 7: An example of a 2D triangular mesh of the unit square $(0, 1) \times (0, 1)$. The blue dots are the **nodes**. The black lines are the **edges of the triangular elements**. Each small triangle is one **finite element**.

- In 3D: elements are **tetrahedra** or **hexahedra (cubes)**.

3D Hexahedral Mesh of the Unit Cube $(0, 1)^3$

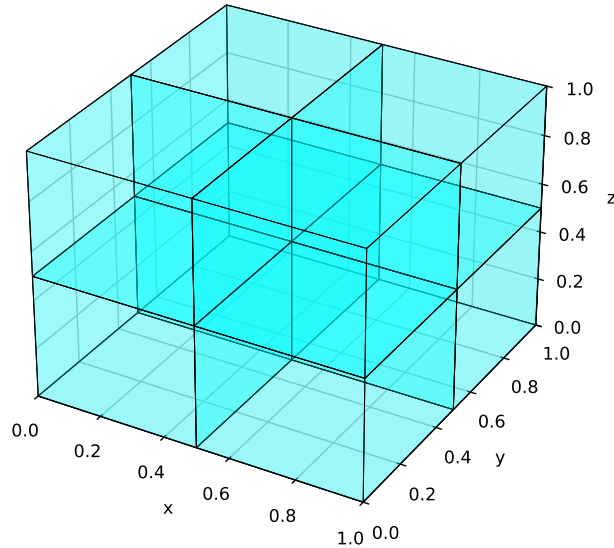


Figure 8: An example of a 3D mesh of the unit cube $(0, 1)^3$, divided into smaller hexahedral elements (little cubes). Each transparent cyan block is one **element**. The black lines are the **edges of the mesh**.

These elements are “building blocks” on which we define our basis functions.

Formally, a **Mesh** (or triangulation) \mathcal{T}_h of a domain Ω is a collection of elements K such that:

1. $\bigcup_{K \in \mathcal{T}_h} K = \Omega$ (the elements cover the whole domain).
2. Two elements only touch on their boundary; they don't overlap inside.
3. Each element has a “small” size related to the **mesh parameter** h , typically the maximum diameter of all elements:

$$h = \max_{K \in \mathcal{T}_h} \text{diam}(K)$$

In 1D, where $K = [x_{i-1}, x_i]$, its **diameter** is just its length:

$$\text{diam}(K) = |x_i - x_{i-1}|$$

In 2D, if K is a triangle, its diameter is the length of the **longest edge**.

In 3D, if K is a tetrahedron, its diameter is the longest distance between two of its vertices. So, $\text{diam}(K)$ gives a **size measure of that element**.

It is called a “mesh” because, when viewed in two or three dimensions, its elements form a grid or net, much like the mesh of a fishing net or the pixels of an image.

In short, a **mesh is the discretization of the geometry of our domain into small, simple elements**. It is the foundation of finite elements. Without a mesh, we wouldn't know *where* to place our basis functions.

❓ So, what exactly is a mesh parameter?

We define the **Mesh Parameter** h (or **mesh size**) as:

$$h = \max_{K \in \mathcal{T}_h} \text{diam}(K) \tag{33}$$

This is a **global measure**: it takes the largest element in the mesh. If the mesh is uniform (all elements equal size), then h is just the common element size. If the mesh is non-uniform (some small, some large elements), then h tells us the size of the **worst (largest) element**.

❓ Why does the Mesh Parameter matter?

- **Accuracy**: Smaller $h \rightarrow$ more elements \rightarrow better approximation of the true solution.
- **Computational cost**: Smaller $h \rightarrow$ bigger system of equations \rightarrow more memory and CPU time.
- **Convergence theory**: Error estimates are usually written like:

$$\|u - u_h\| \leq Ch^p$$

Where p depends on the polynomial degree r . So the quality of the mesh directly controls how fast we converge to the true solution.

For example, suppose $\Omega = (0, 1)$, partitioned into $N + 1$ intervals. Each interval has length $h = \frac{1}{N+1}$. If $N = 9$, then $h = 0.1$. If $N = 99$, then $h = 0.01$, so the mesh is 10 times finer.

✂ 1D Poisson Problem

Our laboratory has the domain $\Omega = (0, 1)$. We take a number of mesh elements of $N + 1 = 20$. Then we have nodes:

$$x_0 = 0, x_1 = h, x_2 = 2h, \dots, x_{20} = 1$$

With $h = \frac{1}{N+1} = \frac{1}{20}$. Each element is $K_i = [x_{i-1}, x_i]$. So the mesh is simply the collection:

$$\mathcal{T}_h = \{[0, h], [h, 2h], [2h, 3h], \dots, [1-h, 1]\}$$

This breaks the continuous problem into “small, simple pieces”. So the domain is now “atomic pieces” K_i . On each element we can define **local polynomials**.

❓ Why do we approximate with polynomials on each piece?

There are four reasons:

- **Because polynomials are simple and computable.** Polynomials have **explicit formulas** for derivatives and integrals. In FEM we need to compute integrals like:

$$\int_{K_i} u'_h(x) \cdot v'_h(x) \, dx$$

And with polynomials these are straightforward.

- **Because polynomials are good local approximators.** By Taylor’s theorem, any smooth function can be approximated locally by a polynomial. On a small element K_i , the solution $u(x)$ doesn’t change much, so a low-degree polynomial (linear, quadratic) already gives a good fit. The smaller the element (smaller h), the better a polynomial of fixed degree approximates the true solution.
- **Because they “glue together” nicely.** If we define one polynomial per element, we can impose **continuity** at shared nodes. This gives us **global continuous functions** built from local building blocks. With polynomials, enforcing continuity at nodes is natural (hat functions are 1 at one node, 0 at others).
- **Because they give sparse algebraic systems.** Each polynomial (hat function) has **local support**: it is nonzero only on 2 neighboring elements (in 1D, for $r = 1$). This locality produces a **sparse stiffness matrix** (tridiagonal in 1D, banded in higher dimensions). Sparse systems are efficient to store and solve, essential for HPC.

Example 5: Physical analogy

Imagine we cut a bent stick (the real solution) into small pieces:

- On each piece, we approximate it with a simple ruler (straight line is a linear polynomial).
- The smaller the pieces, the more the rulers together resemble the original curve.
- If we want higher accuracy per piece, we can replace the ruler with a curved template (quadratic, cubic polynomial).

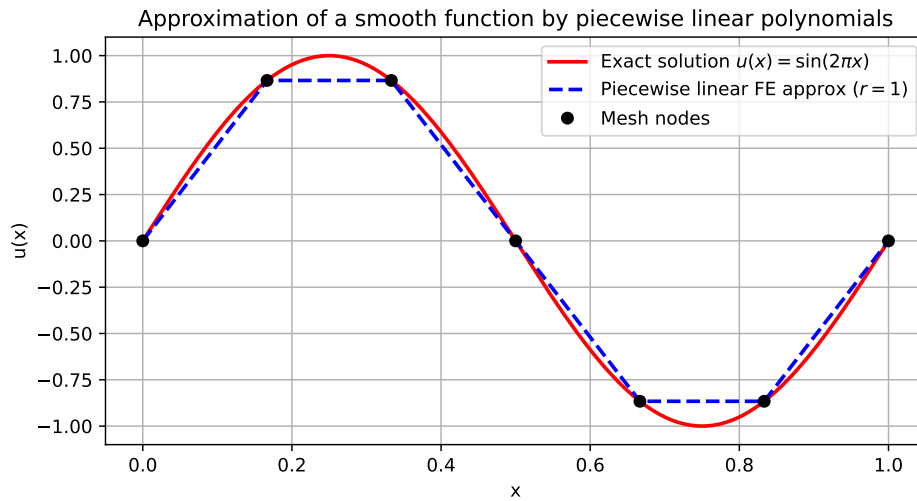


Figure 9: Graphical 1D example showing how a smooth curve can be approximated by piecewise polynomials of degree one (straight lines) on the mesh.

- The **red curve** is the exact function $u(x) = \sin(2\pi x)$.
- The **blue dashed line** is the finite element approximation with $r = 1$: piecewise linear segments between mesh nodes.
- The **black dots** are the mesh nodes, where the FE solution matches the exact one.

As we refine the mesh (N larger, h smaller), the blue curve hugs the red one more closely.

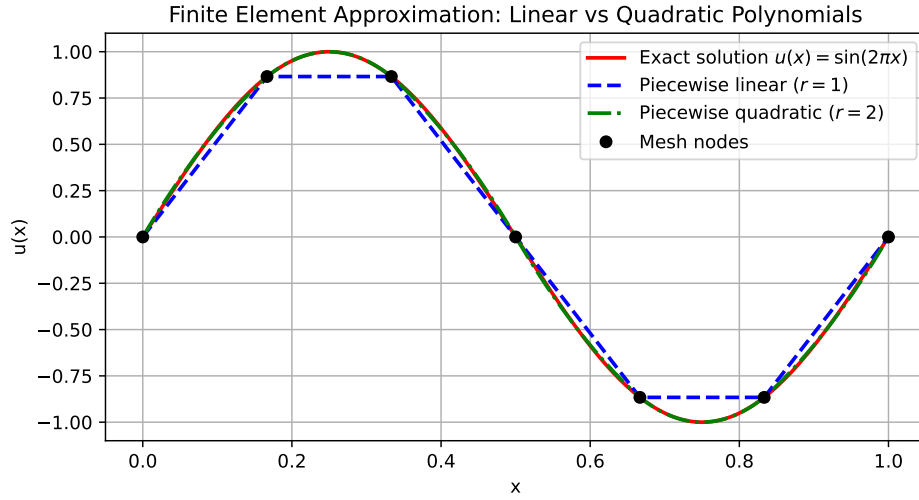


Figure 10: Graphical 1D example showing how a smooth curve can be approximated by piecewise polynomials of degree one (straight lines) on the mesh.

- The **red curve** is the exact function $u(x) = \sin(2\pi x)$.
- The **blue dashed curve** is the piecewise linear approximation ($r = 1$): straight line segments.
- The **green dash-dot curve** is the piecewise quadratic approximation ($r = 2$): parabolas on each element.

We can see that the quadratic elements hug the sine curve much better, especially between the nodes. However, despite the increased precision, the system size, cost, and DoFs (Degrees of Freedom, or the number of equations to be solved) all increase.

Define piecewise polynomials

For a given polynomial degree r :

$$X_h^r(\Omega) = \{v_h \in C^0([0, 1]) : v_h|_{K_i} \in \mathbb{P}_r, \forall i\} \quad (34)$$

Meaning:

- $v_h \in C^0([0, 1])$: every function in $X_h^r(\Omega)$ must be **continuous** across the whole domain. No “jumps” are allowed between one element and the next. So when we glue local polynomials together, they must match at the common endpoints (nodes).

Reason: the weak formulation requires $u_h \in H^1(\Omega)$, and H^1 functions must be continuous.

- $v_h|_{K_i} \in \mathbb{P}_r$: where $|_{K_i}$ means “restricted to the element K_i ”. On each mesh element $K_i = [x_{i-1}, x_i]$, the function is a polynomial of degree $\leq r$. For example:

– If $r = 1$, on each element K_i , $v_h(x) = a + bx$ (a straight line).

– If $r = 2$, then $v_h(x) = a + bx + cx^2$ (a parabola).

So globally, v_h is “piecewise polynomial”: it can change slope or curvature from one element to the next, but it remains continuous.

- $\forall i$: this condition applies **on every element of the mesh**. We cannot have a polynomial on some elements and something else on others, the rule is uniform across the mesh.
- Restricted to each element K_i , it is a polynomial of degree at most r .
- For $r = 1$, that means **straight lines on each interval**.

📌 Impose boundary conditions

From the laboratory problem:

$$u(0) = 0, \quad u(1) = 0$$

The solution must vanish at the endpoints of the domain. However, the continuous weak space already encodes this. From the weak formulation:

$$\begin{aligned} u \in V &= H_0^1(\Omega) \\ &= \{v \in H^1(\Omega) : v(0) = v(1) = 0\} \end{aligned}$$

So in the continuous problem, we don’t enforce the boundary conditions by extra conditions; they are **baked into the function space** itself. So far, we constructed:

$$X_h^r(\Omega) = \{v_h \in C^0([0, 1]) : v_h|_{K_i} \in \mathbb{P}_r\}$$

But these functions don’t necessarily vanish at the boundary. To fix this, we take:

$$V_h = X_h^r(\Omega) \cap H_0^1(\Omega) \tag{35}$$

Meaning:

- Functions must belong to $X_h^r(\Omega)$ (continuous, piecewise polynomials).
- **And** they must vanish at the boundary, just like in $H_0^1(\Omega)$.

In other words, restrict the finite element space so that all functions automatically vanish at the boundary. In practice, this removes the boundary basis functions and leaves only the internal degrees of freedom.

☐ Choose a basis (Lagrangian “hat” functions)

Now we need a basis of V_h . A **Basis** is like a set of “Lego bricks” from which we can build any object in a space. The basis gives us a **small finite set of functions** from which all others in the space can be built. From the finite element space V_h , we can find N **basis functions** $\varphi_1, \dots, \varphi_N$ such that:

$$u_h(x) = \sum_{j=1}^N U_j \cdot \varphi_j(x) \quad \forall u_h \in V_h \quad (36)$$

Where the coefficients U_j are just numbers and the φ_j are the “bricks” (basis functions). In 1D, for $r = 1$, these φ_j are the hat functions. Without a basis, the space is just an abstract definition.

Once we expand the unknown u_h in this basis, the PDE problem reduces to solving for the coefficients U_j . This is how we go from an infinite-dimensional PDE to a finite-dimensional **linear system** $AU = f$ (**from functions to algebra**).

❓ **Why choose a Lagrangian basis?** There are many possible bases, but the **Lagrangian nodal basis** is the most natural for FEM. Its key properties:

1. **Interpolation property.** Each basis function φ_j satisfies:

$$\varphi_j(x_i) = \delta_{ij}$$

It equals **1 at its own node** and **0 at all others**. This makes coefficients U_j directly equal to the **nodal values** of the solution:

$$u_h(x_i) = U_i$$

So the unknowns are literally “the solution at the mesh nodes”.

2. **Local support.** Each φ_j is nonzero only on a small neighborhood of nodes (two elements in 1D). This leads to a **sparse matrix**, which is essential for computational efficiency.
3. **Intuitive geometry.** The basis functions look like little “hats” (for $r = 1$) or “arches” (for $r = 2$), easy to visualize and implement. In higher dimensions, they become pyramids (2D triangles) or tents (3D tetrahedra).
4. **Implementation in FEM libraries.** Packages like `deal.II`, `FEniCS`, `gmsh`, etc. all rely on nodal (Lagrangian) bases as the standard choice. They are the simplest to code, especially for assembling element matrices and evaluating values at quadrature points.

❓ **Could we use another basis?** Yes, hierarchical bases, modal bases (e.g., Legendre polynomials), spectral methods (global polynomials). **But** those are more complex, less intuitive, and not the standard starting point. So for our laboratory, the goal is clarity and efficiency, that’s why we stick to **Lagrangian hat functions**.

Summary

We successfully built the finite element space V_h . Here is a list of the steps we took:

1. **Start from the weak space** (page 32). The PDE requires solutions in:

$$V = H_0^1(\Omega)$$

i.e. continuous functions with square-integrable derivatives, vanishing on the boundary. This space is infinite-dimensional.

2. **Partition the domain (mesh)** (page 41). Divide $\Omega = (0, 1)$ into $N + 1$ small intervals:

$$\mathcal{T}_h = \{K_i = [x_{i-1}, x_i] : i = 1, \dots, N + 1\}, \quad h = \frac{1}{N + 1}$$

3. **Define local polynomial shape** (page 44). On each element K_i , we decide that admissible functions are **polynomials of degree r** :

$$v_h|_{K_i} \in \mathbb{P}_r$$

Where $r = 1$ are straight lines, $r = 2$ are parabolas, etc.

4. **Enforce continuity** (page 46). Require that these piecewise polynomials join continuously across elements:

$$X_h^r(\Omega) = \{v_h \in C^0([0, 1]) : v_h|_{K_i} \in \mathbb{P}_r \ \forall K_i\}$$

5. **Impose boundary conditions** (page 47). Since the PDE requires $u(0) = u(1) = 0$, we restrict to functions that vanish at the endpoints:

$$V_h = X_h^r(\Omega) \cap H_0^1(\Omega)$$

6. **Choose a basis** (page 48). Pick a convenient set of basis functions for V_h .

- Standard choice: **Lagrangian nodal basis** (hat functions).
- They are 1 at one node, 0 at all others, and supported only on neighboring elements.

Thus, any approximate solution is written as:

$$u_h(x) = \sum_{j=1}^{N_h} U_j \cdot \varphi_j(x)$$

With unknown coefficients U_j (the degrees of freedom).

2.2.5.2 From V_h to the Discrete Problem

We want:

$$a(u_h, v_h) = F(v_h) \quad \forall v_h \in V_h$$

With:

$$\bullet \quad a(u, v) = \int_0^1 \mu(x) \cdot u'(x) \cdot v'(x) \, dx$$

$$\bullet \quad F(v) = \int_0^1 f(x) \cdot v(x) \, dx$$

Pick a basis $\{\varphi_j\}_{j=1}^{N_h}$ of V_h . Write the unknown as:

$$u_h(x) = \sum_{j=1}^{N_h} U_j \varphi_j(x) \quad (37)$$

Where:

- U_j are the unknown coefficients (nodal values in the Lagrangian case).
- φ_j are the known basis functions (hat functions for $r = 1$).

Now, we **plug into the weak form**. Take $v_h = \varphi_i$, one basis function. Then:

$$a(u_h, \varphi_i) = F(\varphi_i)$$

Now compute the left-hand side:

$$a(u_h, \varphi_i) = \int_0^1 \mu(x) \cdot \left(\sum_{j=1}^{N_h} U_j \cdot \varphi_j'(x) \right) \cdot \varphi_i'(x) \, dx$$

Since the integral is linear:

$$a(u_h, \varphi_i) = \sum_{j=1}^{N_h} U_j \cdot \int_0^1 \mu(x) \cdot \varphi_j'(x) \cdot \varphi_i'(x) \, dx$$

We now **define**:

$$A_{ij} = \int_0^1 \mu(x) \cdot \varphi_j'(x) \cdot \varphi_i'(x) \, dx \quad (38)$$

$$f_i = \int_0^1 f(x) \cdot \varphi_i(x) \, dx \quad (39)$$

So the weak form equation becomes:

$$\sum_{j=1}^{N_h} A_{ij} \cdot U_j = f_i, \quad i = 1, \dots, N_h \quad (40)$$

Matrix form

That's exactly the linear system:

$$AU = f \quad (41)$$

Where:

- $A = (A_{ij})$ is the **Stiffness Matrix**.
- ❓ **What is the Stiffness Matrix?** In the finite element method, when we discretize a PDE like the Poisson problem, the weak form introduces integrals of derivatives of the basis functions. These integrals become the **entries of the stiffness matrix** (see above):

$$A_{ij} = \int_{\Omega} \mu(x) \cdot \nabla \varphi_j(x) \cdot \nabla \varphi_i(x) \, dx \quad (42)$$

Where A is called the **Stiffness Matrix**. It is **symmetric positive definite (SPD)** if the bilinear form is symmetric and coercive. Its size is $N_h \times N_h$, where N_h is the number of degrees of freedom (basis functions).

❓ **Why is it called stiffness?** The name comes from **structural mechanics**. Originally, FEM was used to model elastic bars, beams, membranes. The relation “force = stiffness \times displacement” in elasticity correspond to the matrix equation:

$$Ku = f$$

Where:

- u are displacement at nodes;
- f are nodal forces;
- K is the stiffness matrix, encoding how “resistant” (stiff) the structure is to deformation.

Even though we now use FEM for general PDEs, the name stuck.

Composition of the Stiffness Matrix

- **Diagonal entries** A_{ii} : measure how strongly a degree of freedom (a node) resists deformation, i.e. the “self-stiffness”.
- **Off-diagonal entries** A_{ij} : measure the coupling between neighboring basis functions (nodes). If two nodes share an element, the integral is nonzero; otherwise, it's zero.

Thus, the stiffness matrix is:

- **Sparse**: only nearby nodes interact.
- **Structured**: for 1D linear elements, it is **tridiagonal**.
- **Conditioning**: its conditions number grows like h^{-2} (with mesh size h).

≡ Key properties (why it's nice computationally)

- **Symmetric:** $A_{ij} = A_{ji}$
- **Positive definite** (for $\mu > 0$): $U^T A U > 0$ for all nonzero vectors U .
- **Sparse/Local:** φ_i overlaps only with a few neighbors, so only a few nonzeros per row.
- **Conditioning** scales with mesh size (roughly $\kappa(A) \sim h^{-2}$ in 1D), motivating preconditioners.

In summary, the stiffness matrix shows how the domain resists changes.

- $U = (U_1, \dots, U_{N_h})^T$ are the **unknown nodal values**.

🔍 **How U is defined.** We write the approximate solution in the finite element space V_h :

$$u_h(x) = \sum_{j=1}^{N_h} U_j \cdot \varphi_j(x)$$

Where:

- $\{\varphi_j\}_{j=1}^{N_h}$ are the basis functions of V_h .
- U_j are scalars: **degrees of freedom (DoFs)**.

Thus, $U = (U_1, U_2, \dots, U_{N_h})^T$.

≡ **Nodal values.** Because we chose the **Lagrangian (nodal) basis**, each φ_j has the property:

$$\varphi_j(x_i) = \delta_{ij}$$

That means:

$$U_j = u_h(x_j)$$

i.e. the unknown coefficients **are literally the approximate solution at the mesh nodes** (internal nodes only, since boundary ones are fixed to zero).

✂ Physical interpretation

- In **structural mechanics:** U are nodal **displacements**.
- In **heat problems:** U are nodal **temperatures**.
- In **Poisson problems** (our lab): U are just nodal **values of the solution**.

In other words, solving $AU = f$ gives us the “best” nodal approximation of the exact PDE solution.

- $f = (f_1, \dots, f_{N_h})^T$ is the **load vector**.

≡ **Definition of the load vector.** For each basis function φ_i , the load vector entry is:

$$f_i = F(\varphi_i) = \int_{\Omega} f(x) \cdot \varphi_i(x) \, dx$$

So the **load vector** f collects the effect of the forcing term $f(x)$ applied to the PDE, projected onto the finite element basis.

❓ **Why it appears.** The weak formulation was:

$$a(u_h, v_h) = F(v_h), \quad \forall v_h \in V_h$$

With:

$$F(v_h) = \int_{\Omega} f(x) v_h(x) dx$$

When we take $v_h = \varphi_i$, we get exactly f_i . Thus, the right-hand side of the system $AU = f$ is the vector with entries f_i .

✂ **Physical meaning**

- In mechanics: f represents **external forces** applied at the nodes.
- In heat transfer: f represents **heat sources** distributed in the domain.
- In general PDEs: it's how the **forcing term** $f(x)$ excites the system.

So just like A encodes “resistance”, f encodes “applied load”.

📖 **Local-to-global composition.** Just like the stiffness matrix, the load vector is built **element by element**:

- On each element K , compute

$$f_{\alpha}^{(K)} = \int_K f(x) \cdot N_{\alpha}(x) dx$$

Where N_{α} are local shape functions.

- Then assemble into the global vector f .

In summary, the load vector f is the FEM representation of the source term $f(x)$. Each entry f_i measures how much the source excites the basis function φ_i . Physically, it is the “external input” applied to the system.

Now we have a **discrete, well-posed algebraic system**. This is exactly what FEM libraries (like `deal.II`) are built to assemble and solve. The next step is coding.

2.2.6 Implementation in deal.II

2.2.6.1 Install & Setup

At the Politecnico di Milano, professors suggest installing `mk`, a project that provides environment modules for scientific computing libraries and packages with portable x86-64 Linux libraries. Developed at the MOX Center at the Politecnico di Milano, it is based on `Lmod`, a tool for managing user environments dynamically. To install it, we can simply follow the instructions in the [README on GitHub](#).

There are other common ways to install `deal.II`. Follow this guide to install `deal.II` (either natively or via Docker, etc.):

Getting `deal.II`



↓ CMakeLists.txt



Now we move to the project skeleton. We assume a structure of this type:

```
1 lab01/
2   CMakeLists.txt
3   src/
4     lab-01.cpp
5     Poisson1D.cpp
6     Poisson1D.hpp
```

The `CMakeLists.txt` file:

```
1 # Minimum CMake version required.
2 cmake_minimum_required(VERSION 3.12)
3 # Project name and language.
4 project(01_poisson_1d LANGUAGES CXX)
5
6 # Set C++ standard to C++11.
7 set(CMAKE_CXX_STANDARD 11)
8 # Require C++11 standard.
9 set(CMAKE_CXX_STANDARD_REQUIRED "ON")
10
11 # Set default build type to Release.
12 if(NOT CMAKE_BUILD_TYPE OR "${CMAKE_BUILD_TYPE}" STREQUAL "")
13     set(CMAKE_BUILD_TYPE "Release" CACHE STRING "" FORCE)
14 endif()
15 message(STATUS)
16 message(STATUS "Build type: ${CMAKE_BUILD_TYPE}")
17 message(STATUS)
18 if("${CMAKE_BUILD_TYPE}" STREQUAL "Debug")
19     add_definitions(-DBUILD_TYPE_DEBUG)
20 endif()
21
22 # Locate MPI compiler.
23 find_package(MPI REQUIRED)
24 set(CMAKE_CXX_COMPILER "${MPI_CXX_COMPILER}")
25
26 # Locate Boost.
27 find_package(Boost 1.72.0 REQUIRED
28     COMPONENTS filesystem iostreams serialization
29     HINTS ${BOOST_DIR} $ENV{BOOST_DIR} $ENV{mkBoostPrefix})
```

```

30 message(STATUS "Using the Boost-`${Boost_VERSION}` configuration
    found at `${Boost_DIR}`")
31 message(STATUS)
32 include_directories(`${Boost_INCLUDE_DIRS}`)
33
34 # Locate deal.II and initialize its variables.
35 find_package(deal.II 9.3.1 REQUIRED
36     HINTS `${DEAL_II_DIR}` $ENV{DEAL_II_DIR} $ENV{mkDealiiPrefix}
    })
37 deal_ii_initialize_cached_variables()
38
39 # Add useful compiler flags.
40 set(CMAKE_CXX_FLAGS "${CMAKE_CXX_FLAGS} -Wfloat-conversion -
    Wmissing-braces -Wnon-virtual-dtor")
41
42 # Add the executable and link it to deal.II.
43 add_executable(lab-01 lab-01.cpp Poisson1D.cpp Poisson1D.hpp)
44 deal_ii_setup_target(lab-01)

```

Where:

- Build type (Release or Debug):

```

1 # Set default build type to Release.
2 if(NOT CMAKE_BUILD_TYPE OR "${CMAKE_BUILD_TYPE}" STREQUAL "")
3     set(CMAKE_BUILD_TYPE "Release" CACHE STRING "" FORCE)
4 endif()
5 message(STATUS)
6 message(STATUS "Build type: `${CMAKE_BUILD_TYPE}`")
7 message(STATUS)
8 if("${CMAKE_BUILD_TYPE}" STREQUAL "Debug")
9     add_definitions(-DBUILD_TYPE_DEBUG)
10 endif()

```

Sets **default build type** to release (faster and optimized).

- MPI:

```

1 # Locate MPI compiler.
2 find_package(MPI REQUIRED)
3 set(CMAKE_CXX_COMPILER "${MPI_CXX_COMPILER}")

```

MPI (Message Passing Interface) is the standard for distributed parallelism (multiple nodes, HPC clusters). `deal.II` uses MPI for parallel FEM solvers. Even if the first lab is serial, MPI will still be useful in the future.

- Boost:

```

1 # Locate Boost.
2 find_package(Boost 1.72.0 REQUIRED
3     COMPONENTS filesystem iostreams serialization
4     HINTS `${BOOST_DIR}` $ENV{BOOST_DIR} $ENV{mkBoostPrefix}
    })
5 message(STATUS "Using the Boost-`${Boost_VERSION}` configuration
    found at `${Boost_DIR}`")
6 message(STATUS)
7 include_directories(`${Boost_INCLUDE_DIRS}`)

```

Boost is a large C++ library, like a “standard library extension”. The version ≥ 1.72 is required with the components:

- **filesystem**: utilities to traverse folders, read/write files.
- **iostreams**: extensions for input/output streams.
- **serialization**: save/load objects in binary/text formats.

It is needed because `deal.II` itself depends on Boost for many utilities.

- `find_package(deal.II ...)`: Locates our `deal.II` installation and imports its CMake configuration.
- `deal_ii_initialize_cached_variables()`: Initializes compiler flags, include paths, etc.
- Compiler flags:

```
1 # Add useful compiler flags.
2 set(CMAKE_CXX_FLAGS "${CMAKE_CXX_FLAGS} -Wfloat-conversion -
    Wmissing-braces -Wnon-virtual-dtor")
```

Adds extra warnings to help catch common FEM bugs:

- `-Wfloat-conversion`: warns when ints are silently converted to floats (dangerous in mesh indexing).
- `-Wmissing-braces`: warns about missing braces in initializers.
- `-Wnon-virtual-dtor`: warns if a base class has virtual methods but no virtual destructor (classic memory leak risk).
- `add_executable(...)`: Defines the actual program we want to compile (Lab 01 solver).
- `deal_ii_setup_target(...)`: Connects our target to `deal.II`'s libraries, so we can use all its functionality.

Remark 2: CMakeLists

A `CMakeLists.txt` file is essentially the *recipe* that CMake uses to configure and build our project. We can think of it as a “build script” written in a declarative mini-language.

In the context of `deal.II` labs, the `CMakeLists.txt` file plays a central role because:

- It tells **CMake** the **project name** and which **languages** we are using (C++ in our case).
- It specifies the **minimum CMake version** required.
- It imports the `deal.II` **library** and makes its headers and compiled code available to our project.
- It defines which **source files** should be compiled into an executable.
- It links our executable against `deal.II` (and possibly other libraries like MPI or LAPACK if enabled).

2.2.6.2 Program Structure

In the first Poisson 1D laboratory, we will create three source files:

- `lab-01.cpp`
- `Poisson1D.cpp`
- `Poisson1D.hpp`

This split follows a classic C++ organization:

- Header (`.hpp`): contains the **class declaration**. It's the "blueprint": all member variables and method signatures are written here. No implementation details.
- Implementation (`.cpp`): contains the **class implementation**: actual code for each method declared in the header. Here is where we'll find the implementation.
- Driver (`lab-01.cpp`): contains the `main()` function. This is the entry point: it creates an instance of `Poisson1D`, calls `run()`, and handles exceptions.

This program structure mirrors the workflow of the Finite Element Method (FEM):

- Declare the **problem** (class declaration = PDE + parameters).
- Implement the **steps** (methods = weak form \rightarrow discrete system).
- Run the **pipeline** (main = assemble + solve).

So the program is not "just code files". It's intentionally structured to **mirror the mathematical procedure** we derived in the written part of the lab.

2.2.6.3 General Structure

We stopped in theory with:

$$a(u, v) = F(v) \quad \forall v \in V$$

Restricted to the finite element space V_h , this became:

$$\sum_{j=1}^{N_h} U_j a(\varphi_j, \varphi_i) = F(\varphi_i), \quad i = 1, \dots, N_h$$

Which is the **linear system**:

$$Au = f$$

With:

- $A_{ij} = a(\varphi_j, \varphi_i)$ (**stiffness matrix**)
- $f_i = F(\varphi_i)$ (**load vector**)
- $u = (U_1, \dots, U_{N_h})^T$ (**vector of unknown coefficients**).

So mathematically, we “only” need to **assemble A , assemble f , and solve $Au = f$** .

🌀 Mapping math objects to deal.II objects

We wrap everything in a class `Poisson1D` to keep the code modular (easy to reuse in future labs, 2D or 3D). Inside the class we store:

- **Discretization parameters**: number of elements N , polynomial degree r .
- **Mesh**: the triangulation of $\Omega = (0, 1) \rightarrow \text{Triangulation}<\text{dim}>$
- **Basis functions & polynomial degree**: Finite Element space definition $\rightarrow \text{FE_Q}<\text{dim}>(r)$
- **Integration of bilinear or linear forms**: quadrature rules

$\rightarrow \text{QGauss}<\text{dim}>$ and `FEValues`

🔍 **What is a quadrature rule?** A **Quadrature Rule** is a **numerical method used to approximate the definite integral of a function**. It involves selecting specific points (called nodes) within the integration interval and assigning weights to these points. The integral is then approximated by a weighted sum of the function values at these nodes.

Common quadrature rules include the trapezoidal rule, Simpson’s rule, and Gaussian quadrature (which is the most widely used). In the context of finite element methods (FEMs), quadrature rules are essential for accurately integrating functions over elements, especially when dealing with polynomial basis functions.

❓ Why Gaussian quadrature and not trapezoidal or Simpson?

Gaussian quadrature is preferred in FEM because it **provides the highest degree of accuracy for a given number of integration points**. It is particularly effective for integrating polynomial functions, which are commonly used as basis functions in FEM. In contrast, the trapezoidal and Simpson's rules may require more points to achieve the same level of accuracy, making them less efficient for this purpose.

With “*highest degree of accuracy*” we mean that, for n integration points, **Gaussian quadrature can exactly integrate polynomials of degree up to $2n - 1$** , while the trapezoidal rule is exact for polynomials of degree 1 and Simpson's rule is exact for polynomials of degree 3. This efficiency is crucial in FEM, where computational resources are often limited.

- **System matrix (sparse):** $A \rightarrow \text{SparseMatrix<double>}$
- **Sparsity structure:** pattern of nonzeros $\rightarrow \text{SparsityPattern}$
- **Load vector & Solution vector:** $f, u \rightarrow \text{Vector<double>}$

We use the static member `dim` to make the code dimension-independent (if we later change `dim = 2`, we can reuse the same structure for 2D). However, every mathematical entity from the variational formulation has a “natural home” in `deal.II`.

Note: It's normal that this mapping feels not immediate the first time. It is like learning a new programming framework:

- At the math level, we already know what we need (mesh, basis, test functions, bilinear/linear forms, linear system).
- At the code level, `deal.II` already has these structures, but the names and abstractions are new.

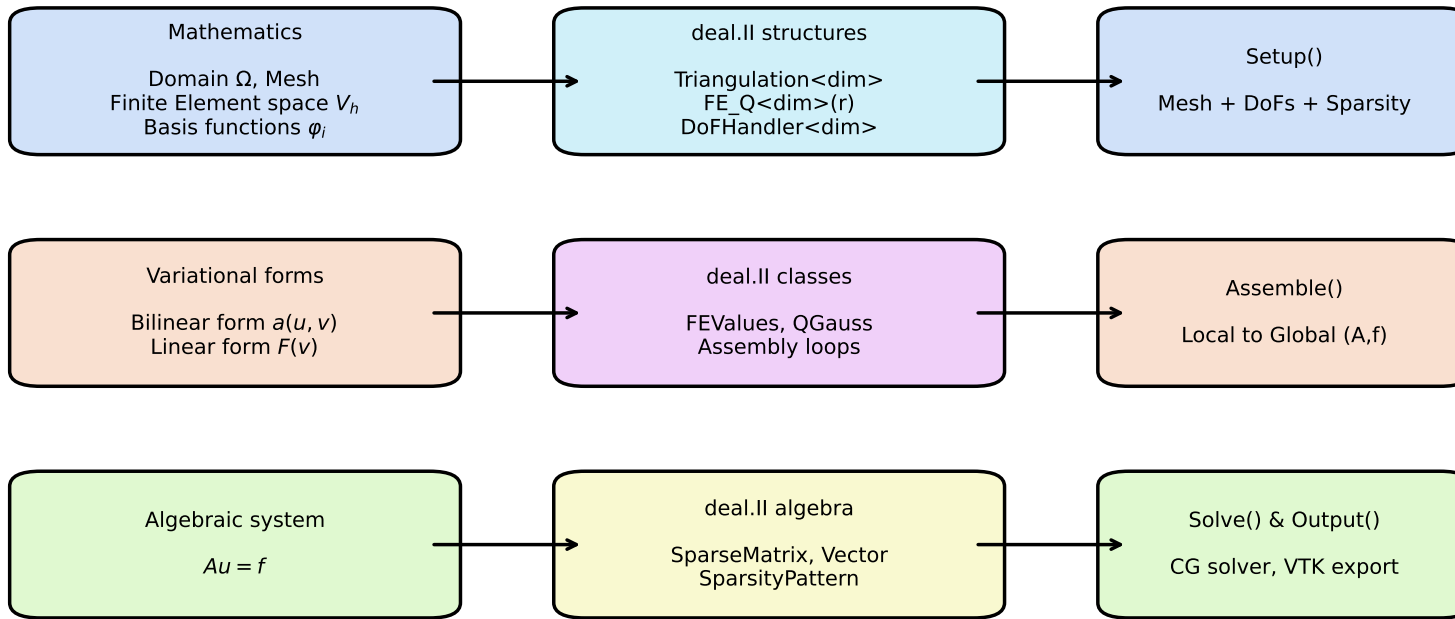
However, once learned, the same structure applies to all future PDE solvers in `deal.II`.

≡ Why split into `setup`, `assemble`, `solve`, `output`?

After mapping mathematical objects to `deal.II` objects, we can create a powerful plan. Typically, the best solution is a 4-step workflow:

1. **Setup.** Before any computation, we need to **initialize** all the structures: mesh, FE space, DoFs (Degree of Freedoms), sparsity pattern, vectors. This is a one-time preparation step.
2. **Assemble.** Local integrals (element stiffness matrices, local RHS) must be computed and inserted into global A and f . This mirrors the theory: local basis function \rightarrow global system.
3. **Solve.** The heart of the problem: solve the linear system $Au = f$. In theory, “find u in V_h ”. In code, apply a solver (solvers that have already been seen in the Numerical Linear Algebra course, such as Conjugate Gradient, GMRES, etc.).
4. **Output.** Once we have u , we need to use it: visualize (ParaView), compute errors, post-process quantities. This is not math anymore, but engineering practice: without output, the solution is useless.

The next sections will cover each step in detail.

Figure 11: Map of translation from math \rightarrow code \rightarrow implementation flow.

Regarding the figure on the previous page:

- **Mathematics** (left column). This is what we derived in the theory part (weak \rightarrow Galerkin \rightarrow FEM). It is pure **math**, independent of any programming language.
- **deal.II Objects** (middle column). Here we see the **software representation** of each math object.

1. Geometry & discretization

- `Triangulation<dim>` \rightarrow the mesh Ω_h
- `FE_Q<dim>(r)` \rightarrow basis functions of degree r
- `DoFHandler<dim>` \rightarrow numbering of the unknowns (degrees of freedom, DoFs)

2. Assembly tools

- `FEValues`, `QGauss` \rightarrow integration over elements (numerical quadrature)
- Assembly loops \rightarrow compute local A^K , f^K and scatter them into the global system

3. Algebraic structures

- `SparseMatrix<double>` \rightarrow the stiffness matrix A
- `Vector<double>` \rightarrow the load vector f and solution u
- `SparsityPattern` \rightarrow structure of nonzeros (saves memory and computation)

Each **mathematical ingredient** has a `deal.II` class implementing it.

- **Solver Pipeline** (right column). Finally, the **workflow** of the finite element solver. This is the *four-step structure*: setup, assemble, solve and output. This is the **concrete implementation**. It correspond 1-to-1 with the previous two columns.

2.2.6.4 Header File

The following header defines a **Poisson 1D solver** with the classic FEM workflow:

$$\text{setup()} \rightarrow \text{assemble()} \rightarrow \text{solve()} \rightarrow \text{output()}$$

Each member maps 1-to-1 to a mathematical object.

```

1 #ifndef POISSON1D_HPP
2 #define POISSON1D_HPP
3
4 #include <deal.II/base/function.h>
5 #include <deal.II/base/quadrature_lib.h>
6
7 #include <deal.II/dofs/dof_handler.h>
8 #include <deal.II/fe/fe_q.h>
9
10 #include <deal.II/grid/tria.h>
11
12 #include <deal.II/lac/sparsity_pattern.h>
13 #include <deal.II/lac/sparse_matrix.h>
14 #include <deal.II/lac/vector.h>
15
16 #include <memory>
17
18 using namespace dealii;
19
20 /**
21  * Minimal Poisson 1D solver skeleton.
22  * Only the core fields from our math  $\rightarrow$  deal.II mapping.
23  */
24 class Poisson1D
25 {
26 public:
27     // Physical dimension (1D, 2D, 3D)
28     static constexpr unsigned int dim = 1;
29
30     //  $\mu(x)$  - diffusion coefficient (Lab 01:  $\mu \equiv 1$ ).
31     class DiffusionCoefficient : public Function<dim>
32     {
33     public:
34         // Constructor.
35         DiffusionCoefficient() = default;
36
37         // Evaluation.
38         double value(const Point<dim> &, const unsigned int = 0) const
39             override {
40             return 1.0;
41         }
42     };
43
44     //  $f(x)$  - forcing term (Lab 01: -1 on  $(1/8, 1/4]$ , 0 elsewhere).
45     class ForcingTerm : public Function<dim>
46     {
47     public:
48         // Constructor.
49         ForcingTerm() = default;
50
51         // Evaluation.
52         double value(const Point<dim> &p, const unsigned int = 0) const
53             override {
54             const double x = p[0];
55             return (x > 1.0/8.0 && x <= 1.0/4.0) ? -1.0 : 0.0;
56         }
57     };
58
59     // ... other members ...
60 };

```

```

54     }
55 };
56
57 // Constructor: N = (N+1) elements on [0,1], r = FE degree.
58 Poisson1D(const unsigned int &N_, const unsigned int &r_)
59     : N(N_), r(r_) {}
60
61 // FEM pipeline (defined later).
62 void setup(); // mesh, FE, DoFs, sparsity, allocate A,f,u
63 void assemble(); // local integrals → global A,f and apply
        Dirichlet
64 void solve(); // linear solver (CG)
65 void output() const; // VTK write
66
67 protected:
68 // Discretization parameters
69 const unsigned int N; // N+1 elements
70 const unsigned int r; // polynomial degree
71
72 // Problem data
73 DiffusionCoefficient diffusion_coefficient;
74 ForcingTerm forcing_term;
75
76 // Geometry & FE space
77 Triangulation<dim> mesh;
78 std::unique_ptr<FiniteElement<dim>> fe; // e.g., FE_Q<
        dim>(r)
79 std::unique_ptr<Quadrature<dim>> quadrature; // e.g., QGauss
        <dim>(r+1)
80 DoFHandler<dim> dof_handler;
81
82 // Algebraic objects: A u = f
83 SparsityPattern sparsity_pattern;
84 SparseMatrix<double> system_matrix;
85 Vector<double> system_rhs;
86 Vector<double> solution;
87 };
88
89 #endif //POISSON1D_HPP

```

 Source



Public section

- **static constexpr unsigned int dim = 1;** We hard-code the **physical dimension** to 1. It simplifies the lab (no templates), while preserving deal.II's dimension-aware types (`Triangulation<dim>`, `DoFHandler<dim>`, ...). If we later want 2D/3D, we'd typically turn the class into `template<int dim>` and reuse the same structure.
- **Problem data as Function<dim>**

```

1 class DiffusionCoefficient : public Function<dim> { ... };
2 class ForcingTerm : public Function<dim> { ... };

```


`deal.II` algorithms expect coefficients and source terms as “**Function objects**”, a polymorphic interface for values/derivatives at points. We override `value()` function to return $\mu(x)$ and $f(x)$. However, for this lab:

- $\mu(x) \equiv 1$
- $f(x) = -1$ on $\left(\frac{1}{8}, \frac{1}{4}\right]$, and 0 elsewhere.

Keeping them as members makes it easy to pass them to assembly and boundary utilities (e.g., `VectorTools`, `MatrixTools`).

❓ Function objects? In `deal.II`, coefficients, source terms, boundary data, exact solutions, etc. are modeled by classes derived from `dealii::Function<dim>`. `Function<dim>` class is abstract and provides some default implementations. Since it is abstract, we cannot create objects directly using this class. Instead, we need to create a derivative, such as the `ForcingTerm` class. `Function<dim>` class exposes **virtual methods** like:

- `value(const Point<dim>&, unsigned int component=0)`
- `gradient(const Point<dim>&, unsigned int component=0)`
- `vector_value(...), vector_gradient(...)`, etc.

Because they’re virtual, algorithms (assembly, interpolation, error post-processing) can accept a **reference to the base type** `Function<dim>&` and work with *any* concrete subclass we provide; that’s **runtime polymorphism**. Here we have override only the value function, but we could override also other methods if we need it.

• Constructor

```
1 Poisson1D(const unsigned int &N_, const unsigned int &r_)
2 : N(N_), r(r_) {}
```

- `N` controls the **mesh resolution** (here: the implementation uses $N+1$ elements on $[0, 1]$).
- `r` is the FE **polynomial degree** (so V_h is \mathbb{P}_r continuous).

Both are stored as `const` so they’re fixed for the life of the object.

• Pipeline methods. This mirrors the **four canonical FEM phases**.

- `setup()`. Build everything static: mesh, FE, DoFs, sparsity, allocate `A`, `f`, `u`.
- `assemble()`. Compute local element matrices/vectors and scatter into global `A`, `f`; apply Dirichlet.
- `solve()`. Run a linear solver (CG here, as A is SPD² for Poisson).
- `output()`. Write results (VTK) for ParaView, etc.

²A real square matrix A is Symmetric Positive Definite (SPD) if $A^T = A$ and $x^T A x > 0$ for all nonzero vectors x . Consequences: all eigenvalues are real and strictly positive; A admits a Cholesky factorization $A = R^T R$; it defines an inner product $\langle x, y \rangle_A = x^T A y$; Krylov solvers like Conjugate Gradient (CG) are applicable and guaranteed to converge. In FEM: stiffness matrices from coercive elliptic problems with homogeneous Dirichlet BCs are SPD.

✂ Protected section (the state of our solver)

• Discretization parameters

```
1 const unsigned int N; // N+1 elements on [0,1]
2 const unsigned int r; // FE degree (P_r)
3
```

These determine mesh size and polynomial degree; together they define V_h .

• Problem data (instances)

```
1 DiffusionCoefficient diffusion_coefficient;
2 ForcingTerm          forcing_term;
```

Kept as objects (not pointers). They're cheap and provide an easy API during assembly and BCs.

• Geometry & FE

```
1 Triangulation<dim>          mesh;
2 std::unique_ptr<FiniteElement<dim>> fe;
3 std::unique_ptr<Quadrature<dim>> quadrature;
4 DoFHandler<dim>             dof_handler;
```

- `Triangulation<dim>`: the **mesh** \mathcal{T}_h .
- `FiniteElement<dim>` is an **abstract base**; `FE_Q<dim>` derives from it. Storing a `unique_ptr<FiniteElement<dim>>` lets we choose the concrete FE at runtime (here `FE_Q<1>(r)`, but later we could switch type/degree without changing the class definition).
`fe` is our **finite element type**, it tells `deal.II`
 - * What the **local basis functions** are on each cell K ;
 - * Where the **degrees of freedom (DoFs)** live (endpoints, midpoints, ...);
 - * How to get **shape values** $\phi_i(x_q)$ and **gradients** $\phi'_i(x_q)$ at quadrature points;
 - * How many **DoFs per cells** there are, etc.
- Same idea for `Quadrature<dim>`: we'll usually pick `QGauss<dim>(r+1)` in `setup()`.
- `DoFHandler<dim>` binds FE to the mesh and assigns **global DoF indices** (the algebraic unknowns).

Lifetime ordering: class members are destroyed in the **reverse** order of their declaration in C++. Here, `dof_handler` is declared **after** `mesh`, so it is destroyed **before** `mesh` → this is the safe order required by `deal.II` (the handler must not outlive the mesh).

- **Algebraic structures**

```
1 SparsityPattern      sparsity_pattern;  
2 SparseMatrix<double> system_matrix;  
3 Vector<double>       system_rhs;  
4 Vector<double>       solution;
```

- `SparsityPattern` captures where nonzeros can appear (from FE connectivity).
- `SparseMatrix<double>` holds the global **stiffness matrix** A .
- `Vector<double>`: RHS f and solution u .

⚠ Strict style nit: many teams avoid using namespace `dealii`; in headers to prevent symbol pollution; for a lab it's okay, but in production we'd prefer `dealii::` prefixes or put `using` in the `.cpp`.

2.2.6.5 Setup: turning math objects into deal.II objects

The setup process has four parts:

1. Mesh + boundary IDs

```

1 // Create the mesh.
2 {
3     printf("Initializing the mesh\n");
4     GridGenerator::subdivided_hyper_cube(
5         mesh, N + 1, 0.0, 1.0, true
6     );
7     printf(
8         "    Number of elements = %d\n",
9         mesh.n_active_cells()
10    );
11
12    // Write the mesh to file.
13    const std::string mesh_file_name = "mesh-" +
14        std::to_string(N + 1) + ".vtk";
15    const GridOut grid_out;
16    std::ofstream grid_out_file(mesh_file_name);
17    grid_out.write_vtk(mesh, grid_out_file);
18    printf("    Mesh saved to %s\n", mesh_file_name.c_str());
19 }

```

The mesh is the scaffold that turns the continuous PDE on Ω into a finite-dimensional problem we can actually compute.

- **Math picture (what we want)**

- Domain: the closed interval $[0, 1]$.
- Partition (mesh): split $[0, 1]$ into small sub-intervals (cells/elements). If we have N cells, the vertices are $N + 1$ points: $x_0 = 0 < x_1 < \dots < x_M = 1$.
- Boundary: the two endpoint $x = 0$ (left) and $x = 1$ (right).

- **deal.II objects (how it represents that picture).** Triangulation<dim> is the mesh container (cells + faces + links). The name “triangulation” comes from numerical PDE jargon: *any* partition of a domain into simple elements (segments in 1D, triangles/quads in 2D, tets/hexes in 3D) is often called a “triangulation”, even when the cells aren’t literal triangles.

❓ **What does a Triangulation store?** Geometry and topology of the mesh. It stores **vertices** (coordinates) and **cells** (their vertex indices), plus who’s adjacent to whom (**links**). This is the scaffold on which we place basis functions and do integrals cell-by-cell.

In 1D:

- A **cell** is an interval $[x_i, x_{i+1}]$;
- A **face** is a 0-D endpoint (vertex).
- **Boundary faces** are endpoints located on the boundary of the domain (here, just $x = 0$ and $x = 1$).

In summary, it creates a 1D mesh on $[0, 1]$ with $N + 1$ **elements** (so $N + 2$ **nodes** for $r = 1$). The last boolean parameter in the `subdivided_hyper_cube` invocation means that the `colorize` parameter is set to

`true (colorize=true)`, and assigns **boundary id 0** to $x = 0$ and **id 1** to $x = 1$. We'll use these IDs to impose Dirichlet in `assemble()`.

❓ **Why VTK export now (write_vtk)?** So we can see the mesh and quickly catch wrong counts/IDs.

✂ API Meaning

- (a) `subdivided_hyper_cube(mesh, M, a, b, colorize)`. In 1D, this creates a line segment $[a, b]$ split into M equal cells. Here, $M = N + 1$, $a = 0.0$ and $b = 1.0$. So we get $N + 1$ intervals.
- (b) **What does “active” mean?** Triangulations can be adaptively refined, creating a tree of parent/child cells. “**Active cells**” are the *leaves* (the current mesh we compute on). Immediately after creation, every cell is active.
- (c) `colorize = true` (crucial for boundary IDs)
 - If `false`, *all* boundary faces get the **same** `boundary_id` (typically 0). That's OK for “Dirichlet everywhere = 0”, but useless for different BCs on different sides.
 - If `true`, `deal.II` assigns **distinct IDs** per “side” of the hyper-cube:
 - In 1D:
 - * **ID 0**: left endpoint $x = a$ (the “minus” face along x).
 - * **ID 1**: right endpoint $x = b$ (the “plus” face along x).
 - In 2D:
 - * ID 0: $-x$ (left)
 - * ID 1: $+x$ (right)
 - * ID 2: $-y$ (bottom)
 - * ID 3: $+y$ (top)
 - In 3D:
 - * ID 0: $-x$
 - * ID 1: $+x$
 - * ID 2: $-y$
 - * ID 3: $+y$
 - * ID 4: $-z$
 - * ID 5: $+z$

Because the IDs are distinct, we *could* assign different functions to 0 and 1 if we wanted mixed boundary conditions.

❓ **Why is it called colorize?** In the context of meshing, “**colorize**” refers to labeling parts with distinct tags. `deal.II` uses integer tags called `boundary_id`. Setting `colorize=true` tells the generator to **color** each side with a different `boundary_id` so we can target them individually for boundary conditions.

2. Finite element + quadrature

```

1 // Initialize the finite element space.
2 {
3     printf("Initializing the finite element space\n");
4
5     // Finite elements in one dimension are obtained with
6     // the FE_Q class (which for higher dimensions represents
7     // hexahedral finite elements).
8     // In higher dimensions, we must use FE_Q for
9     // hexahedral elements or FE_SimplexP for tetrahedral
10    // elements. They are both derived from
11    // FiniteElement, so that the code is generic.
12    fe = std::make_unique<FE_Q<dim>>(r);
13
14    printf(
15        "    Degree                = %d\n",
16        fe->degree
17    );
18    printf(
19        "    DoFs per cell          = %d\n",
20        fe->dofs_per_cell
21    );
22
23    // Construct the quadrature formula of the
24    // appropriate degree of exactness.
25    // This formula integrates exactly the mass
26    // matrix terms (i.e. products of basis functions).
27    quadrature = std::make_unique<QGauss<dim>>(r + 1);
28
29    printf(
30        "    Quadrature points per cell = %d\n",
31        quadrature->size()
32    );
33 }

```

❓ **Finite element (FE_Q): What does the math need?** We decide to approximate the solution in a space:

$$V_h = \{v \in C^0([0, 1]) \mid v|_K \in \mathbb{P}_r \text{ for every cell } K \in \mathcal{T}_h\}$$

So on **each cell** K we use polynomials of degree r , and we glue cells together with continuity at the nodes.

❓ **Finite element (FE_Q): How deal.II represents that**

- **FE_Q<dim>(r): Lagrange \mathbb{P}_r elements** on a (hyper)cube cell (Q = hypercube elements, segments in 1D, quads in 2D, hexes in 3D). In 1D, the reference cell is $[0, 1]$. The **local basis** are the Lagrange shape functions $\{\phi_i\}_{i=0}^r$ that are 1 at the one node and 0 at the others (nodal basis).
In other words, **FE_Q(r)** says “on each cell, use $r+1$ nodal polynomials and glue cells continuously”.
- **DoFs per cell** in 1D: `fe -> dofs_per_cell = r + 1`. For example, with $r = 1$, 2 DoFs per cell (endpoints); $r = 2$ 3 DoFs per cell (endpoints + midpoint).
- **Global DoFs** with M cells and degree r in 1D:

$$N_{\text{dofs}} = M \cdot r + 1$$

Because adjacent cells share nodes. In our code, $M = N + 1$, so for $r = 1$: $N_{\text{dofs}} = (N + 1) \cdot 1 + 1 = N + 2$.

❓ Quadrature (QGauss): What does the math need? For Poisson, on each cell K we must compute:

- **Stiffness:** $A_{ij}^K = \int_K \mu \cdot \phi_j' \cdot \phi_i' dx$
- **Load:** $f_i^K = \int_K f \phi_i dx$

These are **integrals of polynomials (or polynomials \times coefficient)** over K . We approximate them with Gauss-Legendre quadrature.

❓ Quadrature (QGauss): How deal.II represents that.

In `deal.II`, QGauss is a **numerical integration rule**: it tells `deal.II` which points x_q to sample on a cell and *which weights* w_q to multiply by, so that an integral is approximated by a weighted sum

$$\int_K g(x) dx \approx \sum_{q=1}^{n_q} g(x_q) \cdot w_q \quad (\text{on cell } K)$$

Specifically, **Gauss-Legendre** with n_q points is **exact** for all **polynomials up to degree $2n_q - 1$** on an **interval**. That's why we like it for FEM on (hyper)cube cells.

QGauss controls **how we integrate** on each cell during assembly (and post-processing): i.e., **how many sample points** inside the cell we use, and with which **weights**, to approximate integrals.

- **Triangulation / mesh:** how many cells, their size/shape, boundary tags. This **sets where the domain is cut and how fine the grid is**.
- **Finite element FE_Q(r):** which basis we use on each cell (degree r , continuity). This **sets how “complex” the polynomial we can represent per cell is**.
- **Quadrature QGauss(n_q):** how many **sample points** per cell we use to compute the integrals that build A and f . This **sets how accurately we evaluate those integrals, not the mesh, not the basis**.

❓ What does QGauss actually give us? For an interval (our 1D cell), `QGauss<1>(n_q)` returns n_q reference points and weights that are **exact** for all **polynomials up to degree $2n_q - 1$** .

⚠ Undershooting n_q . If we pick too few points, we'll get consistency/accuracy issues (quietly!). The standard rule is generally to use $r + 1$.

3. DoFHandler: global numbering of unknowns

```

1 // Initialize the DoF handler.
2 {
3     printf("Initializing the DoF handler\n");
4
5     // Initialize the DoF handler with the mesh
6     // we constructed.
7     dof_handler.reinit(mesh);
8
9     // "Distribute" the degrees of freedom.
10    // For a given finite element space,
11    // initializes info on the control variables
12    // (how many they are, where
13    // they are collocated, their "global indices", ...).
14    dof_handler.distribute_dofs(*fe);
15
16    printf("  Number of DoFs = %d\n", dof_handler.n_dofs());
17 }

```

❓ **What problem it solves (conceptually).** After we pick the FE space V_h with $\text{FE_Q<1>}(\mathbf{r})$ and we have a mesh \mathcal{T}_h , we need a **single global index** for every unknown (degree of freedom, DoF) in the problem. That global numbering is what lets us build the global vector u, f and the sparse matrix A .

- **Locally (per cell)** we have $r + 1$ shape functions $\{\phi_i\}_{i=0}^r$.
- **Globally** many of those DoFs are **shared** at interfaces (e.g., the right vertex of one cell is the left vertex of the next).
- The **DoFHandler** walks the mesh and **assign unique global indices** to those shared DoFs exactly once, so the global system reflects continuity correctly.

❓ What the two calls do

```

1 // attach to triangulation
2 dof_handler.reinit(mesh);
3 // assign global DoF indices using 'fe'
4 dof_handler.distribute_dofs(*fe);

```

- **reinit(mesh):** tells the handler which mesh to use.
- **distribute_dofs(*fe):** asks **fe** where DoFs live on each cell and then produces a global numbering that respects sharing across cell interfaces.

In general, **triangulation first, then DoFHandler, then distribute DoFs**, and only *after that* we can build the sparsity pattern and allocate matrices/vectors.

❓ **How many DoFs do we get in 1D?** Let M be the number of cells (in our code $M = N + 1$). For $\text{FE_Q}(\mathbf{r})$ in 1D:

$$\#\text{DoFs} = M \cdot r + 1$$

The first cell contributes $r + 1$ DoFs, and each subsequent cell contributes r new ones (the interface node is shared), so:

$$(r + 1) + (M - 1) \cdot r = Mr + 1$$

Example 6: A tiny concrete picture

If $r = 1$ and $N = 3$:

- Mesh: $M = N + 1 = 4$ cells, nodes at $x_0 = 0, x_1, x_2, x_3, x_4 = 1$.
- Global DoFs (before BCs): indices 0, 1, 2, 3, 4 (so $n_dofs = 5 = N+2$).
- Cells and their local to global maps:
 - Cell 0 $[x_0, x_1]$: local (0, 1) \rightarrow global (0, 1)
 - Cell 1 $[x_1, x_2]$: local (0, 1) \rightarrow global (1, 2)
 - Cell 2 $[x_2, x_3]$: local (0, 1) \rightarrow global (2, 3)
 - Cell 3 $[x_3, x_4]$: local (0, 1) \rightarrow global (3, 4)
- During assembly on Cell 1, for example, when we add `cell_matrix(0, 1)` we write into global `A(1, 2)`; on Cell 2 the same local entry writes into `A(2, 3)`, etc. Shared nodes cause **sums** into the same rows/cols (that's how continuity/gluing shows up algebraically).

4. Sparse structure + algebra shells

```

1 // Initialize the linear system.
2 {
3     printf("Initializing the linear system\n");
4
5     // First, we need to initialize the sparsity pattern.
6     // This object describes the structure of the system
7     // matrix (i.e. which entries are nonzero).
8     // We use a DynamicSparsityPattern object to generate
9     // the sparsity pattern, and then copy it into a
10    // SparsityPattern object,
11    // which is more efficient for computations.
12    printf("  Initializing the sparsity pattern\n");
13    DynamicSparsityPattern dsp(dof_handler.n_dofs());
14    DoFTools::make_sparsity_pattern(dof_handler, dsp);
15    sparsity_pattern.copy_from(dsp);
16
17    // Then, we use the sparsity pattern to initialize
18    // the system matrix
19    printf("  Initializing the system matrix\n");
20    system_matrix.reinit(sparsity_pattern);
21
22    // Finally, we initialize the right-hand side and
23    // solution vectors.
24    printf("  Initializing the system right-hand side\n");
25    system_rhs.reinit(dof_handler.n_dofs());
26    printf("  Initializing the solution vector\n");
27    solution.reinit(dof_handler.n_dofs());
28 }

```

The goal of this step is to encode **which pairs of DoFs can couple** (i.e., where A_{ij} might be nonzero), and allocate the sparse matrix A and vectors f, u with the **right sizes and layout**.

From FE connectivity → nonzero pattern. In FEM, DoFs are the unknowns (one per basis function). Two DoFs **couple** if their basis functions **overlap on at least one cell**. In the matrix A , this means the entry A_{ij} **can be nonzero**. So the **sparsity pattern** is just the list of all index pairs (i, j) where A_{ij} might be nonzero. We **precompute** this once (fast) before assembly so the sparse matrix knows exactly which slots to allocate.

Example 7: 1D

Let $r = 1$, 4 cells and then 5 DoFs. Cells (with their **global** DoFs):

- Cell 0: $[x_0, x_1] \rightarrow$ DoFs (0,1)
- Cell 1: $[x_1, x_2] \rightarrow$ DoFs (1,2)
- Cell 2: $[x_2, x_3] \rightarrow$ DoFs (2,3)
- Cell 3: $[x_3, x_4] \rightarrow$ DoFs (3,4)

Each cell has **2 local DoFs**: its left and right vertices. With 4 cells, we might have global DoFs 0, 1, 2, 3, 4. The sparsity pattern is built by inserting **all pairs** from each cell's set $I \times I$:

- From cell 0: (0, 0), (0, 1), (1, 0), (1, 1)
- From cell 1: (1, 1), (1, 2), (2, 1), (2, 2)
- Etc.

Collecting unique pairs gives this **tridiagonal** pattern:

$$\begin{bmatrix} \text{x} & \text{x} & & & \\ \text{x} & \text{x} & \text{x} & & \\ & \text{x} & \text{x} & \text{x} & \\ & & \text{x} & \text{x} & \text{x} \\ & & & \text{x} & \text{x} \end{bmatrix}$$

Those x are the positions we **pre-allocate**. Later, assembly just **adds numbers** into these slots.

Why “precompute” the pattern? Making the sparse matrix grow on-the-fly is expensive and unsafe. Instead, we do:

```

1 DynamicSparsityPattern dsp(n_dofs);
2 for (each cell K) {
3     I = global dof indices on K;
4     for (i in I) for (j in I) dsp.add(i,j); // mark possible
      nonzeros
5 }
6 sparsity_pattern.copy_from(dsp);
7 system_matrix.reinit(sparsity_pattern); // allocate exact
      slots
8
```

Now assembly can do constant-time adds into known positions.

❓ Why this structure?

- **Build the graph dynamically (cheap inserts):** `DynamicSparsityPattern dsp(dof_handler.n_dofs());` The **sparsity pattern** tells us which entries of the global matrix may be non zero. This data structure is an insertion-friendly container. While we scan each cell and its local DoFs, we “declare” couplings (i, j) by inserting them into `dsp`. Inserts are frequent and irregular, so we need a structure that doesn’t reallocate like crazy.

❓ **Why are we talking about graphs?** `deal.II` never draws a graph, but under the hood uses an abstract adjacency graph of the sparse matrix:

- Vertices are DoFs (global unknown indices $0 \dots N - 1$).
- Edges (i, j) are potential nonzero A_{ij} (i.e., DoF i couples with DoF j on at least one cell).

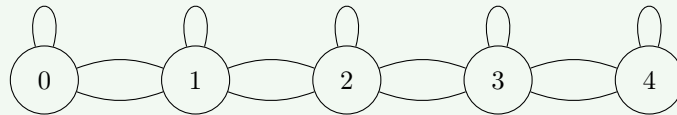
`DoFTools::make_sparsity_pattern(dof_handler, dsp)` walks the mesh cell by cell, looks at the **local** DoFs on that cell, and for every pair (i, j) in that local set, it marks an entry in `dsp`. That is literally building the **adjacency** of the global matrix, just not visually.

Example 8: Graph 1D

For example, with $r = 1$ and a uniform mesh, the degrees of freedom (DoFs) are 0, 1, 2, 3 and 4 along the line. Cells: [0, 1], [1, 2], [2, 3], [3, 4]. Each cell contributes couplings among its two DoFs:

- Cell [0, 1] → Edges (0, 0)
- Cell [0, 1] → Edges (0, 0), (0, 1), (1, 0), (1, 1)
- Cell [1, 2] → Edges (1, 1), (1, 2), (2, 1), (2, 2)
- Etc.

Collecting unique edges gives this **graph** (self-edges are the diagonal):



We never see a drawing, but `dsp` stores exactly this connectivity. Then:

- `sparisty_pattern.copy_from(dsp)` freezes it in a compressed format;
- And `system_matrix.reinit(sparisty_pattern)` allocates numeric storage *only* for those (i, j) .

- **Freeze the graph into a compressed pattern (CSR-like):**

```
1 sparsity_pattern.copy_from(dsp);
```

Converts that flexible graph into a compact, cache-friendly layout (row-compressed). This step is all about **memory efficiency and fast access** downstream.

- **Create global Stiffness Matrix A :**

```
1 system_matrix.reinit(sparsity_pattern);
```

Where `sparsity_pattern` tells which entries (i, j) are allowed to exist. After this, the matrix has the right shape and memory allocated, but its entries are all zero.

- **Right-hand side:**

```
1 system_rhs.reinit(dof_handler.n_dofs());
```

Initializes the **right-hand side vector** f . Its size equals the number of global unknowns (DoFs). This vector will later be filled with the load term integrals $\int f\varphi_i$. In other words, it is the input forcing vector for the linear system.

- **Create Solution vector:**

```
1 solution.reinit(dof_handler.n_dofs());
```

Initializes the **solution vector** u . Same size as `system_rhs`. At the beginning, it is just a vector of zeros. After solving, it will contain the approximate solution at each DoF. In other words, it is the unknown vector that will store the result after the solver runs.

After setup, we are ready to assemble the system: $Au = f$.

- `system_matrix`: A
- `solution`: u
- `system_rhs`: f

 Source



Output:

```
1 =====
2 Setup started
3 Initializing the mesh
4   Number of elements = 40
5   Mesh saved to mesh-40.vtk
6 -----
7 Initializing the finite element space
8   Degree                = 1
9   DoFs per cell         = 2
10  Quadrature points per cell = 2
```

```
11 -----
12 Initializing the DoF handler
13   Number of DoFs = 41
14 -----
15 Initializing the linear system
16   Initializing the sparsity pattern
17   Initializing the system matrix
18   Initializing the system right-hand side
19   Initializing the solution vector
```

2.2.6.6 Assemble: compute A and f

This is the part at the top of `assemble()`:

```

1 // Number of local DoFs for each element.
2 const unsigned int dofs_per_cell = fe->dofs_per_cell;
3
4 // Number of quadrature points for each element.
5 const unsigned int n_q = quadrature->size();
6
7 // FEValues instance.
8 // This object allows to compute basis functions, their
9 // derivatives, the reference-to-current element mapping
10 // and its derivatives on all quadrature points
11 // of all elements.
12 FEValues<dim> fe_values(
13     *fe,
14     *quadrature,
15     // Here we specify what quantities we need FEValues
16     // to compute on quadrature points.
17     // For our test, we need:
18     // - the values of shape functions
19     // - the derivative of shape functions
20     // - the position of quadrature points
21     // - the product J_c(x_q)*w_q
22     update_values |
23     update_gradients |
24     update_quadrature_points |
25     update_JxW_values
26 );
27
28 // Local matrix and right-hand side vector.
29 // We will overwrite them for each element within the loop.
30 FullMatrix<double> cell_matrix(dofs_per_cell, dofs_per_cell);
31 Vector<double> cell_rhs(dofs_per_cell);
32
33 // We will use this vector to store the global indices
34 // of the DoFs of the current element within the loop.
35 std::vector<types::global_dof_index> dof_indices(dofs_per_cell);
36
37 // Reset the global matrix and vector, just in case.
38 system_matrix = 0.0;
39 system_rhs = 0.0;

```

- **dofs_per_cell**. Each element (cell) of the mesh has its own set of *local* basis functions (shape functions). This number depends on:

- The finite element type ($\text{FE_Q}<\text{dim}>(r) \rightarrow$ polynomial degree);
- The dimension (dim).

For example, 1D linear elements ($r = 1$), then 2 local DoFs per cell.

- **n_q = quadrature->size()**. Quadrature rule defines how many integration points we use *per cell*. Needed because we approximate integrals by weighted sums at quadrature points.
- **FEValues object**. This is the **bridge between reference element and physical cell**. It knows how to evaluate:
 - Values of shape functions (`update_values`)

- Gradients of shape functions (`update_gradients`)
- Coordinates of quadrature points (`update_quadrature_points`)
- Jacobian \times weight factors (`update_JxW_values`)

Essentially, this object does all the geometric bookkeeping for us.

? Why is FEValues needed?

- ? What we want to compute.** From laboratory 1, we know the weak form turns into local contributions like (page 51):

$$A_{ij}^{(K)} = \int_K \mu(x) \cdot \nabla \varphi_i(x) \cdot \nabla \varphi_j(x) \, dx$$

And (page 50):

$$f_i^{(K)} = \int_K f(x) \cdot \varphi_i(x) \, dx$$

For each element K . So we need:

- * Basis functions $\varphi_i(x)$;
- * Their gradients $\nabla \varphi_i(x)$;
- * Quadrature weights and Jacobians for mapping integrals from reference element to physical cell.

✗ The “manual” alternative. In principle we could:

1. Hard-code the formulas for each basis function;
2. Transform coordinates from the reference element (e.g. $[-1, 1]$) to the physical element;
3. Compute the Jacobian determinant J and its inverse transpose for gradients;
4. Loop over quadrature nodes, evaluating shape functions and gradients by hand.

This is **tedious, error-prone, and messy** (especially in 2D/3D or for higher order elements).

✓ What FEValues does. FEValues is the **automation tool**:

- * Given:
 - The finite element space (`FE_Q`),
 - The quadrature rule (`QGauss`),
 - The flags (`update_values | update_gradients | ...`),
- * It precomputes, for **all quadrature points of a given cell**:
 - $\varphi_i(x_q) \rightarrow$ basis values;
 - $\nabla \varphi_i(x_q) \rightarrow$ basis gradients, mapped to physical cell;
 - $x_q \rightarrow$ actual coordinates of quadrature points;
 - $J(x_q)w_q \rightarrow$ the correct measure for integration.

So instead of writing integrals by hand, we just write:

```
1 fe_values.shape_value(i, q)
2 fe_values.shape_grad(i, q)
3 fe_values.quadrature_point(q)
4 fe_values.JxW(q)
```

And it gives the correct quantity.

- **Local containers** (`cell_matrix`, `cell_rhs`). Each cell contributes a **local stiffness matrix** and a **local load vector**. These are small (size = `dofs_per_cell` × `dofs_per_cell`). We recompute them for each element, then add them into the big global system.
- **dof_indices vector**. Temporary storage: maps local DoFs of the cell to global DoF indices. For example, on cell 3, local DoFs might correspond to global DoFs [5, 6].
- **Reset global system**. Before assembly, set matrix and RHS to zero, so we don't accumulate leftovers from a previous call.

✂ Element-wise assembly of local matrices and vectors into the global system

```

1 for (const auto &cell : dof_handler.active_cell_iterators())
2 {
3     // Reinitialize the FEValues object on current element.
4     // This precomputes all the quantities we requested when
5     // constructing FEValues (see the update_* flags above)
6     // for all quadrature nodes of the current cell.
7     fe_values.reinit(cell);
8
9     // We reset the cell matrix and vector
10    // (discarding any leftovers from previous element).
11    cell_matrix = 0.0;
12    cell_rhs    = 0.0;
13
14    for (unsigned int q = 0; q < n_q; ++q)
15    {
16        // Here we assemble the local contribution for
17        // current cell and current quadrature point,
18        // filling the local matrix and vector.
19
20        // Here we iterate over *local* DoF indices.
21        for (unsigned int i = 0; i < dofs_per_cell; ++i)
22        {
23            for (unsigned int j = 0; j < dofs_per_cell; ++j)
24            {
25                // FEValues::shape_grad(i, q) returns
26                // the gradient of the i-th basis function
27                // at the q-th quadrature node, already mapped
28                // on the physical element:
29                // we don't have to deal with the
30                // mapping, it's all hidden inside FEValues.
31                cell_matrix(i, j) += diffusion_coefficient.value(
32                    fe_values.quadrature_point(q)) // mu(x)
33                    * fe_values.shape_grad(i, q) // (I)
34                    * fe_values.shape_grad(j, q) // (II)
35                    * fe_values.JxW(q);           // (III)
36            }
37
38            cell_rhs(i) += forcing_term.value(
39                fe_values.quadrature_point(q)
40            ) * fe_values.shape_value(i, q) * fe_values.JxW(q);
41        }
42    }
43

```



```

44 // At this point the local matrix and
45 // vector are constructed: we need to sum them into the
46 // global matrix and vector. To this end, we need to
47 // retrieve the global indices of the DoFs of current cell.
48 cell->get_dof_indices(dof_indices);
49
50 // Then, we add the local matrix and vector into
51 // the corresponding positions of the global matrix
52 // and vector.
53 system_matrix.add(dof_indices, cell_matrix);
54 system_rhs.add(dof_indices, cell_rhs);
55 }

```

- `for (const auto &cell : dof_handler.active_cell_iterators())`
`dof_handler` is the object that knows the mesh (triangulation) and the distribution of DoFs on it. `active_cell_iterators()` returns **iterators to all active cells** in the mesh.

❓ **What is an active cell?** `deal.II` supports **adaptive meshes**: some cells can be refined into smaller children. The **active cells** are those that are **leaves of the refinement tree**, i.e. the cells we actually want to assemble on. If we're using a uniform mesh (like in our laboratory), then **all cells are active**. So this loop literally means: “*for each element of the mesh on which the solution is represented, do the following steps*”.

❓ **Why loop over cells?** Finite element assembly is **element-by-element**:

1. Compute the *local* contributions (cell matrix and RHS).
2. Scatter them into the *global* system.

That's why we need to visit each cell in turn.

- `fe_values.reinit(cell)`; `fe_values` was created outside the loop with a finite element (`fe`), a quadrature rule (`quadrature`), and some update flags (`update_values`, `update_gradients`, ...). However, at that particular moment, it was not linked to any specific cell. So, calling `reinit(cell)` means: “*take this cell, map the reference element to its physical shape, and precompute all the quantities we asked for at quadrature points (shape values, gradients, JxW , coordinates, ...)*”.

❓ **Why it's necessary.** Every cell can have different geometry (different size, position, refinement). The mapping (and therefore Jacobian, gradients, quadrature point positions) changes per cell. `reinit(cell)` makes sure that `fe_values.shape_grad(i,q)` or `fe_values.JxW(q)` (see below) correspond to **this specific cell**.

- `cell_matrix = 0.0`; `cell_rhs = 0.0`; These two variables are the **local contributions** for the current cell. They are small (size = `dofs_per_cell` × `dofs_per_cell` for the matrix, and `dofs_per_cell` for the RHS). Since we are looping over all cells, we need to **clear them out** before computing the contributions for this cell. Otherwise, leftovers from the previous cell would pollute the new computations.

- `for (unsigned int q = 0; q < n_q; ++q) {...}`. **Iterate all quadrature points on the current cell** to accumulate the cell's local matrix and RHS via numerical integration.

❓ **Why it exists.** Our integrals:

$$A_{ij}^{(K)} = \int_K \mu \cdot \nabla \phi_i \cdot \nabla \phi_j \, dx, \quad f_i^{(K)} = \int_K f \cdot \phi_i \, dx$$

Are approximated by sums over quadratures nodes x_q :

$$\begin{aligned} A_{ij}^{(K)} &\approx \sum_{q=1}^{n_q} \mu(x_q) \cdot \nabla \phi_i(x_q) \cdot \nabla \phi_j(x_q) \cdot JxW(q) \\ f_i^{(K)} &\approx \sum_{q=1}^{n_q} f(x_q) \cdot \phi_i(x_q) \cdot JxW(q) \end{aligned}$$

Here $JxW(q)$ is the mapped weight $|\det J_K| \cdot w_q$ from the reference element to the physical cell.

❓ **What are x_q ?** They are the **quadrature points**, i.e. the positions inside each cell where the integral is sampled. When we replace integrals with quadrature, we need both:

- the **weights** w_q (how much each sample contributes);
- the **points** x_q (where to evaluate the integrand).

So x_q are the specific coordinates where we evaluate the shape functions, their gradients, and the data $f(x)$, $\mu(x)$, etc.

❓ **Why do we need them?** Look at our weak form:

$$a(u, v) = \int_{\Omega} \mu(x) \cdot \nabla u(x) \cdot \nabla v(x) \, dx, \quad F(v) = \int_{\Omega} f(x) \cdot v(x) \, dx$$

The quadrature approximation is:

$$\begin{aligned} a(u, v) &\approx \sum_{q=1}^{n_q} \mu(x_q) \cdot \nabla u(x_q) \cdot \nabla v(x_q) \cdot JxW(q) \\ F(v) &\approx \sum_{q=1}^{n_q} f(x_q) \cdot v(x_q) \cdot JxW(q) \end{aligned}$$

Here we see explicitly: we need to know **where** to evaluate $\mu(x)$, $f(x)$, $\phi_i(x)$, $\nabla \phi_i(x)$. That “where” is exactly the quadrature point x_q .

❓ **Where does $JxW(q)$ come from?** In FEM, we don't integrate directly on each physical cell K . We map everything back to a **reference cell** \hat{K} (like $[-1, 1]$ in 1D, the unit square in 2D, ...). The map $F_K : \hat{K} \rightarrow K$ has a **Jacobian matrix**:

$$J_K \left(\hat{\xi} \right) = \frac{\partial x}{\partial \hat{\xi}} \quad (43)$$

When we change variables in an integral, the measure transforms as:

$$\int_K g(x) dx = \int_{\hat{K}} g\left(F_K\left(\hat{\xi}\right)\right) \cdot \left|\det J_K\left(\hat{\xi}\right)\right| d\hat{\xi}$$

On the reference cell, we approximate the integral with quadrature:

$$\int_{\hat{K}} g\left(F_K\left(\hat{\xi}\right)\right) \cdot \left|\det J_K\left(\hat{\xi}\right)\right| d\hat{\xi} \approx \sum_{q=1}^{n_q} g\left(F_K\left(\hat{\xi}_q\right)\right) \cdot \left|\det J_K\left(\hat{\xi}_q\right)\right| \cdot w_q$$

Where w_q are the quadrature weights on \hat{K} .

`deal.II` packages the product:

$$\left|\det J_K\left(\hat{\xi}_q\right)\right| \cdot w_q$$

Into one quantity:

```
1 fe_values.JxW(q)
```

Why we need it. If we didn't multiply by $JxW(q)$:

- Our integral would be computed as if the cell had **unit size and shape**.
- For example, in 1D, integrating over $[0, h]$ would give the same result as over $[0, 1]$.
- That's completely wrong: the measure (length, area, volume) of each cell must appear in the integral.

$JxW(q)$ is the **correct measure of the little piece of the cell around quadrature point x_q** .

- **for (unsigned int i = 0; i < dofs_per_cell; ++i) {...}**. Each cell has `dofs_per_cell` local shape functions $\{\varphi_i\}$. This loop means: “for each local basis function φ_i on this element, compute its contribution”.

Why is it needed?

1. **For the matrix $A^{(K)}$** we need contributions for every pair (i, j) . That's why inside this loop there's another nested loop over j . So we fill an entries of the local stiffness matrix.
2. **For the RHS $f^{(K)}$** each equation corresponds to a test function φ_i . So for each i , we compute:

$$f_i^{(K)} \approx \sum_q f(x_q) \cdot \varphi_i(x_q) \cdot JxW(q)$$

- **Fill Stiffness Matrix**

```
1 for (unsigned int j = 0; j < dofs_per_cell; ++j) {
2   cell_matrix(i, j) += diffusion_coefficient.value(
3     fe_values.quadrature_point(q)) // mu(x)
4     * fe_values.shape_grad(i, q)   // (I)
5     * fe_values.shape_grad(j, q)   // (II)
6     * fe_values.JxW(q);             // (III)
7 }
```

Inside the surrounding loops over the cell and the quadrature point q , that line accumulates the quadrature contribution to:

$$A_{ij}^{(K)} \approx \sum_{q=1}^{n_q} \mu(x_q) \cdot \nabla \phi_i(x_q) \cdot \nabla \phi_j(x_q) \cdot JxW(q)$$

Which is the discrete version of:

$$A_{ij}^{(K)} = \int_K \mu(x) \cdot \nabla \phi_i(x) \cdot \nabla \phi_j(x) dx \text{ (local form)}$$

Summing over all cells later gives the global entries A_{ij} used in $Au = f$.

A few precise points about what happens here:

- **Role of j :** for a fixed i , we pair the test function ϕ_i with every trial function ϕ_j on the cell. That's why this loop runs over all local DoFs.

The result is the full dense local matrix $\left(A_{ij}^{(K)}\right)_{i,j=0}^{\text{dofs_per_cell}-1}$.

- **What each factor supplies:**

- * $\mu(x_q)$ is:

```
1 diffusion_coefficient.value(  
2     fe_values.quadrature_point(q)  
3 )
```

- * `fe_values.shape_grad(i,q)` is $\nabla \phi_i(x_q)$ in **physical** coordinates.

- * `fe_values.shape_grad(j,q)` is $\nabla \phi_j(x_q)$.

- * `fe_values.JxW(q)` is the mapped weight $\left|\det J_K\left(\hat{\xi}_q\right)\right| \cdot w_q$.

- **Symmetry:** since $\nabla \phi_i \cdot \nabla \phi_j = \nabla \phi_j \cdot \nabla \phi_i$ and $\mu \geq 0$, the local (and global) matrix is symmetric: $A_{ij} = A_{ji}$. Many codes exploit this to halve work, but it's fine (and clearer) to assemble all (i, j) .
- **Cost structure:** the nested `i, j` loops make the local work $O(n_q \cdot \text{dofs_per_cell}^2)$ per cell (big O notation). For $r = 1$ in 1D, `dofs_per_cell = 2`, so this is tiny; in higher order/dimension, careful placement of the `mu(x_q)` load (hoist it outside the `j` loop), and reuse of `shape_grad(i,q)` values help with performance.
- **Connection to the notes:** the exact same bilinear form shown in our laboratory 1 solution:

$$A_{ij} = a(\phi_j, \phi_i) = \int_{\Omega} \mu \cdot \phi_j' \cdot \phi_i' dx$$

Is what we're discretizing here via quadrature on each cell.

After this `j` loop finishes (for the current i and current q), we've added the q -th quadrature contribution to the entire **row** i of the local matrix. The outer loops over q (quadrature points) and then over i complete the whole local matrix for the cell; afterwards we scatter it to the global matrix with `system_matrix.add(dof_indices, cell_matrix)`.

- **Assemble load vector (right-hand side)**

```

1 cell_rhs(i) += forcing_term.value(
2             fe_values.quadrature_point(q)
3             ) * fe_values.shape_value(i, q) *
4             fe_values.JxW(q);

```

We start from the weak formulation of the Poisson problem:

$$a(u, v) = F(v), \quad \forall v \in V$$

With:

$$a(u, v) = \int_{\Omega} \mu(x) \cdot u'(x) \cdot v'(x) dx, \quad F(v) = \int_{\Omega} f(x) \cdot v(x) dx$$

When we discretize, the **load vector entry** for basis/test function ϕ_i is:

$$f_i = \int_{\Omega} f(x) \cdot \phi_i(x) dx$$

In the code each part corresponds to the quadrature approximation of this integral:

- `forcing_term.value(fe_values.quadrature_point(q))` is $f(x_q)$, the source term evaluated at the quadrature point x_q .
- `fe_values.shape_value(i, q)` is $\phi_i(x_q)$, the value of the i -th basis (test) function at the quadrature point.
- `fe_values.JxW(q)` is the **Jacobian times weight**, it converts the integral over a possibly deformed cell into a sum of weighted contributions at quadrature points. Formally, it's:

$$JxW(q) = \det(J_T(x_q)) \cdot w_q$$


Where $\det(J_T)$ is the Jacobian determinant of the mapping from the reference element, and w_q is the quadrature weight.

- `cell_rhs(i) += ...` we sum these contributions over all quadrature points q . This approximates:

$$f_i \approx \sum_q f(x_q) \cdot \phi_i(x_q) \cdot JxW(q)$$

This line is building the discrete version of the **load vector**. For each degree of freedom (basis function ϕ_i), it accumulates the weighted contributions of the source term f over the cell, using numerical quadrature. We can think of it as: “take the forcing term at each integration point, multiply by the shape function, scale by the correct measure of volume (JxW), and sum them up to get the correct right-hand-side entry”.

- `cell->get_dof_indices(dof_indices);`

 **The context.** Up to this point, we’ve assembled the **local stiffness matrix** (`cell_matrix`) and the **local load vector** (`cell_rhs`) for one element (`cell`). These are written in terms of the **local basis functions**

on that cell. But the **global linear system** is assembled in terms of **global degrees of freedom (DoFs)**, one big vector \mathbf{u} and one big matrix \mathbf{A} for the whole mesh. So, we need a map: *which global indices do our local basis functions correspond to?*

🔍 What does `get_dof_indices` do? Each `cell` in `deal.II` has a small number of **local DoFs** (e.g. 2 in 1D linear case, 3 in quadratic case, etc.). The method:

```
1 cell->get_dof_indices(dof_indices);
```

Fills the vector `dof_indices` with the **global numbering** assigned to those local DoFs by the `DoFHandler`. For example, in 1D with $N = 3$ cells, linear elements ($r=1$):

- Nodes: x_0, x_1, x_2, x_3 .
- Global DoFs: numbered $[0, 1, 2, 3]$.
- Cell 0 (interval $[x_0, x_1]$): local DoFs \rightarrow global indices $[0, 1]$.
- Cell 1 ($[x_1, x_2]$): local DoFs \rightarrow $[1, 2]$.
- Cell 2 ($[x_2, x_3]$): local DoFs \rightarrow $[2, 3]$.

When we call `get_dof_indices` on cell 1, we'll get 1, 2.

Example 9: Physical analogy

Think of each `cell` like a small team in a company:

- Locally, the team has roles “Alice = $i=0$, Bob = $i=1$ ”.
- But globally, Alice is employee #123, Bob is employee #124 in the company's HR system.
- `get_dof_indices` is the lookup that tells us “local slot \rightarrow global employee number”, so we can update the **global payroll system** (the linear system) correctly.

• Scatter-Add from the element (cell) to the global system

```
1 system_matrix.add(dof_indices, cell_matrix);
2 system_rhs.add(dof_indices, cell_rhs);
```

They are just compact shorthands for the “triple loop” we'd otherwise write:

– Matrix

```
1 for (unsigned int i = 0; i < dofs_per_cell; ++i)
2   for (unsigned int j = 0; j < dofs_per_cell; ++j)
3     system_matrix.add(
4       dof_indices[i],
5       dof_indices[j],
6       cell_matrix(i,j)
7     );
```

This adds each local entry $(A^K)_{ij}$ into the **global** entry $A_{\text{glob}(i), \text{glob}(j)}$

– RHS vector

```

1 for (unsigned int i = 0; i < dofs_per_cell; ++i)
2     system_rhs(dof_indices[i]) += cell_rhs(i);

```

This adds the local load entry f_i^K into the global $f_{\text{glob}(i)}$.

Here `dof_indices[i]` is exactly the global DoF index for the i -th local basis function (provided by `cell->get_dof_indices(...)`), so each cell contributes to the **same** global rows/columns where nodes are shared. Over all cells, these adds build the global linear system $Au = f$ (the discrete version of $a(u, v) = F(v)$).

⚠ Boundary Conditions

```

1 // Boundary conditions.
2 {
3     // We construct a map that stores,
4     // for each DoF corresponding to a Dirichlet condition,
5     // the corresponding value.
6     // E.g., if the Dirichlet condition is
7     // u_i = b, the map will contain the pair (i, b).
8     std::map<types::global_dof_index, double> boundary_values;
9
10    // This object represents our boundary data
11    // as a real-valued function
12    // (that always evaluates to zero).
13    Functions::ZeroFunction<dim> bc_function;
14
15    // Then, we build a map that,
16    // for each boundary tag, stores the
17    // corresponding boundary function.
18    std::map<
19        types::boundary_id,
20        const Function<dim> *
21    > boundary_functions;
22    boundary_functions[0] = &bc_function;
23    boundary_functions[1] = &bc_function;
24
25    // interpolate_boundary_values fills
26    // the boundary_values map.
27    VectorTools::interpolate_boundary_values(
28        dof_handler,
29        boundary_functions,
30        boundary_values
31    );
32
33    // Finally, we modify the linear system
34    // to apply the boundary conditions.
35    // This replaces the equations
36    // for the boundary DoFs with the corresponding
37    // u_i = 0 equations.
38    MatrixTools::apply_boundary_values(
39        boundary_values,
40        system_matrix,
41        solution,
42        system_rhs,
43        true
44    );
45 }

```

- `std::map<types::global_dof_index, double> boundary_values` is essentially preparing a **container to store Dirichlet boundary conditions**.
 - `types::global_dof_index` is just `deal.II`'s typedef for an unsigned integer that labels a degree of freedom (DoF) in the **global numbering** created by the `DoFHandler`. Every unknown of the system (i.e. each node where we want to compute the solution) gets such an index.
 - `double` is the prescribed value of the solution at that DoF, coming from the boundary condition.

So this `map` will be filled later with pairs of the form:

(i, b) meaning: DoF i must take the value b .

For our Poisson 1D (with homogeneous Dirichlet BCs $u(0) = u(1) = 0$), this means we will eventually store something like:

- (DoF index at $x=0$, 0.0)
- (DoF index at $x=1$, 0.0)

And possibly more if the mesh has multiple boundary faces. In other words, this line declares a data structure that will **hold all the boundary constraints** needed to later enforce them in the linear system.

- `Functions::ZeroFunction<dim> bc_function;` creates an object that represents the **mathematical function** $u(x) = 0$ in the whole domain of dimension `dim`.
 - `Functions::ZeroFunction<dim>` is a class provided by `deal.II` that inherits from `Function<dim>`.
 - It is a simple function object: whenever we evaluate it at some point $x \in \mathbb{R}^{\text{dim}}$, it always returns 0.0.
 - The template parameter `<dim>` just means it works in 1D, 2D, or 3D, depending on our problem setup.

? Why do we need it? Because boundary conditions in `deal.II` are expressed as **functions defined on the boundary**. Even if the condition is simply homogeneous Dirichlet ($u = 0$), we still need to pass a function object. So here, `bc_function` is the *prescribed boundary function* that tells the solver: “*on the boundary, the solution must equal zero*”.

Later on, this object is associated with the boundary ids (e.g. left and right ends of the interval in 1D), and then interpolated into the discrete finite element space to actually generate the values for each boundary DoF.

- **Set the Dirichlet functions**

```
1 std::map<
2     types::boundary_id,
3     const Function<dim> *
4 > boundary_functions;
5 boundary_functions[0] = &bc_function;
6 boundary_functions[1] = &bc_function;
```


First of all, we prepare a `map` between boundary identifiers and the corresponding *boundary conditions*.

- `types::boundary_id` is just a `deal.II` typedef (an integer type) used to **tag different parts of the boundary** of the mesh.
- The value is a pointer to a `const Function<dim>` object, because different boundaries may have different prescribed functions.

So this `map` will tell `deal.II` “on boundary with id X , apply function Y as boundary condition”.

About assignments:

- `boundary_functions[0] = &bc_function;` Boundary with `id = 0` (e.g. in 1D, this corresponds to $x = 0$) is assigned the function `bc_function`. Recall `bc_function` is `ZeroFunction<dim>`, so: “on boundary 0, impose $u = 0$ ”.
- `boundary_functions[1] = &bc_function;` Boundary with `id = 1` (e.g. in 1D, the point $x = 1$) is also assigned the same zero function. So “on boundary 1, impose $u = 0$ ”.

🔍 Why two lines? In our lab problem (Poisson in 1D), the domain is $\Omega = (0, 1)$ and the BCs are homogeneous Dirichlet:

$$u(0) = 0, \quad u(1) = 0$$

`deal.II` distinguishes boundaries using IDs. By default: left endpoint of the 1D interval \rightarrow id 0; right endpoint \rightarrow id 1. So we explicitly say: **both boundary ids (0 and 1) are constrained with the zero Dirichlet function.**

• Computes boundary condition values

```
1 VectorTools::interpolate_boundary_values(
2   dof_handler,
3   boundary_functions,
4   boundary_values
5 );
```

This function from `deal.II` computes the actual values of the boundary conditions on the degrees of freedom (DoFs) that live on the boundary, and fills the `boundary_values` map we created earlier.

1. Inputs

- `dof_handler`: knows the finite element space and which DoFs are attached to which cells/faces. It can tell us which DoFs sit on the boundary.
- `boundary_functions`: the map that says: “on boundary $id = X$, apply function Y ”.
- `boundary_values`: the map that will be filled.

2. Interpolation process

- For each boundary id in `boundary_functions`, `deal.II` finds all the DoFs lying on that boundary part.

- It then evaluates the corresponding function (here `bc_function`, i.e. always 0.0) at the DoF locations.
- It records the pair (`global_dof_index`, `value`) into `boundary_values`.

3. **Result:** after this call, `boundary_values` contains entries like:

$$\{0 \rightarrow 0.0, 19 \rightarrow 0.0\}$$

Assuming DoF 0 and DoF 19 happen to be the endpoints of our 1D mesh with 20 subintervals.

❓ Why is this interpolation needed? Because the function is continuous (mathematical), but the finite element solution space is discrete: it only knows about DoFs. We must translate “ $u(x) = 0$ on boundary” into “DoF #*i* = 0.0” for every DoF lying on the boundary. So this line is the **bridge** between the abstract boundary condition (function on the boundary) and the concrete algebraic system (specific entries in vectors/-matrices).

• **Impose Dirichlet BCs on the linear system**

```
1 MatrixTools::apply_boundary_values(
2     boundary_values,
3     system_matrix,
4     solution,
5     system_rhs,
6     true
7 );
```

Inputs:

- `boundary_values`: the map $\{i \mapsto b_i\}$ saying “DoF *i* must take value b_i ”.
- `system_matrix` A , `system_rhs` f , and the current `solution` vector u (used/updated).
- The last flag `true` means **also eliminate columns** (keeps the system symmetric and clean).

≡ What `apply_boundary_values` does (Dirichlet enforcement). For each constrained DoF i in `boundary_values`:

1. **Zero the entire row** i of A .
2. **Put a 1 on the diagonal:** $A_{ii} \leftarrow 1$.
3. **Set the RHS:** $f_i \leftarrow b_i$.
4. If `eliminate_columns == true` (our case), **also zero column** i and **correct the RHS** of the *unconstrained* equations to account for the known value $u_i = b_i$:

$$f_j \leftarrow f_j - A_{ji}^{(\text{old})} \cdot b_i \quad \text{for all unconstrained } j$$

Then set $A_{ji} \leftarrow 0$ for all $j \neq i$.

5. **Set the solution entry:** $u_i \leftarrow b_i$ (so the vector is consistent for output/initial guesses).

Net effect: the i -th equation becomes exactly $u_i = b_i$ and the rest of the system is modified so those fixed values no longer appear implicitly on the left-hand side.

🔍 Why the last true matters

- **true (eliminate columns)**: preserves symmetry/positive definiteness (important for CG), avoids spurious nonzeros, and makes the algebra cleaner.
- **false**: leaves columns intact; sometimes used to keep certain preconditioner patterns, but less common for symmetric SPD problems.

So this single call rewrites our system so that **boundary DoFs are hard-set to the prescribed values** and the remaining unknowns solve a system that already accounts for those fixed notes.

In conclusion, the assembly routine builds the algebraic system corresponding to our PDE. First, it computes the local stiffness matrices and load vectors on each element using quadrature, then it inserts them into the global matrix and right-hand side. Finally, boundary conditions are enforced by directly modifying the system so that boundary DoFs take the prescribed values. After this step, the discrete problem is fully defined as a linear system $Au = f$, ready to be solved with the chosen linear solver.

📄 Source



2.2.6.7 Solve phase

Once the assembly stage is completed and boundary conditions have been enforced, we are left with a well-posed linear system of equations:

$$Au = f$$

Where A is the global stiffness matrix, f is the right-hand side vector, and u is the vector of unknown DoFs. The next step is to actually **solve this system numerically**.

In finite element problems (FEMs), the system matrix is typically **symmetric and positive definite** (SPD) for elliptic PDEs like the Poisson equation. This property makes the **Conjugate Gradient (CG) method** an excellent choice, since it is designed specifically for large, sparse SPD systems. The code sets up a solver with a tolerance proportional to the residual norm of the right-hand side, specifies a maximum number of iterations, and then calls the CG routine to compute the solution vector. For now, the solver uses no preconditioner, meaning convergence may be slower on more challenging problems, but the overall workflow is clear:

1. Define a stopping criterion (`SolverControl`).
2. Create the CG solver object (`SolverCG`).
3. Apply it to the matrix, right-hand side, and unknown vector (`solve`).

The result is that the unknown vector `solution` now contains the discrete approximation of the PDE solution at the mesh nodes.

```

1 void Poisson1D::solve()
2 {
3     printf("=====\n");
4
5     // Here we specify the maximum number of iterations of the
6     // iterative solver, and its tolerance.
7     SolverControl solver_control(1000, 1e-6 * system_rhs.l2_norm())
8     ;
9
10    // Since the system matrix is symmetric and positive definite (
11    // SPD),
12    // we solve the system using the conjugate gradient method.
13    SolverCG<Vector<double>> solver(solver_control);
14
15    printf(" Solving the linear system\n");
16    // We don't use any preconditioner for now,
17    // so we pass the identity matrix as preconditioner.
18    solver.solve(system_matrix, solution, system_rhs,
19    PreconditionIdentity());
20    std::cout << " " << solver_control.last_step()
21    << " CG iterations"
22    << std::endl;
23 }
```

- **SolverControl**

```

1 SolverControl solver_control(
2     1000, 1e-6 * system_rhs.l2_norm()
3 );
```

`SolverControl` is a `deal.II` **utility class** that defines the **stopping criteria** for iterative solvers. Every iterative solver (like CG, GMRES, etc.) needs to know *when to stop*. That can be either:

- When the residual becomes smaller than a given tolerance, or
- When a maximum number of iterations is reached.

The arguments:

- 1000 is the **maximum number of iterations**. If the solver hasn't converged within 1000 iterations, it stops anyway. This prevents infinite loops or wasted computation.
- `1e-6 * system_rhs.l2_norm()` is the **tolerance on the residual norm**. Where `system_rhs.l2_norm()` computes the Euclidean norm of the right-hand side vector f . Multiplying by 10^{-6} sets the tolerance proportional to the size of the problem data. This means: we ask the solver to reduce the residual until:

$$\|r\| \leq 10^{-6} \cdot \|f\|$$

Where $r = Au - f$ is the residual vector.

Why this choice? Using a **relative tolerance** $\frac{\|r\|}{\|f\|} < 10^{-6}$ is standard, because it makes the convergence criterion independent of the scale of the problem. For example, if f is very large, then asking for an absolute residual smaller than 10^{-6} would be meaningless. By scaling with $\|f\|$, the solver stops when the residual is *six orders of magnitude smaller than the forcing term*.

In other words, this line says “**run the iterative solver for at most 1000 steps, but stop earlier if the residual has dropped below 10^{-6} times the size of the right-hand side**”.

• SolverCG

```
1 SolverCG<Vector<double>> solver(solver_control);
```

- `SolverCG` is `deal.II`'s implementation of the **Conjugate Gradient (CG) method**. The CG method is an iterative algorithm designed for solving **symmetric positive definite (SPD)** linear systems $Au = f$. In our Poisson problem, the stiffness matrix A is SPD (because the bilinear form $a(u, v) = \int \mu \cdot \nabla u \cdot \nabla v$ is coercive), so CG is the ideal solver.
- The solver is templated on the vector type it operates with. Here we use `<Vector<double>` (`deal.II`'s own vector class) to represent the solution, RHS, and residual vectors. This ensures compatibility with the algebra objects created during assembly.
- The solver object is constructed and linked with the `SolverControl` defined earlier. This means the CG solver will follow those stopping rules:
 - * Maximum 1000 iterations, or

* Residual norm below $10^{-6} \|f\|$.

• **solve**

```
1 solver.solve(
2     system_matrix,
3     solution,
4     system_rhs,
5     PreconditionIdentity()
6 );
```

- **system_matrix** is the global stiffness matrix A assembled in the previous phase. It encodes how basis functions interact (the bilinear form).
- **solution** is the vector u of unknowns. On entry, it usually contains zero (or a guess). On exit, it will contain the computed approximation of the PDE solution at the mesh DoFs.
- **system_rhs** is the right-hand side vector f . It represents the load functional, i.e. the forcing term integrated against basis functions.
- **PreconditionIdentity()** specifies the **preconditioner** to use. Here it's just the *identity preconditioner* (i.e. no preconditioning). In practice, the solver just uses the raw system matrix. For small or simple problems, this is fine; for larger systems, one would replace it with something like **PreconditionJacobi**, **PreconditionSSOR**, or even more advanced preconditioners.

When this function returns, **solution** contains the discrete FE approximation u_h . **solver_control.last_step()** tells us how many CG iterations were needed.

 [Source](#)



Output:

```
1 =====
2 Solving the linear system
3 Linear system solved in 37 CG iterations
```

2.2.6.8 Output phase

After assembling and solving the linear system, the final step is to **visualize the computed finite element solution**. The output phase is responsible for exporting the discrete solution (stored in the vector `solution`) together with the mesh information, into a file format that can be inspected with external visualization tools such as ParaView. In `deal.II`, this task is managed by the `DataOut` class, which collects numerical results defined on the mesh and writes them in common scientific formats (e.g. VTK).

```

1 void Poisson1D::output() const
2 {
3     printf("=====\n");
4
5     // The DataOut class manages writing the results to a file.
6     DataOut<dim> data_out;
7
8     // It can write multiple variables (defined on the same mesh)
9     // to a single file. Each of them can be added by calling
10    // add_data_vector, passing the
11    // associated DoFHandler and a name.
12    data_out.add_data_vector(dof_handler, solution, "solution");
13
14    // Once all vectors have been inserted, call build_patches
15    // to finalize the DataOut object,
16    // preparing it for writing to file.
17    data_out.build_patches();
18
19    // Then, use one of the many write_* methods to write
20    // the file in an appropriate format.
21    const std::string output_file_name =
22        "output-" + std::to_string(N + 1) + ".vtk";
23    std::ofstream output_file(output_file_name);
24    data_out.write_vtk(output_file);
25
26    printf("Output written to %s\n", output_file_name.c_str());
27    printf("=====\n");
28 }

```

- `DataOut<dim> data_out;` `DataOut` is a `deal.II` utility class that handles the export of finite element data for visualization. It knows how to:
 - Collect solution vectors (and possibly multiple variables).
 - Reconstruct them on each cell.
 - Write them into output formats like VTK, VTU, DX, etc.

Like most `deal.II` classes, it is templated on the **dimension of the problem** (1D, 2D, 3D). This is needed so that it knows how to traverse the mesh and build patches (pieces of the mesh decorated with solution values).

❓ Why do we need it? By itself, the vector `solution` is just a list of numbers, one per degree of freedom. `DataOut` takes those numbers, matches them with the geometry of the mesh (`dof_handler`), and generates the geometric + data description that visualization software understands. In other words, this line creates an empty `DataOut` object, which will be filled with the solution data and then asked to write an output file.

- `data_out.add_data_vector(dof_handler, solution, "solution");`

This call **registers a vector of values** (in our case, the finite element solution) with the `DataOut` objects. It links:

- The **mesh and DoF structure** (`dof_handler`);
- The **numerical data** (`solution` vector);
- And a **name** ("`solution`") that will appear in the output file.

Input parameters:

- **dof_handler**: Tells `DataOut` how the DoFs are placed on the mesh, so it knows where each entry of the solution vector belongs.
- **solution**: The vector of computed values at all DoFs. This is the result of the solver, now ready to be visualized.
- **"solution"**: A label for the data field. If we open the `.vtk` file in `ParaView`, we'll see this name in the list of available scalar fields.

❓ Why do we need it? We can add **multiple data vectors** with different names (e.g. "`temperature`", "`flux`", "`error_indicator`"). Here, we just add the single primary unknown, the scalar solution of the Poisson equation. In other words, this line tells `DataOut`: *"here is the solution vector, defined over the mesh in `dof_handler`. Save it as a field called `solution`".*

- `data_out.build_patches();` This command tells the `DataOut` object: *"take the mesh + DoF information, interpolate the solution, and build the geometric representation that will be written to file"*. Concretely, it constructs **patches**: small pieces of the domain (usually one per cell) where the solution values are stored in a format compatible with visualization software.

❓ Why "patches"? In finite elements, the solution is represented by shape functions on each cell. For output, visualization tools expect a piecewise polynomial field that can be plotted as colors, contours, etc. `build_patches()` evaluates the solution on each cell and prepares this piecewise description. By default, one patch corresponds to one cell of the mesh. If the FE degree is > 1 , `deal.II` subdivides the cell appropriately so that curved shape functions are represented smoothly in the output.

In other words, this step **finalizes the `DataOut` object**, making it ready for export. Before this call, `data_out` only know "there's a solution vector"; after it, it has all the geometric and field data structured for writing.

- **Write `vtk`**

```
1 const std::string output_file_name =
2   "output-" + std::to_string(N + 1) + ".vtk";
3 std::ofstream output_file(output_file_name);
4 data_out.write_vtk(output_file);
```

1. **File name construction.** Builds the name of the output file as a string. It will look like `output-20.vtk` if $N + 1 = 20$ (i.e. the number of mesh nodes). This way, the filename encodes the resolution of the mesh, useful when running with different discretizations.

2. **Open file stream.** Creates an output stream and opens the file with the chosen name. If the file already exists, it will be overwritten.
3. **Write data in VTK format.** Writes the content of `data_out` (mesh + solution values) into the file, in VTK format. VTK is a standard format for scientific visualization, compatible with tools like **ParaView**. Once written, we can load the `.vtk` file in one of these programs to see plots, color maps, or isosurfaces of our computed solution.

In other words, this block **exports the numerical solution to disk** in a standard visualization format.

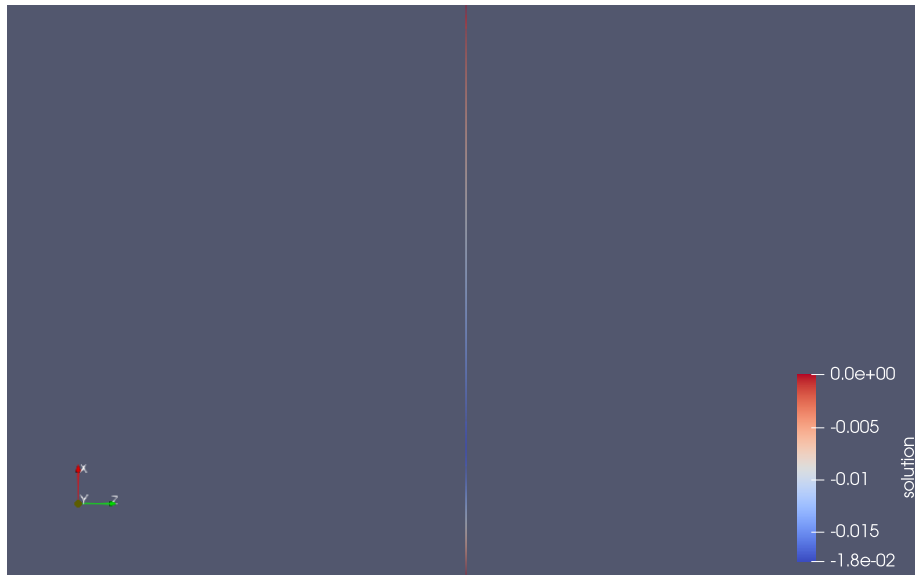


Figure 12: Solution in ParaView.

- The **domain is 1D** (the Poisson problem in $(0, 1)$), but **ParaView** always tries to render in 3D space. That's why we see a thin vertical line at the center.
- The **color map** represents our finite element solution along that 1D mesh.
- The **scale bar** on the right shows that the solution is close to zero, with small negative values (down to about -1.8×10^{-2}).
- The **axes triad** in the bottom left confirms: the mesh is along the x axis, with $y = z = 0$.

 Source



2.2.6.9 Extensions

In the basic implementation of our Poisson solver, all parameters are *hard-coded* inside the C++ source:

- The number of mesh elements $N + 1$;
- The polynomial degree r ;
- The diffusion coefficient $\mu(x)$;
- The right-hand side $f(x)$, etc.

This means that if we want to change, for example, the mesh size or the degree of the finite elements, we need to **edit the code and recompile**.

The class `ParameterHandler` in `deal.II` solves this inconvenience: it lets us **define, document, and read parameters from a text file** at runtime:

- We register each parameter in the handler with a name, default value, and description.
- We then parse an input `.prm` file.
- The solver reads the values directly from that file, so we can change parameters without touching or recompiling the C++ code.

≡ `ParameterHandler`: Example workflow

1. In our solver class, we declare a `ParameterHandler prm;` object.
2. In a dedicated method (say `declare_parameters()`), we register entries, e.g.:

```
1 prm.declare_entry(
2     "N", "39", Patterns::Integer(),
3     "Number of elements in the mesh"
4 );
5 prm.declare_entry(
6     "r", "1", Patterns::Integer(),
7     "Polynomial degree of FE space"
8 );
```

3. In another method (e.g. `parse_parameters(const std::string &filename)`), we load the file:

```
1 prm.parse_input(filename);
2 N = prm.get_integer("N");
3 r = prm.get_integer("r");
```

4. Then we can run our program with a parameter file `parameters.prm`:

```
1 subsection Poisson problem
2     set N = 100
3     set r = 2
4 end
```

✔ Why ParameterHandler is useful

- **Flexibility:** we can run different problem configurations just by editing the text file.
- **Reproducibility:** parameter files can be saved and shared.
- **Scalability:** in larger PDE projects, the number of parameters grows quickly (mesh files, time steps, tolerances, preconditioners, ...). Hard-coding them becomes impractical.

🔧 Profiling: TimerOutput

The goal is to turn our solver from “*it runs*” into “*it runs and we **know** why it takes that long*”. So we can reason about scalability, pick better solvers/preconditioners, and justify design changes like mesh resolution or FE degree.

After we write and test the code, we want to measure performance to find bottlenecks and possibly introduce optimizations. `TimerOutput` gives us an at-a-glance table with wall times/percentages per section; if we later need flame graphs or per-function hotspots, switch to an external profiler. **What it measures:**

- **Setup (initialization):** mesh creation/refinement, DoF enumeration, sparsity pattern allocation. Helps check overhead of changing N , r , or reading meshes from file.
- **Assembly:** local integrals to global matrix/vector. Typically dominates at moderate sizes; reveals impact of quadrature order, FE degree, cache behavior, and boundary handling.
- **Solve:** linear solver and preconditioner. On large problems this is often the **bottleneck**; timing it lets us compare CG vs GMRES, or Jacobi vs (S)SOR vs SSOR, etc.
- **Output:** I/O and data formatting (e.g., VTK). Useful to know if file writing is skewing short runs.

✂ How it works (conceptually)

We create a `TimerOutput` object once (`.hpp` file):

```

1 #include <deal.II/base/timer.h>
2
3 class Poisson1D
4 {
5     public:
6         ...
7         // Constructor: N = (N+1) elements on [0,1], r = FE degree.
8         Poisson1D(const unsigned int &N_, const unsigned int &r_)
9             : N(N_), r(r_),
10             // Print one line per timer section, wall times only.
11             timer(
12                 std::cout, TimerOutput::summary,
13                 TimerOutput::wall_times

```

```

14         )
15     {}
16
17     // FEM pipeline (defined later).
18     void setup();
19     void assemble();
20     void solve();
21     void output() const;
22     void print_timing() const; // new
23 protected:
24     // Discretization parameters
25     ...
26
27     // Problem data
28     ...
29
30     // Geometry & FE space
31     ...
32
33     // Algebraic objects:  $A u = f$ 
34     ...
35
36     // Profiling
37     mutable TimerOutput timer;
38 }

```

We wrap each **phase** in a timed scope (.cpp file):

```

1 void Poisson1D::setup()
2 {
3     TimerOutput::Scope t(timer, "1_setup");
4     // ...
5 }
6
7 void Poisson1D::assemble()
8 {
9     TimerOutput::Scope t(timer, "2_assembly");
10    // ...
11 }
12
13 void Poisson1D::solve()
14 {
15     TimerOutput::Scope t(timer, "3_solve");
16     // ...
17 }
18
19 void Poisson1D::output() const
20 {
21     TimerOutput::Scope t(timer, "4_output");
22     // ...
23 }
24
25 void Poisson1D::print_timing() const
26 {
27     timer.print_summary();
28 }

```

On exit, it prints a **summary table** with times per label and percentages of total wall-time.

2.3 Poisson 1D: Convergence & Error Analysis

2.3.1 Why Convergence & Error Analysis?

In the previous laboratory (page 24) we built a **finite element solver** for the 1D Poisson problem. At that stage, the solver could generate a mesh, assemble the stiffness matrix, impose boundary conditions, solve the linear system, and output results. However, having code that “runs” is not enough: we must ask ourselves whether it is **mathematically correct**. This is where the second lab (this section) comes into play.

Verification vs. Validation

- **Verification** asks: “*are we solving the equations correctly?*”. It focuses on the **implementation of the numerical method**. We want to ensure that our FEM discretization of Poisson’s equation converges at the rates predicted by theory.
- **Validation** asks: “*are we solving the correct equations?*”. This concerns the **mathematical model**. For example, is Poisson’s equation with Dirichlet boundary conditions the right physical model for heat diffusion in a bar?

This lab is entirely about **verification**, not validation. Our task is to prove that the FEM code correctly implements the Galerkin formulation.

Method of Manufactured Solutions (MMS)

In practice, we rarely know the exact solution to a PDE. To verify convergence, however, we need one. The **Method of Manufactured Solutions (MMS)** provides a systematic way:

1. **Choose a smooth exact solution** $u_{\text{ex}}(x)$, even arbitrarily (e.g. $u_{\text{ex}}(x) = \sin(2\pi x)$).
2. **Derive the forcing term** $f(x)$ by plugging u_{ex} into the PDE:

$$-u_{\text{ex}}''(x) = f(x)$$

For the sine example, this gives $f(x) = 4\pi^2 \sin(2\pi x)$.

3. Impose **boundary conditions** consistent with $u_{\text{ex}}(0)$ and $u_{\text{ex}}(1)$.

By construction, u_{ex} is the exact solution of the PDE we feed to our solver. We can then compute the numerical error $u_h - u_{\text{ex}}$ and verify the theoretical convergence rates.

Why not use trivial “patch tests”?

A **Patch test** is a very simple verification check used in structural mechanics and early FEM development. The idea: choose a problem whose exact solution belongs **exactly to the finite element space** V_h . For example, if we use linear finite element ($r = 1$), take $u_{\text{ex}}(x) = ax + b$. Since the finite element basis can represent this function exactly, the solver should reproduce u_{ex} with **zero error** (up to machine precision). While useful, patch tests do **not** tell us whether our solver converges at the right rates for general functions:

- With $u_{\text{ex}} \in V_h$, we always get zero error, independent of mesh size.
- Therefore, we learn nothing about the *approximation properties* of our FEM code.

That is why here we go beyond patch tests, we choose **Manufactured solutions that are not in the FE space**. These produce a nonzero error that decrease as $h \rightarrow 0$. Measuring that decrease is what confirms convergence.

Deepening: Method of Manufactured Solutions (MMS)

❓ **The problem we want to solve.** For example, take the Poisson problem:

$$-u''(x) = f(x), \quad x \in (0, 1), \quad u(0) = u(1) = 0$$

Normally, we **don't know** $u(x)$, and we use FEM to approximate it numerically. But if we want to *check our FEM code*, we need to know what the **exact** $u(x)$ is, so we can measure the error $(u - u_h)$. That's the purpose of MMS.

❓ **How does MMS work?** Instead of starting from $f(x)$ and trying to *find* $u(x)$, we **reverse the logic**.

1. **Choose any smooth, convenient function $u_{\text{ex}}(x)$.** For example:

$$u_{\text{ex}}(x) = \sin(2\pi x)$$

We can compute all its derivatives easily.

2. **Plug it into the PDE to manufacture the corresponding $f(x)$.** Take the PDE operator, here $-\frac{\partial^2}{\partial x^2}$, and apply it to u_{ex} :

$$f(x) = -u_{\text{ex}}''(x) = 4\pi^2 \sin(2\pi x)$$

Now we have constructed an artificial right-hand side $f(x)$.

3. **Build the boundary conditions consistently.** For Dirichlet BCs, set:

$$u(0) = u_{\text{ex}}(0) = 0, \quad u(1) = u_{\text{ex}}(1) = 0$$

And this works for us since $\sin(0) = \sin(2\pi) = 0$.

4. **Solve the manufactured PDE with our FEM code.** Our FEM solver does not know the “trick”. It just solves:

$$-u_h''(x) = f(x), \quad x \in (0, 1), \quad u_h(0) = u_h(1) = 0$$

Since f was built *exactly* from u_{ex} , the exact solution of this PDE is indeed $u_{\text{ex}}(x)$ itself.

❓ **Why isn't it magic?** We are not giving a function and asking the code to “return” it. Instead, we are *creating* a problem whose solution we **already know**:

1. **Constructing a full PDE** whose analytic solution we know.
2. **Feeding the PDE** (through its forcing term f and BCs) to our FEM solver.
3. **Comparing** the numerical result u_h with our known u_{ex}

So the “black box” isn’t guessing u_{ex} ; it’s solving a PDE that was *designed* so that u_{ex} is its exact solution.

? Why did we choose u_{ex} outside the FEM space? Because if u_{ex} were representable exactly (e.g. a linear function for linear FE), the FEM would reproduce it perfectly for any mesh, giving zero error and no convergence information. By picking u_{ex} that is **not** in the finite element space, like a sine, the solver can only approximate it. When we refine the mesh, $u_h \rightarrow u_{\text{ex}}$, and the error decreases at a predictable rate:

$$|u - u_h|_{L^2} = O(h^{r+1}) \quad |u - u_h|_{H^1} = O(h^r)$$

We can then measure these rates and verify that the implementation behaves as theory predicts.

📖 Analogy. In a similar way, when testing a sorting algorithm, we might generate random lists of numbers (the “manufactured input”) and know the expected sorted output. We then run the algorithm and compare its output to our known correct result. The algorithm isn’t “magically” producing the sorted list; it’s being tested against a case where we already know the answer. Think of MMS like a **unit test** for our numerical solver.

| In programming | In PDE verification |
|---|--|
| We create a function $\mathbf{f}()$ and check if its output matches what we expect. | We create a PDE (with known u_{ex}) and check if the solver approximates it with the right accuracy. |
| The test is artificial, not a real-world case. | MMS PDE is artificial, not physical, but mathematically consistent. |

In summary, MMS is a systematic way to create test problems with known solutions, allowing us to verify that our numerical methods are implemented correctly and converge as expected.

2.3.2 Problem Setup for MMS

🔍 How to choose a smooth exact solution

The key idea is to pick something we like, as long as it is smooth enough. Typical choices are **polynomials**, **trigonometric functions** (e.g. sines and cosines), or **exponentials**, because their derivatives are easy to compute.

However, the solution must satisfy three primary requirements:

1. The exact solution u_{ex} must satisfy the **boundary conditions** of the problem (e.g., homogeneous Dirichlet $u(0) = u(1) = 0$).

Example 10: Choose a smooth exact solution

If we pick $u_{\text{ex}}(x) = \sin(2\pi x)$, it automatically vanishes at both ends:

$$u_{\text{ex}}(0) = \sin(0) = 0, \quad u_{\text{ex}}(1) = \sin(2\pi) = 0$$

2. The exact solution u_{ex} must be **sufficiently smooth** (at least C^2) so that plugging into $-u'' = f$ makes sense and the theory applies.

Example 10 (continue): Choose a smooth exact solution

Taking $u_{\text{ex}}(x) = \sin(2\pi x)$ is a good choice since it is infinitely differentiable:

$$u'_{\text{ex}}(x) = 2\pi \cos(2\pi x), \quad u''_{\text{ex}}(x) = -4\pi^2 \sin(2\pi x) \implies u_{\text{ex}} \in C^\infty$$

3. It should **not belong to our FE space** (so that error is not identically zero). For example, avoid linear functions when using $r = 1$ elements.

Example 10 (continue): Choose a smooth exact solution

The choice $u_{\text{ex}}(x) = \sin(2\pi x)$ is suitable since it is not a polynomial and cannot be exactly represented by piecewise linear functions.

📖 Deriving the forcing term

Once we have chosen a suitable exact solution $u_{\text{ex}}(x)$, we can derive the corresponding forcing term $f(x)$ by substituting u_{ex} into the Poisson equation:

$$-u''_{\text{ex}}(x) = f(x)$$

That's our **manufactured forcing term**³.

³Note: the manufactured forcing term is not necessarily physically meaningful, but it serves our purpose for verifying the numerical method.

Example 11: Deriving the forcing term

For our example $u_{\text{ex}}(x) = \sin(2\pi x)$, we compute:

$$u_{\text{ex}}''(x) = -4\pi^2 \sin(2\pi x) \implies f(x) = 4\pi^2 \sin(2\pi x)$$

Thus, the manufactured solution $u_{\text{ex}}(x) = \sin(2\pi x)$ satisfies the Poisson equation with the forcing term $f(x) = 4\pi^2 \sin(2\pi x)$ and homogeneous Dirichlet boundary conditions.

Defining the PDE problem

We can now summarize the complete PDE problem for the Method of Manufactured Solutions (**manufactured PDE**):

$$\begin{cases} -u''(x) = 4\pi^2 \sin(2\pi x), & x \in (0, 1) \\ u(0) = 0, \\ u(1) = 0 \end{cases}$$

with the exact solution:

$$u_{\text{ex}}(x) = \sin(2\pi x)$$

This setup allows us to implement the finite element method, compute the numerical solution u_h , and then compare it to the exact solution u_{ex} to analyze convergence and error.

? What do we gain?

By using the Method of Manufactured Solutions:

- We know the **exact solution** u_{ex} , allowing us to compute the error $e_h = u_{\text{ex}} - u_h$ directly.
- We can **compute the error in different norms** (e.g., L^2 , H^1) to assess the accuracy of our numerical method.
- We can **check if the solver exhibits the expected convergence rates**:
 - $e_{L^2} = O(h^{r+1})$, means the error in the L^2 norm decreases proportionally to h^{r+1} as the mesh is refined.

? Why? Because the L^2 error is related to the smoothness of the exact solution and the order of the finite element space. As we refine the mesh (reduce h), the approximation becomes more accurate, leading to a faster decrease in the error.

It's obvious that more elements mean more mesh points and more computational work, but also a better approximation of the exact solution.

- $e_{H^1} = O(h^r)$, means the error in the H^1 norm decreases proportionally to h^r as the mesh is refined.

🔍 **Why?** The reason behind the convergence rates is rooted in the mathematical properties of the finite element method. The L^2 norm measures the error in the function values, while the H^1 norm measures the error in both the function values and their first derivatives. As the mesh is refined, the finite element space can better approximate the exact solution, leading to a faster decrease in the L^2 error. However, since the H^1 norm also considers the derivative, which is generally less smooth than the function itself, the convergence rate is typically one order lower.

2.3.3 What changes from the first Poisson 1D solver

The PDE and solver skeleton are **the same** as in the first Poisson 1D solver lab. The second laboratory adds a **verification layer** on top of the existing solver, to check that the numerical solution is correct and converges to the exact solution as the mesh is refined. This verification layer is based on the **Method of Manufactured Solutions (MMS)**, (see Section 2.3.2, page 104).

✔ New capability in Poisson1D: computing errors

We extend the header file `Poisson1D.hpp` with the declaration of a new method:

```
1 double compute_error(const VectorTools::NormType &norm_type) const;
```

This method performs **a-posteriori error evaluation** against a **known exact solution** (MMS). The implementation is in `Poisson1D.cpp`:

```
1 double Poisson1D::compute_error(
2     const VectorTools::NormType &norm_type
3 ) const
4 {
5     // The error is an integral,
6     // and we approximate that integral using a quadrature formula.
7     // To make sure we are accurate enough,
8     // we use a quadrature formula with one node more than
9     // what we used in assembly.
10    const QGauss<dim> quadrature_error = QGauss<dim>(r + 2);
11
12    // First we compute the norm on each element,
13    // and store it in a vector.
14    Vector<double> error_per_cell(mesh.n_active_cells());
15    VectorTools::integrate_difference(
16        dof_handler,
17        solution,
18        ExactSolution(),
19        error_per_cell,
20        quadrature_error,
21        norm_type
22    );
23
24    // Then, we add out all the cells.
25    const double error = VectorTools::compute_global_error(
26        mesh, error_per_cell, norm_type
27    );
28
29    return error;
30 }
```

- It integrates the element-wise error using `deal.II`'s

`VectorTools::integrate_difference(...)`

then collapses to a global norm with

`VectorTools::compute_global_error(...)`

This yields either the L^2 or H^1 norm of the error, depending on the input argument `norm_type`. Later we will see how to use this method in the convergence analysis.

- For accuracy, it uses a **richer quadrature** than assembly (we choose `QGauss(r+2)`), so the **integration of the error** does not become the bottleneck.

❓ Why richer quadrature? The error is the difference between the numerical solution and the exact solution. The numerical solution is a polynomial of degree r (the FE degree), while the exact solution is generally not a polynomial. Therefore, the error is not a polynomial of degree r , but a more complex function. **To accurately integrate this function, we need a quadrature that can handle higher-degree polynomials.** Using `QGauss(r+2)` ensures that we can accurately capture the behavior of the error function, leading to more reliable error estimates. Indeed, with `QGauss(r+2)`, $n = r + 2$, we can exactly integrate polynomials of degree up to $2n - 1 = 2(r + 2) - 1 = 2r + 3$, which is sufficient for our purposes.

❓ Why isn't the integration of errors the bottleneck? In numerical methods, the accuracy of error estimation is crucial for assessing the quality of the solution. If the quadrature used for integrating the error is not sufficiently accurate, it can lead to significant discrepancies in the error estimates. By using a richer quadrature like `QGauss(r+2)`, we ensure that the **integration process is precise enough to capture the nuances of the error function.** This **prevents the integration step from becoming a limiting factor in the overall accuracy of the error estimation**, allowing us to trust the results of our convergence analysis.

❓ Why does this method exist? In numerical simulations, especially when solving PDEs, it is essential to assess the accuracy of the computed solution. The `compute_error` method provides a systematic way to quantify the difference between the numerical solution and a known exact solution (from MMS). It lets us to **quantify** whether the method achieves the **theoretical convergence rates**:

- $\|u - u_h\|_{L^2} = O(h^{r+1})$ for the L^2 norm;
- $\|u - u_h\|_{H^1} = O(h^r)$ for the H^1 norm.

Implementation note: `ExactSolution::value(...)` and `ExactSolution::gradient(...)` must be consistent, because

```
VectorTools::integrate_difference(...)
```

Uses both to compute the L^2 and H^1 norms of the error.

✂ Modifications to Forcing Term and Exact Solution

To implement the Method of Manufactured Solutions (MMS), we need to modify the forcing term class to correspond to a known exact solution. Also, we need to implement the exact solution class. These changes are necessary to verify the correctness of our numerical solution.

❓ **Why change the ForcingTerm?** In the first Poisson 1D solver lab, the forcing term was a simple constant function defined as:

```

1 class ForcingTerm : public Function<dim>
2 {
3 public:
4     // Constructor.
5     ForcingTerm() : Function<dim>() {}
6
7     // Evaluation.
8     virtual double value(
9         const Point<dim> &p,
10        const unsigned int /*component*/ = 0
11    ) const override
12    {
13        if (p[0] <= 1.0 / 8 || p[0] > 1.0 / 4.0)
14            return 0.0;
15        else
16            return -1.0;
17    }
18 };

```

Listing 1: Original Forcing Term

Where -1.0 in the interval $(\frac{1}{8}, \frac{1}{4}]$ and 0.0 elsewhere. This choice was arbitrary and did not correspond to any specific exact solution.

For MMS, we need a forcing term that corresponds to our chosen exact solution. We select a manufactured solution (e.g., $u(x) = \sin(\pi x)$) and derive the corresponding forcing term using the Poisson equation $-u''(x) = f(x)$. This ensures that our numerical solution can be verified against a known exact solution (see Section 2.3.2, page 104). The modified `ForcingTerm` class is:

```

1 class ForcingTerm : public Function<dim>
2 {
3 public:
4     // Constructor.
5     ForcingTerm() : Function<dim>() {}
6
7     // Evaluation.
8     virtual double value(
9         const Point<dim> &p,
10        const unsigned int /*component*/ = 0
11    ) const override
12    {
13        return 4.0 * M_PI * M_PI * std::sin(2.0 * M_PI * p[0])
14        ;
15    }
16 };

```

Listing 2: Modified Forcing Term for MMS

This corresponds to the forcing term derived from the manufactured solution $u(x) = \sin(2\pi x)$:

$$f(x) = -u''(x) = 4\pi^2 \sin(2\pi x)$$

- ❓ **Why add the `ExactSolution` class?** The `ExactSolution` class is introduced to provide a reference solution against which we can compare our numerical solution. This class **implements the exact solution and its gradient**, which are essential for computing the error norms. The implementation is as follows:

```

1 // Exact solution.
2 class ExactSolution : public Function<dim>
3 {
4     public:
5         // Constructor.
6         ExactSolution() {}
7
8         // Evaluation.
9         virtual double
10        value(
11            const Point<dim> &p,
12            const unsigned int /*component*/ = 0) const override
13        {
14            // Points 3 and 4.
15            return std::sin(2.0 * M_PI * p[0]);
16        }
17
18        // Gradient evaluation.
19        // deal.II requires this method to return a Tensor
20        // (not a double), i.e. a dim-dimensional vector.
21        // In our case, dim = 1, so that the Tensor will in
22        // practice contain a single number.
23        // Nonetheless, we need to return an object
24        // of type Tensor.
25        virtual Tensor<1, dim>
26        gradient(
27            const Point<dim> &p,
28            const unsigned int /*component*/ = 0) const override
29        {
30            Tensor<1, dim> result;
31
32            // Points 3 and 4.
33            result[0] = 2.0 * M_PI * std::cos(2.0 * M_PI * p[0]);
34
35            return result;
36        }
37
38        static constexpr double A = -4.0 / 15.0 * std::pow(0.5,
39        2.5);

```

Listing 3: Exact Solution Class for MMS

This class provides the exact solution $u(x) = \sin(2\pi x)$ (in `value(...)`) and its gradient $u'(x) = 2\pi \cos(2\pi x)$ (in `gradient(...)`). The gradient value is returned as a `Tensor<1, dim>` because `deal.II` requires this format for gradient evaluations, even in 1D where it effectively behaves like a vector with a single component.

❓ **What does Tensor mean?** A **tensor** is a generalization of scalars (rank 0), vectors (rank 1), and matrices (rank 2) to arbitrary rank. It's the natural object for representing quantities in continuum mechanics, PDEs, and FEM:

- **Rank 0 tensor:** scalar field value $u(x)$;
- **Rank 1 tensor:** vector quantity, e.g. gradient 2D $\nabla u = (\partial_x u, \partial_y u)$;
- **Rank 2 tensor:** matrix quantity, e.g. stress tensor, Jacobian of a mapping.
- **Higher-rank tensors:** more complex relationships in advanced applications, e.g. elasticity, electromagnetism, etc.

In `deal.II`, the `Tensor<rank, dim>` is a **template class** representing a tensor of given rank in `dim` dimensions. For example:

- `Tensor<0, dim>` is just a scalar (like `double`);
- `Tensor<1, dim>` is a vector of length `dim` (like `std::array<double, dim>`);
- `Tensor<2, dim>` is a `dim x dim` matrix.

So when we compute the **gradient of a scalar field** in `dim` dimensions, we get a **rank-1 tensor** `Tensor<1, dim>`.

- In 1D, this is essentially a vector with one entry (the derivative $\partial_x u$);
- In 2D, it's a vector with two entries (the partial derivatives $\partial_x u$ and $\partial_y u$);
- In 3D, it's a vector with three entries (the partial derivatives $\partial_x u$, $\partial_y u$, and $\partial_z u$).

Remark 3: Gradient

The **Gradient** of a scalar field $u(x)$ in 1D is simply its derivative:

$$\nabla u(x) = \frac{\partial u}{\partial x}$$

In higher dimensions, the gradient is a vector of partial derivatives. For example, in 2D, the gradient is:

$$\nabla u(x, y) = \begin{bmatrix} \frac{\partial u}{\partial x} \\ \frac{\partial u}{\partial y} \end{bmatrix} = \left(\frac{\partial u}{\partial x}, \frac{\partial u}{\partial y} \right)$$

And in 3D, it's:

$$\nabla u(x, y, z) = \begin{bmatrix} \frac{\partial u}{\partial x} \\ \frac{\partial u}{\partial y} \\ \frac{\partial u}{\partial z} \end{bmatrix} = \left(\frac{\partial u}{\partial x}, \frac{\partial u}{\partial y}, \frac{\partial u}{\partial z} \right)$$

The gradient points in the direction of the steepest increase of the function and its magnitude indicates how steep that increase is.

✓ New capability in main: convergence driver

The `main.cpp` (or `lab-02.cpp`) file is modified to turn the solver into a **convergence driver**. A convergence driver **runs the solver** multiple times on a sequence of refined meshes, **computes the errors**, and **estimates the convergence rates**.

```

1 #include <deal.II/base/convergence_table.h>
2
3 #include <fstream>
4 #include <iostream>
5 #include <vector>
6
7 #include "Poisson1D.hpp"
8
9 int main(int /*argc*/, char * /*argv*/[])
10 {
11     ConvergenceTable table;
12
13     const std::vector<unsigned int> N_values = {
14         9, 19, 39, 79, 159, 319
15     };
16     const unsigned int degree = 2;
17
18     std::ofstream convergence_file("convergence.csv");
19     convergence_file << "h,eL2,eH1" << std::endl;
20
21     for (const unsigned int &N : N_values)
22     {
23         Poisson1D problem(N, degree);
24
25         problem.setup();
26         problem.assemble();
27         problem.solve();
28         problem.output();
29
30         const double h = 1.0 / (N + 1.0);
31         const double error_L2 = problem.compute_error(
32             VectorTools::L2_norm
33         );
34         const double error_H1 = problem.compute_error(
35             VectorTools::H1_norm
36         );
37
38         table.add_value("h", h);
39         table.add_value("L2", error_L2);
40         table.add_value("H1", error_H1);
41         convergence_file << h << "," << error_L2
42             << "," << error_H1 << std::endl;
43     }
44
45     table.evaluate_all_convergence_rates(ConvergenceTable::
46         reduction_rate_log2);
47
48     table.set_scientific("L2", true);
49     table.set_scientific("H1", true);
50
51     table.write_text(std::cout);
52
53     return 0;
54 }

```

Listing 4: `main.cpp` for convergence analysis

The key changes are:

- **ConvergenceTable** `table`; A helper class to store and analyze convergence data. `ConvergenceTable` is part of `deal.II`'s base module that **simplifies the collection and presentation of convergence results**. For example, it can automatically compute convergence rates based on the errors and mesh sizes provided.
- **Mesh ladder** `N_values = {9, 19, 39, 79, 159, 319}` A vector of mesh sizes (number of elements) to run the solver on. This creates a sequence of increasingly refined meshes for convergence analysis. They are taken from lab instructions (*"with polynomial degree $r = 1$, solve the Poisson 1D problem, with finite elements, setting $N + 1 = 10, 20, 40, 80, 160, 320$ "*). Since our 1D mesh has $N + 1$ elements, the **mesh size** is:

$$h = \frac{1}{N+1} \in \left\{ \frac{1}{10}, \frac{1}{20}, \frac{1}{40}, \frac{1}{80}, \frac{1}{160}, \frac{1}{320} \right\}$$

Each step **halves** h is essential for estimating convergence rates.

- **Fix the polynomial degree degree = 2** The polynomial degree of the finite element basis functions is fixed to $r = 2$ (quadratic elements). This choice affects the expected convergence rates:

- L^2 norm: $O(h^{r+1}) = O(h^3)$;
- H^1 norm: $O(h^r) = O(h^2)$.

We can later rerun the convergence analysis with different polynomial degrees to observe how the rates change.

- **CSV for plotting**

```
1 std::ofstream convergence_file("convergence.csv");
2 convergence_file << "h,eL2,eH1" << std::endl;
```

We create a CSV file to store the mesh size and errors for external plotting. The header row defines the columns: `h` (mesh size), `eL2` (L^2 error), and `eH1` (H^1 error). Each iteration appends a new row with the current mesh size and computed errors:

```
1 convergence_file << h << "," << error_L2 << "," << error_H1 <<
  std::endl;
```

This file can be used later for plotting convergence graphs using tools like Python's `Matplotlib` or Excel.

- **Loop over meshes, solve, compute the errors and store in table**

```
1 for (const unsigned int &N : N_values)
2 {
3     Poisson1D problem(N, degree);
4     problem.setup();
5     problem.assemble();
6     problem.solve();
7     problem.output();
8
9     const double h = 1.0 / (N + 1.0);
```

```

10     const double error_L2 = problem.compute_error(
11         VectorTools::L2_norm
12     );
13     const double error_H1 = problem.compute_error(
14         VectorTools::H1_norm
15     );
16
17     table.add_value("h", h);
18     table.add_value("L2", error_L2);
19     table.add_value("H1", error_H1);
20     convergence_file << h << "," << error_L2 << "," <<
        error_H1 << std::endl;
21 }

```

For each mesh size in `N_values`, we:

- Instantiate a new `Poisson1D` object with the current number of elements and fixed polynomial degree.
- Call the full solver pipeline: `setup()`, `assemble()`, `solve()`, and `output()`.
 - ❓ **Why call `output()` here?** Calling `output()` within the loop allows us to generate and save the solution for each mesh size. This is **useful for visual inspection of how the solution improves with mesh refinement**. It also provides a **record of the numerical solutions corresponding to each level of mesh refinement**, which can be valuable for debugging and analysis.
- Compute the mesh size h and the errors in L^2 and H^1 norms using the new `compute_error(...)` method.
- Store the mesh size and errors in the `ConvergenceTable` for later analysis.
- Append the results to the CSV file for external plotting.

The constant `h = 1.0 / (N + 1.0)` computes the mesh size based on the number of elements. This is crucial for convergence analysis, as we need to know how the error behaves as h decreases. About the errors, we call:

- `problem.compute_error(VectorTools::L2_norm)` to compute the L^2 norm of the error;
- `problem.compute_error(VectorTools::H1_norm)` to compute the H^1 norm of the error.

• Compute \log_2 convergence rates

```

1 table.evaluate_all_convergence_rates(ConvergenceTable::
    reduction_rate_log2);
2 table.set_scientific("L2", true);
3 table.set_scientific("H1", true);
4 table.write_text(std::cout);

```

After collecting all the data, we call `evaluate_all_convergence_rates(...)` to **compute the convergence rates** based on the errors and mesh sizes. We use `ConvergenceTable::reduction_rate_log2` to get the rates in base 2, which is standard in numerical analysis. The `set_scientific`

(...) calls `format` the error values in scientific notation for better readability. Finally, `write_text(...)` outputs the convergence table to the console, showing the mesh sizes, errors, and estimated convergence rates.

❓ What is a convergence driver?

A **convergence driver** is a program or script that **systematically tests a numerical method by solving a problem on a series of increasingly refined meshes**. The goal is to observe how the error between the numerical solution and the exact solution decreases as the mesh is refined, thereby estimating the convergence rates of the method. Key features of a convergence driver include:

- **Mesh Refinement:** It runs the solver on a sequence of meshes with decreasing mesh sizes (e.g., halving the mesh size at each step).
- **Error Computation:** It computes the error norms (e.g., L^2 , H^1) between the numerical solution and a known exact solution (from MMS).
- **Convergence Rate Estimation:** It analyzes how the errors decrease with mesh refinement to estimate the convergence rates, which can be compared against theoretical predictions.
- **Data Collection and Presentation:** It collects the results in a structured format (e.g., tables, CSV files) for easy analysis and visualization.

By automating this process, a convergence driver helps verify the correctness and efficiency of numerical methods, ensuring they perform as expected in practice.

❓ What we should expect from the convergence analysis?

When we run the convergence driver, we should expect to see the following results in the output convergence table:

- **Decreasing Errors:** As the mesh is refined (i.e., as h decreases), the errors in both the L^2 and H^1 norms should decrease. This indicates that the numerical solution is converging to the exact solution.
- **Convergence Rates:** The estimated convergence rates should align with the theoretical predictions based on the polynomial degree r of the finite element basis functions:
 - For the L^2 norm, we expect a convergence rate of approximately $r+1$. For example, with $r = 2$, we expect a rate of about 3.
 - For the H^1 norm, we expect a convergence rate of approximately r . For example, with $r = 2$, we expect a rate of about 2.
- (Tip) **Scientific Notation:** The errors should be presented in scientific notation for better readability, especially as they become very small with mesh refinement.
- **Consistency:** The results should be consistent across different runs of the convergence driver, indicating that the numerical method is stable and reliable.

If the observed convergence rates match the theoretical expectations, it validates the correctness of the implementation and the effectiveness of the numerical method. If there are discrepancies, it may indicate issues in the implementation or the need for further investigation into the numerical method's properties.

The output of the convergence driver should look like this:

`output.txt`



The source code is available at:

`Source code`



References

- [1] Quarteroni Alfio Maria. Numerical methods for partial differential equations. Slides from the HPC-E master's degree course on Politecnico di Milano, 2024.

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