Interpolating amplitudes

Víctor Bresó,[a] **Gudrun Heinrich,**[b] **Vitaly Magerya,**[c] **Anton Olsson**[b]

[a]*Institute for Theoretical Physics, University of Heidelberg, 69120 Heidelberg, Germany*

[b]*Institute for Theoretical Physics, Karlsruhe Institute of Technology, 76131 Karlsruhe, Germany*

[c]*Theoretical Physics Department, CERN, 1211 Geneva 23, Switzerland*

E-mail: v.breso@thphys.uni-heidelberg.de, gudrun.heinrich@kit.edu, vitaly.magerya@cern.ch, anton.olsson@kit.edu

ABSTRACT: While the calculation of scattering amplitudes at higher orders in perturbation theory has reached a high degree of maturity, their usage to produce physical predictions within Monte Carlo programs is often hampered by the slow evaluation of the multi-loop amplitudes, especially so for amplitudes calculated numerically. As a remedy, interpolation frameworks have been successfully used in lower dimensions, but for higher-dimensional problems, such as the five dimensions of a $2 \to 3$ phase space, efficient and reliable solutions are sparse.

This work aims to fill this gap by reviewing state-of-the-art interpolation methods, and by assessing their performance for concrete examples drawn from particle physics. Specifically, we investigate interpolation methods based on polynomials, splines, spatially adaptive sparse grids, and neural networks (multilayer perceptron and Lorentz-Equivariant Geometric Algebra Transformer). Our additional aim is to motivate further studies of the interpolation of scattering amplitudes among both physicists and mathematicians.

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Contents

1 Introduction

Particle physics today demands precision calculations of scattering amplitudes to find hints of physics beyond the Standard Model (BSM) in the data from current colliders. Even more precision is needed to ensure the feasibility of exploiting the much more precise data expected from future colliders.

Impressive progress has been made in the calculation of QCD corrections at next-to-next-to-leading order and beyond to the most important processes at the Large Hadron Collider (LHC) [1–3], however most of them are restricted to processes involving relatively few kinematic scales or masses. This is due to the fact that analytic calculations of the required two-loop amplitudes become rapidly unfeasible as the number of external legs and/or particle masses is increasing. For numerical methods the growth in complexity with the number of scales is more tractable. Therefore, the domains of two-loop amplitudes beyond $2 \to 2$ scattering, involving 5 or more kinematic scales, as well as the domains of multi-loop corrections in electro-weak or BSM theories, involving many different masses, are the ones where numerical methods to calculate the virtual amplitudes can prove extremely useful. On the other hand, the usefulness in phenomenological applications is strongly tied to the speed and accuracy at which these amplitudes can be evaluated. In a realistic Monte Carlo evaluation of total or differential cross sections, typically millions of phase-space points need to be evaluated. For this important use case it is unfeasible to embark on a lengthy numerical evaluation of the amplitude for each individual phase-space point.

Therefore, a promising way to make the usage of numerical methods for multi-loop amplitudes more practical is to precompute the values of the amplitudes at some set of points, often a grid, and rely on interpolation to evaluate them at other phase-space points, i.e. for events produced by the Monte Carlo program. However, interpolation for $2 \to 3$ processes needs to be performed on a five-dimensional phase space, which makes it a highly non-trivial task.

The intention of this work is to present a selection of state-of-the-art multidimensional interpolation methods and study their practical usage and performance, having the physics use case in mind. While there is vast mathematical literature on interpolation, the test functions used in mathematics often have different properties than the functions related to loop amplitudes. The purpose of this article is to connect the mathematical literature with the physics use cases that so far were mostly limited to interpolation in dimensions lower than five.

The remaining part of this paper is structured as follows: in Section 2 we give a brief introduction to amplitudes and cross sections. We formulate the interpolation problem and define the error metrics and test functions we use to benchmark the approximation methods. In Sections 3–6, four categories of methods are described. Section 3 is about polynomial interpolation, Section 4 about B-splines, Section 5 about sparse grids and Section 6 about machine learning techniques. In these sections, the main results are presented in the form of plots of the approximation error against the amount of training data. We conclude in Section 7 by summarizing the results of the previous sections. Further details on the parametrization of the test functions are given in Appendix A.

2 Setting the stage

2.1 What is an amplitude?

In a proton–proton collider of collision energy $\sqrt{s}$, the number of times a reaction

$$\underbrace{p + p}_{\text{protons}} \rightarrow \underbrace{a(q_1) + b(q_2)}_{\text{partons}} \rightarrow \underbrace{c(p_1) + d(p_2) + \dots}_{\text{particles}} \tag{2.1}$$

takes place is proportional to the *differential cross section* of the process [4], which, assuming that the squared masses of partons a and b are much smaller than s, is

$$d\sigma = \frac{1}{2\hat{s}} \, |\mathcal{M}(q_1, q_2, p_1, p_2, \dots)|^2 \, d\Phi \, d\rho_{a,b}(\hat{s}, s), \tag{2.2}$$

where $\mathcal{M}$ is the *scattering amplitude* for the process $a + b \rightarrow c + d + \dots$, $d\Phi$ is the element of the Lorentz-invariant phase space, given in terms of the four-momenta q_i, p_i, and masses m_i as

$$d\Phi = (2\pi)^4 \, \delta^4(q_1 + q_2 - \sum_i p_i) \prod_i \frac{d^4 p_i}{(2\pi)^4} 2\pi\delta(p_i^2 - m_i^2) \, \theta(p_i^{(0)}), \tag{2.3}$$

and $d\rho$ is the probability of finding partons a and b with collision energy $\sqrt{\hat{s}}$ in the colliding proton pair, given via the *parton distribution functions* f_a, f_b as

$$d\rho_{a,b}(\hat{s}, s, \mu_F) = d\hat{s} \int f_a(x_1, \mu_F) \, f_b(x_2, \mu_F) \, \delta(\hat{s} - s x_1 x_2) \, dx_1 \, dx_2. \tag{2.4}$$

Parton distribution functions themselves are well studied and readily available via [5]. The amplitude is normally calculated within perturbation theory as an expansion in a small coupling parameter, e.g. the strong coupling α_s:

$$|\mathcal{M}|^2 \equiv \mathcal{A} = \sum_{k=0}^{\infty} \left(\frac{\alpha_s}{2\pi}\right)^k \mathcal{A}_k. \tag{2.5}$$

Each subsequent term of this expansion is much harder to calculate than the previous one, so when calculating $\mathcal{A}_2$, one can consider $\mathcal{A}_0$ and $\mathcal{A}_1$ to be readily available. Tools exist for the automated calculation of $\mathcal{A}$ up to the next-to-leading order [6–10]; beyond that, the calculations are usually custom-made for each process.

The differential cross section depends on the parameters that fully characterize the phase space. These are two for $2 \rightarrow 2$ processes, five for $2 \rightarrow 3$, nine for $2 \rightarrow 4$, etc. There is a freedom to choose these parameters; common choices are energy or Mandelstam variables, $s_{ij} = (p_i + p_j)^2$, and angular variables. In what follows, we denote these parameters as $\vec{x}$, and choose them such that the physical region of the process is a hypercube: $\vec{x} \in (0; 1)^d$.

The primary use of amplitudes is to calculate cross sections—either the total values over the whole phase space: $\sigma \equiv \int d\sigma$, or differential over some phase-space partitioning defined either via some observable quantity $\mathcal{O}$: $d\sigma/d\mathcal{O}$, or via a sequence of them, as in e.g. [11].

2.2 Our goal

Assume that we can calculate most parts of a squared amplitude $\mathcal{A}$ quickly and precisely, but one part, e.g. a subleading order in α_s, is slow or expensive to evaluate. Let us denote this part as $a : (0;1)^d \to \mathbb{R}$. We aim to approximate a by some function $\widetilde{a}$, from the knowledge of the values of a at some *data points* $\vec{x}_1, \ldots, \vec{x}_n$: $a_i \equiv a(\vec{x}_i)$. We are interested in algorithms to choose $\vec{x}_i$ and to construct $\widetilde{a}$ such that it is "close enough" to a, while requiring as few data points as possible, as to minimize the expensive evaluations of a.

2.3 How to define the approximation error?

There are different ways to precisely define what "close enough" means, and no single definition works equally well for all observables and phase-space regions of interest, so a choice of what to prioritize must be made.

In this paper we choose $\mathrm{d}\sigma/\mathrm{d}\vec{x}$ as the probability density of interest, and define the approximation error as the distance between probability densities $\mathrm{d}\sigma/\mathrm{d}\vec{x}$ based on $\widetilde{a}$ and a, measured via the L^1 norm:[1]

$$\varepsilon = \frac{||\widetilde{f} - f||_1}{||f||_1}, \quad \text{where} \quad f(\vec{x}) \equiv a(\vec{x}) \underbrace{\frac{1}{2\hat{s}} \left| \frac{\mathrm{d}(\Phi, \rho)}{\mathrm{d}\vec{x}} \right|}_{\equiv \text{ weight } w(\vec{x})}. \tag{2.6}$$

The choice of the L^1 norm ensures that this quantity is independent of the choice of variables $\vec{x}$. In statistics, it is known as *total variation distance* (up to an overall normalization). This distance weighs different phase-space regions proportional to their contribution to the total cross section (via the factor w), and guarantees that for any phase-space subregion R, using $\widetilde{a}(\vec{x})$ instead of $a(\vec{x})$ will result in the error of σ_R being no more than $\varepsilon \left(\frac{\alpha_s}{2\pi}\right)^k ||f||_1$. We target ε of at most 1%.

Note that the precision of the total cross section comes at the expense of precision in tails of differential distributions: for parts of the phase space that do not contribute much to the total cross section, such as the very-high-energy region, only low precision is guaranteed by a bound on ε. An alternative definition of the error, $\varepsilon = \max |\widetilde{a}/a - 1|$, would ensure equal relative precision for all bins of any differential distribution, but would come at the expense of the interpolation spending most effort on phase-space regions where only few (or zero) experimental data points can be expected at the LHC. This is the trade-off involved in error target choices; to apply the methods we study, each application would need to choose its own appropriate error measure.

2.4 How to prioritize different phase-space regions?

Summarizing Section 2.3, we approximate $a(\vec{x})$, and encode the relative importance of different phase-space regions into $w(\vec{x})$. But can we incorporate this importance information to improve the approximation procedure? There are multiple options:

1. Instead of constructing an approximation for $a(\vec{x})$ directly, we can construct an approximation $\widetilde{f}(\vec{x})$ for $f(\vec{x}) \equiv a(\vec{x}) w(\vec{x})$, and then set $\widetilde{a}(\vec{x}) = \widetilde{f}(\vec{x})/w(\vec{x})$.

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[1]Here and throughout, we define the L^p-norm $||f||_p$ as $\left(\int |f(\vec{x})|^p \, \mathrm{d}\vec{x} \right)^{1/p}$.

2. For methods based on regression, we can choose the data points x_i such that they cluster more in regions where $w(\vec{x})$ is greater.

3. For adaptive methods, we can approximate $a(\vec{x})$, but use the quantity $a\,w$ in the adaptivity condition, so that regions where $a\,w$ (and not just a) is approximated the worst are refined first.

4. We can find a variable transformation from $\vec{x}$ to $\vec{y}$ that cancels w, and interpolate in $\vec{y}$ instead of $\vec{x}$. In other words, choose τ with $\vec{x} = \tau(\vec{y})$ such that $w(\vec{x})\,|\,\mathrm{d}\tau(\vec{x})/\mathrm{d}\vec{y}\,| = 1$, so that $\int a\,w\,\mathrm{d}x = \int a\,\mathrm{d}y$.

   We know of no general way to construct such transformations in the multidimensional case, but a popular approach is to approximate τ as its rank-1 decomposition: $\tau(\vec{y}) = \prod_i \tau_i(y_i)$; this is the basis of the VEGAS integration algorithm [12]. Higher-rank approximations are, of course, also possible.

2.5 The test functions

In the remainder of the article we assess the performance of the most promising interpolation algorithms studied in numerical analysis when applied to the following five test functions.

Test function f_1:

   Leading-order (tree-level) amplitude for $q\bar{q} \to t\bar{t}H$ taken as a 5-dimensional function over the phase space as described in [13]. Specifically,

$$a_1 = \langle \mathcal{M}_0^{q\bar{q}t\bar{t}H} | \mathcal{M}_0^{q\bar{q}t\bar{t}H} \rangle, \quad f_1 = a_1 \times \left| \frac{\mathrm{d}\Phi_{t\bar{t}H}}{\mathrm{d}(\mathrm{frac}_{s_{t\bar{t}}}, \theta_H, \theta_t, \varphi_t)} \right| \times \frac{1}{2\hat{s}} \frac{\mathrm{d}\rho_{q\bar{q}}}{\mathrm{d}\beta^2} \times J_{t\bar{t}H}, \quad (2.7)$$

   with the phase space parameters set as

$$\beta^2 = \frac{10}{100} + \frac{86}{100} x_1, \quad \mathrm{frac}_{s_{t\bar{t}}} = x_2, \quad \theta_H = \pi x_3, \quad \theta_t = \pi x_4, \quad \varphi_t = 2\pi x_5, \quad (2.8)$$

$$J_{t\bar{t}H} = \left| \frac{\mathrm{d}(\beta^2, \mathrm{frac}_{s_{t\bar{t}}}, \theta_H, \theta_t, \varphi_t)}{\mathrm{d}\vec{x}} \right| = \frac{86}{50} \pi^3. \quad (2.9)$$

   The phase space parameters are described in more detail in Appendix A.1. To specify $\rho_{q\bar{q}}$ it is possible to use eq. (2.4) together with one of the well known parton distribution functions, but to be more self-contained, we use the following generic form of ρ:

$$\frac{1}{2\hat{s}} \frac{\mathrm{d}\rho_{q\bar{q}}}{\mathrm{d}\beta^2} \propto \frac{(1 - c_1\beta^2)^2}{(1 - c_2\beta^2)(1 - c_3\beta^2)}, \quad (2.10)$$

   and set $c = \{1.0132, 0.9943, 0.3506\}$, which approximates ρ computed using the parton distribution functions from [14]. The overall proportionality constant is omitted here because it cancels in the error definition of eq. (2.6).

   The amplitude a_1 possesses multiple discrete symmetries. For us of immediate interest are the symmetry under $\varphi_t \to -\varphi_t$ (parity invariance), and the symmetry of the swap $\{q, t\} \leftrightarrow \{\bar{q}, \bar{t}\}$. These two symmetries are present in all higher order corrections to
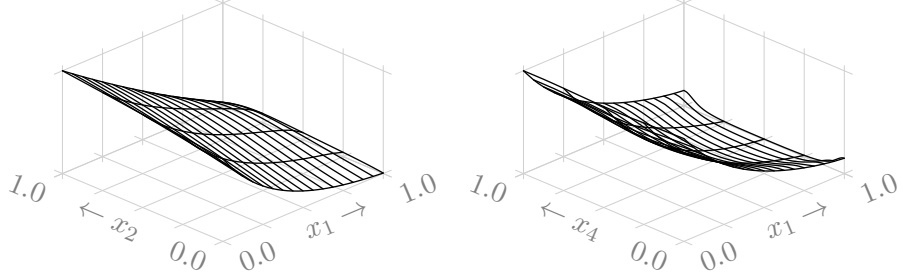
this amplitude too; the leading order is additionally symmetric under the swap $q \leftrightarrow \bar{q}$. In terms of the variables x_i, this works out to

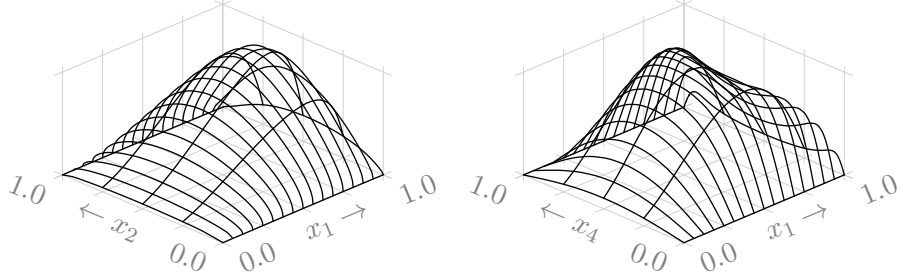$$\varphi_t \to -\varphi_t : \qquad a_1(x_5) = a_1(1-x_5), \qquad (2.11)$$

$$\{q,t\} \leftrightarrow \{\bar{q},\bar{t}\} : \qquad a_1(x_3,x_4) = a_1(1-x_3,1-x_4), \qquad (2.12)$$

$$q \leftrightarrow \bar{q} : \qquad a_1(x_3,x_5) = a_1(1-x_3,x_5+1/2). \qquad (2.13)$$

As an illustration, slices of the amplitude a_1 in x_1–x_2 and x_1–x_4 space are as follows:

The same slices for the function f_1 are:

Test function f_2:

One-loop amplitude contributing to $q\bar{q} \to t\bar{t}H$, taken as a 5-dimensional function. This amplitude has an integrable Coulomb-type singularity at $\mathrm{frac}_{s_{t\bar{t}}} \to 0$, which needs to be tamed for interpolation to work well. We do this by subtracting the singular behaviour using eq. (2.67) from [15], i.e.:

$$a_2 = 2\mathrm{Re}\left[\langle \mathcal{M}_0^{q\bar{q}t\bar{t}H}|\mathcal{M}_1^{q\bar{q}t\bar{t}H}\rangle - \frac{\pi^2}{\beta_{t\bar{t}}}\langle \mathcal{M}_0^{q\bar{q}t\bar{t}H}|\mathbf{T}_{t\bar{t}}|\mathcal{M}_0^{q\bar{q}t\bar{t}H}\rangle\right], \qquad (2.14)$$

$$f_2 = a_2 \times \left|\frac{\mathrm{d}\Phi_{t\bar{t}H}}{\mathrm{d}(\mathrm{frac}_{s_{t\bar{t}}},\theta_H,\theta_t,\varphi_t)}\right| \times \frac{1}{2\hat{s}}\frac{\mathrm{d}\rho_{q\bar{q}}}{\mathrm{d}\beta^2} \times J_{t\bar{t}H}, \qquad (2.15)$$
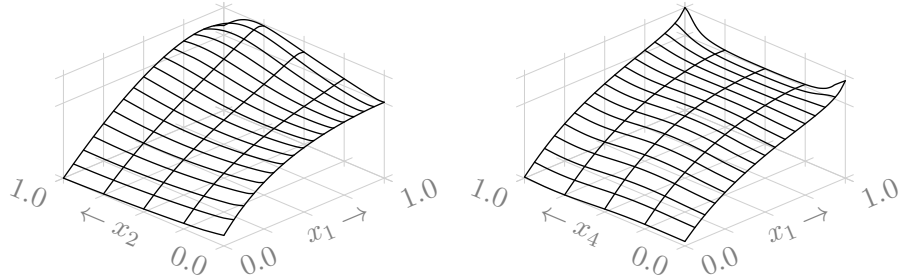
where $\mathbf{T}_{t\bar{t}}$ is a colour operator defined in [15] and $\beta_{t\bar{t}}$ is the velocity of the $t\bar{t}$ system, in our variables given by

$$\beta_{t\bar{t}}^2 \equiv 1 - \left[1 + \mathrm{frac}_{s_{t\bar{t}}}\left(\left(\frac{1+\frac{1}{2}\frac{m_H}{m_t}}{\sqrt{1-\beta^2}} - \frac{1}{2}\frac{m_H}{m_t}\right)^2 - 1\right)\right]^{-1}. \qquad (2.16)$$
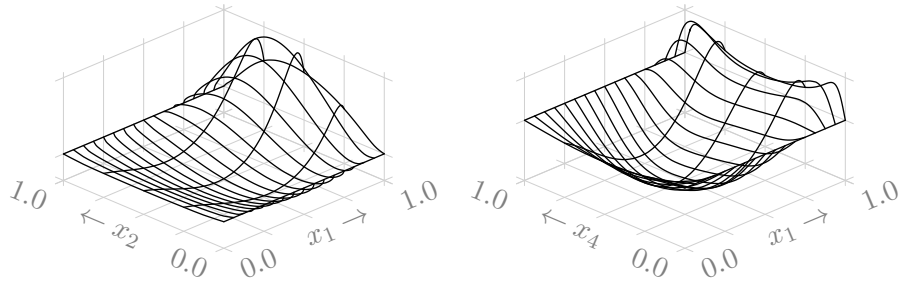
Both the phase space and $\rho_{q\bar{q}}$ are the same as for f_1. The amplitude a_2 possesses two of the symmetries of a_1:

$$a_2(x_5) = a_2(1 - x_5), \quad \text{and} \quad a_2(x_3, x_4) = a_2(1 - x_3, 1 - x_4). \tag{2.17}$$

Slices of the amplitude a_2 in x_1–x_2 and x_1–x_4 space are as follows:

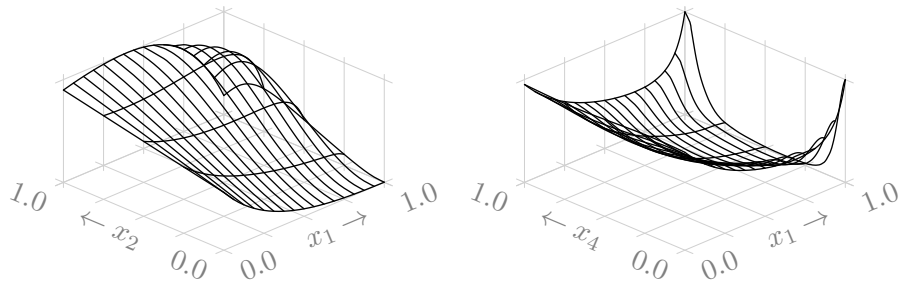The same slices for the function f_2 are:

Test function f_3:

Leading-order (tree-level) amplitude for $gg \to t\bar{t}H$,

$$a_3 = \langle \mathcal{M}_0^{ggt\bar{t}H} | \mathcal{M}_0^{ggt\bar{t}H} \rangle, \quad f_3 = a_3 \times \left| \frac{\mathrm{d}\Phi_{t\bar{t}H}}{\mathrm{d}(\mathrm{frac}_{s_{t\bar{t}}}, \theta_H, \theta_t, \varphi_t)} \right| \times \frac{1}{2\hat{s}} \frac{\mathrm{d}\rho_{gg}}{\mathrm{d}\beta^2} \times J_{t\bar{t}H}, \tag{2.18}$$

with the same kinematics and phase space as for f_1, and $\mathrm{d}\rho_{gg}/\mathrm{d}\beta^2$ chosen via the ansatz of eq. (2.10) with $c = \{1.0134, 0.7344, 0.0987\}$.

The amplitude a_3 possesses the same symmetries as a_1, given in eq. (2.13).

Slices of the amplitude a_3 in x_1–x_2 and x_1–x_4 space are as follows:

The same slices for the function f_3 are:

Test function f_4:

One-loop amplitude contributing to $gg \to t\bar{t}H$, taken as a 5-dimensional function, with the Coulomb-type singularity subtracted in the same way as for a_2, i.e.

$$a_4 = 2\mathrm{Re}\left[\langle \mathcal{M}_0^{ggt\bar{t}H}|\mathcal{M}_1^{ggt\bar{t}H}\rangle - \frac{\pi^2}{\beta_{t\bar{t}}}\langle \mathcal{M}_0^{ggt\bar{t}H}|\mathbf{T}_{t\bar{t}}|\mathcal{M}_0^{ggt\bar{t}H}\rangle\right], \qquad (2.19)$$

$$f_4 = a_4 \times \left|\frac{\mathrm{d}\Phi_{t\bar{t}H}}{\mathrm{d}(\mathrm{frac}_{s_{t\bar{t}}}, \theta_H, \theta_t, \varphi_t)}\right| \times \frac{1}{2\hat{s}}\frac{\mathrm{d}\rho_{gg}}{\mathrm{d}\beta^2} \times J_{t\bar{t}H}, \qquad (2.20)$$
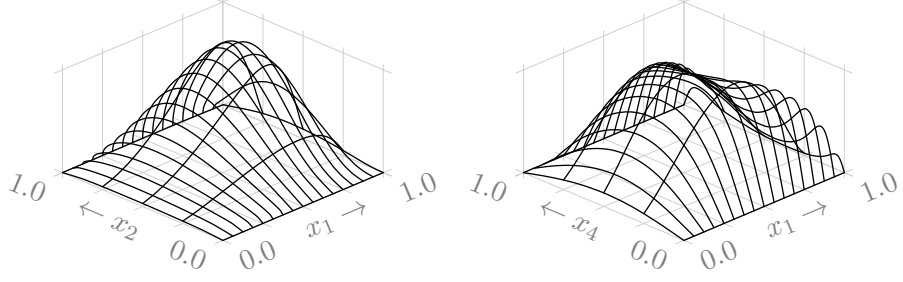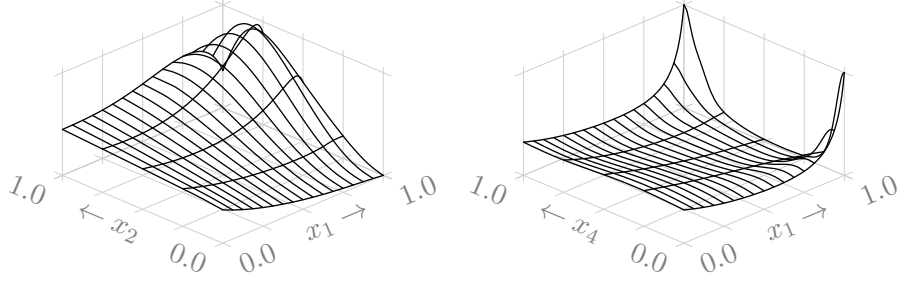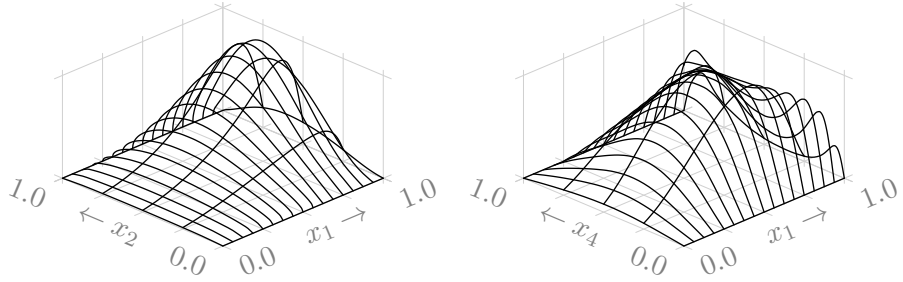
where $\beta_{t\bar{t}}$ is given in eq. (2.16), and the rest is the same as for f_3.

The amplitude a_4 possesses the same symmetries as a_3 and a_1, given in eq. (2.13).

Slices of the amplitude a_4 in x_1–x_2 and x_1–x_4 space are as follows:

The same slices for the function f_4 are:

Test function f_5:

Leading-order (one-loop) amplitude for $gg \to Hg$, taken as a 2-dimensional function,

$$a_5 = \langle \mathcal{M}_1^{ggHg}|\mathcal{M}_1^{ggHg}\rangle, \quad f_5 = a_5 \times \frac{\mathrm{d}\Phi_{Hg}}{\mathrm{d}\theta_H} \times \frac{1}{2\hat{s}}\frac{\mathrm{d}\rho_{gg}}{\mathrm{d}\beta^2} \times J_{Hg}, \qquad (2.21)$$

with the phase-space parameters set as

$$\beta^2 = \frac{33}{100} + \frac{66}{100}x_1, \quad \theta_H = \theta_0 + (\pi - 2\theta_0)x_2, \tag{2.22}$$

$$J_{Hg} = \left|\frac{\mathrm{d}(\beta^2, \theta_H)}{\mathrm{d}\vec{x}}\right| = \frac{66}{100}(\pi - 2\theta_0), \tag{2.23}$$

the phase-space density being

$$\frac{\mathrm{d}\Phi_{Hg}}{\mathrm{d}\theta_H} = \frac{1}{16\pi}\frac{1}{\hat{s}}\sqrt{\lambda(\hat{s}, m_H^2, 0)}\sin\theta_H = \frac{\beta^2\sin\theta_H}{16\pi}, \tag{2.24}$$

and $\mathrm{d}\rho_{gg}/\mathrm{d}\beta^2$ chosen via the ansatz of eq. (2.10), with $c = \{1.0012, 0.9802, 0.3357\}$.

The introduction of θ_0 as a cutoff is needed because a_5 diverges as $1/\sin^2\theta_H$ at $\theta_H \to 0$ and $\theta_H \to \pi$. We choose not to interpolate the region around the divergence, because in practical calculations it should be regulated by infrared subtraction or appropriate kinematic cuts; we only consider the phase-space region where the transverse momentum p_T of the Higgs boson H is greater than a cutoff $p_{T,0}$. Then:

$$\sin\theta_0 = p_{T,0}\frac{2\sqrt{\hat{s}}}{\sqrt{\lambda(\hat{s}, m_H^2, 0)}} = 2\frac{p_{T,0}}{m_H}\frac{\sqrt{1-\beta^2}}{\beta^2}, \tag{2.25}$$

We choose $p_{T,0}$ corresponding to the lower boundary of the β^2 region from eq. (2.22):

$$\frac{p_{T,0}}{m_H} = \frac{1}{2}\frac{\beta_{\min}^2}{\sqrt{1-\beta_{\min}^2}}, \tag{2.26}$$

such that at $\beta^2 < \beta_{\min}^2$ no phase space point passes the p_T cut. This works out to $p_{T,0} \approx 25$ GeV.

The amplitude a_5 is symmetric under the swap of the incoming gluons, i.e.

$$a_5(x_2) = a_5(1 - x_2). \tag{2.27}$$

The amplitude a_5 (left) and the function f_5 (right) depend on x_1 and x_2 as follows:

In all cases we use GoSam [9] to evaluate the amplitudes, and set $m_H^2/m_t^2 = 12/23$.

2.6 How to use test function symmetries?

When the test functions are symmetric under discrete transformations, as ours are, there are multiple ways to take advantage of this:

1. Make the interpolant obey the same symmetries by construction.

2. Duplicate symmetric data points, i.e. if $f(x) = f(1-x)$, then for each x_i also add $1 - x_i$ to the data set (but still count this as a single evaluation of f).

3. Reduce the interpolation domain, i.e. if $f(x) = f(1-x)$, only construct the approximation for $x \in [0, 1/2]$, and use the symmetry to obtain the values in $x \in [1/2, 1]$.

2.7 How to evaluate the approximation error?

To evaluate eq. (2.6) we use Monte Carlo integration. It can be formulated based on different kinds of testing samples:

$$\text{uniform:} \qquad \vec{x}_1, \ldots \vec{x}_m \sim 1, \qquad \varepsilon = \frac{\sum_{i=1}^m |(\tilde{a}_i - a_i) w_i|}{\sum_{i=1}^m |a_i w_i|}, \qquad (2.28)$$

$$\text{partially unweighted:} \qquad \vec{x}_1, \ldots, \vec{x}_m \sim w, \qquad \varepsilon = \frac{\sum_{i=1}^m |\tilde{a}_i - a_i|}{\sum_{i=1}^m |a_i|}, \qquad (2.29)$$

$$\text{leading-order unweighted:} \quad \vec{x}_1, \ldots, \vec{x}_m \sim a_{\text{LO}}\, w, \quad \varepsilon = \frac{\sum_{i=1}^m |(\tilde{a}_i - a_i)/a_{\text{LO},i}|}{\sum_{i=1}^m |a_i/a_{\text{LO},i}|}. \quad (2.30)$$

The first of these is natural for the selected variables $\vec{x}$, the second is important because it is independent of the choice of $\vec{x}$ (and can be approximated by e.g. the widely used RAMBO sampling technique [16]), and the third is important because it is oriented at the approximate probability distribution of physical scattering events, encoded in the leading order amplitude, a_{LO}.

While each sampling method must yield the same result asymptotically, in practice we are interested in using as few testing evaluations as possible. In Figure 1 we compare the error convergence when using the different sampling methods for test function f_2. Here we see that the error becomes stable for all methods after $m \sim 1000$ samples.

Note that a uniform sample can be generated both via Monte Carlo, i.e. randomly, and with a low-discrepancy sequence (such as the Sobol sequence). In Figure 1 we present results for both options, and while sampling from a low-discrepancy sequence gives a more uniform coverage of the parameter space, we see only marginal improvements in the error convergence.
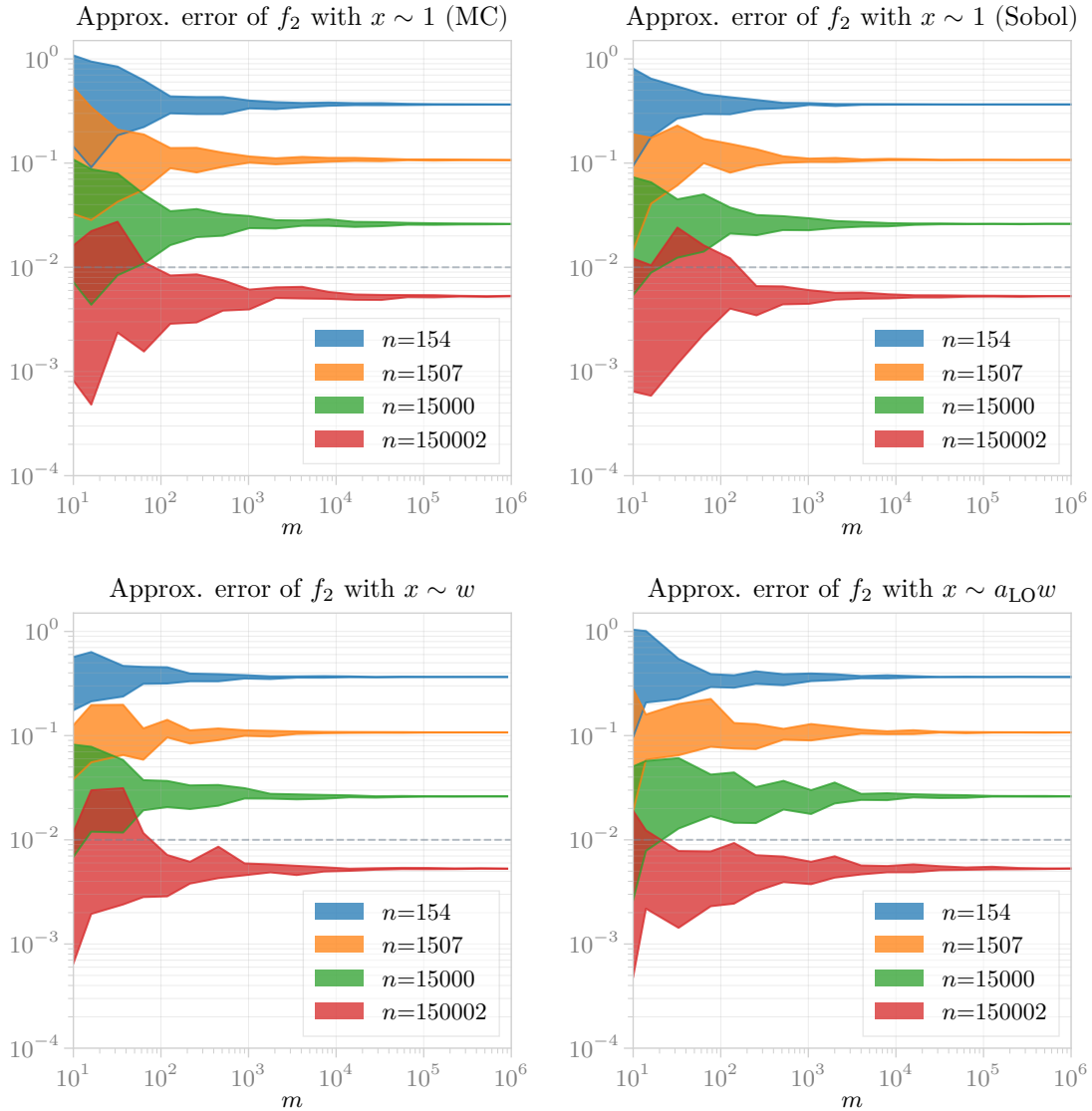
Figure 1: Approximation error ε of f_2, as defined in eq. (2.6), evaluated via eq. (2.28), eq. (2.29), and eq. (2.30), with respect to the number of testing points m. The uniform samples are taken both randomly (MC) and from a low-discrepancy sequence (Sobol). The approximations are constructed using sparse grid interpolation from Section 5, with different numbers of data points n. The error bands are created from 10 independent testing sets for each m.

3 Polynomial interpolation

The classic interpolation method is polynomial interpolation [17, 18]. In the univariate case $\widetilde{f}$ is constructed as a polynomial of degree $n-1$ that exactly passes through the n

interpolation nodes x_i. It can be written in the *Lagrange form* as

$$\widetilde{f}(x) = \sum_{i=1}^{n} f_i \, l_i(x), \qquad l_i(x) \equiv \prod_{j \neq i} \frac{x - x_j}{x_i - x_j}, \tag{3.1}$$

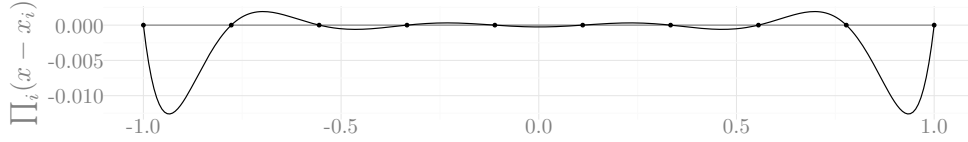or slightly rewritten in the *barycentric form* [19] as:

$$\widetilde{f}(x) = \frac{\displaystyle\sum_{i=1}^{n} \frac{w_i}{x - x_i} f_i}{\displaystyle\sum_{i=1}^{n} \frac{w_i}{x - x_i}}, \qquad w_i = \prod_{j \neq i} \frac{1}{x_i - x_j}. \tag{3.2}$$

The barycentric interpolation formula is general enough that with an appropriate choice of the *weights* w_i, any *rational* interpolation can be expressed by it; the weights given here, however, correspond to the purely polynomial interpolation of eq. (3.1).[2] This is our form of choice for evaluation due to its numerical stability and simplicity.

The error of a polynomial approximation is given by

$$f(x) - \widetilde{f}(x) = \frac{f^{(n)}(\xi)}{n!} \prod_{i=1}^{n} (x - x_i), \tag{3.3}$$

where ξ is some function of x. To minimize this error *a priori* without the precise knowledge of $f^{(n)}$, one can choose the nodes x_i such that they would minimize $\prod_i (x - x_i)$ over the domain of interest. Doing so is important because a naive choice of equidistant nodes leads to the *Runge phenomenon* [21]: the approximation error explodes close to the boundaries, increasingly worse with higher degree of the polynomial. E.g. for 10 nodes on the interval of $[-1; 1]$:

3.1 Chebyshev nodes of the first kind

The product $\prod_i (x - x_i)$ is minimized in the sense of the infinity norm by the *Chebyshev nodes of the first kind*, which are traditionally given for the domain $[-1; 1]$ as

$$x_i = \cos\left(\frac{2i - 1}{2n} \pi \right), \qquad i = 1, \dots, n. \tag{3.4}$$

These nodes achieve a uniform $\prod_i (x - x_i)$ over the interval:

---

[2]Rational interpolation methods, specifically of the non-linear kind, such as the AAA algorithm [20], have established themselves as the most efficient one-dimensional interpolation methods, but generalizations to many dimensions are not developed well enough for us to consider them.

3.2 Chebyshev polynomials

Corresponding to these nodes are the *Chebyshev polynomials of the first kind*:

$$T_k(x) = \cos(k \arccos(x)). \tag{3.5}$$

Specifically, eq. (3.4) are the zeros of $T_n(x)$. These polynomials are orthogonal with respect to the weight $1/\sqrt{1-x^2}$:

$$\int_{-1}^{1} \frac{T_n(x) \, T_m(x)}{\sqrt{1-x^2}} \, \mathrm{d}x = \begin{cases} \pi & \text{if } n = m = 0, \\ \pi/2 & \text{if } n = m \neq 0, \\ 0 & \text{if } n \neq m. \end{cases} \tag{3.6}$$

Note that the nodes in eq. (3.4) are nothing more than equidistant points in $\phi = \arccos(x)$, and the corresponding polynomials are simply an even Fourier series in ϕ. This is why a transformation from the function values $\{f_i\}$ to the coefficients of the decomposition into Chebyshev polynomials $\{c_i\}$,

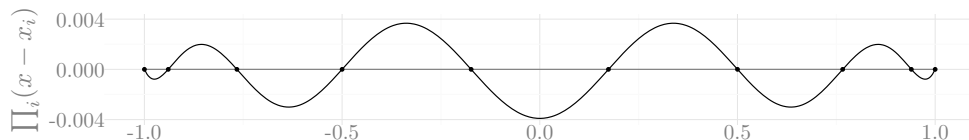$$\widetilde{f}(x) = \sum_i c_i \, T_i(x), \tag{3.7}$$

is just a Fourier transform (specifically, a discrete cosine transform). Still, for interpolation purposes, the barycentric form of eq. (3.2) is preferable, since both eq. (3.7) and the monomial form suffer from rounding errors that prevent their usage for $n \gtrsim 40$.

3.3 Chebyshev nodes of the second kind

A related set of points that avoids the Runge phenomenon is *Chebyshev nodes of the second kind* (a.k.a. *Chebyshev–Lobatto nodes*), traditionally given as

$$x_i = \cos\left(\frac{i-1}{n-1}\pi\right), \qquad i = 1, \ldots, n. \tag{3.8}$$

Unlike eq. (3.4), these points are not located at the zeros of $T_n(x)$, but rather at the extrema and the end points, with the advantage of being nested: the set of n of these is exactly contained in the set of $2n - 1$. This comes at the price of $\prod_i(x - x_i)$ not being uniform over the interval:

The property of being nested is important for adaptive interpolation constructions, because larger grids can reuse the results of smaller ones that they contain.

Unfortunately the inclusion of the end points can make this construction impractical for scattering amplitudes. For example, f_2 can not be evaluated at exactly $x_2 = 0$ due to loss of numerical precision, and evaluation at $x_1 = 1$ is possible, but best avoided, because evaluation time typically grows when approaching this boundary.

3.4 Approximation error scaling

It is known that polynomial interpolation at Chebyshev nodes is logarithmically close to the best polynomial interpolation of the same degree [17]. The approximation error itself depends on how smooth the function f is [18, 22, 23]. If f has $\nu - 1$ continuous derivatives and the variation of $f^{(\nu)}$ is bounded, then

$$||f - \widetilde{f}||_2 \leq \frac{4\,||f^{(\nu)}||_1}{\pi\nu(n-\nu)^\nu}, \quad \text{for } n > \nu. \tag{3.9}$$

If f is analytic, and can be analytically continued to an ellipse in the complex plane with focal points at ± 1 and the sum of semimajor and semiminor axes ρ (a *Bernstein ellipse*), then

$$||f - \widetilde{f}||_2 \leq \frac{4M\rho^{-n}}{\rho - 1}, \quad \text{where } M = \max|f(x)| \text{ in the ellipse.} \tag{3.10}$$

3.5 Gauss nodes

Closely related to Chebyshev nodes, and often considered superior, are *Gauss nodes* and *Gauss–Lobatto nodes*, which are the location of zeros and extrema (respectively) of the Legendre polynomials. These have the advantage that a quadrature built on them (*Gauss quadrature*) is exact for polynomials up to degree $2n - 1$, while the same for Chebyshev nodes (*Clenshaw–Curtis quadrature*) is only exact for polynomials up to degree $n - 1$. In practice, however, the approximation error of both is very close [24, 25], and since Gauss nodes are much harder to compute compared to eq. (3.4), we do not consider them further.

3.6 Multiple dimensions

The simplest generalization to multiple dimensions is to take the set of nodes $\{\vec{x}_i\}$ to be the outer tensor product of the Chebyshev nodes of eq. (3.4) for each dimension,

$$\{\vec{x}_i\} = \{x_{i_1}\} \otimes \cdots \otimes \{x_{i_d}\}, \tag{3.11}$$

with possibly different node count in each dimension, n_i. This corresponds to interpolation via nested application of eq. (3.2), or via the decomposition

$$\widetilde{f}(\vec{x}) = \sum_{i_1=1}^{n_1} \cdots \sum_{i_d=1}^{n_d} c_{i_1 \ldots i_d}\, T_{i_1}(x_1) \cdots T_{i_d}(x_d). \tag{3.12}$$

A detailed study of the interpolation error of this construction is presented in [26]. Roughly speaking, it is similar to eq. (3.9) and eq. (3.10), except instead of n one must use n_i, which are of the order of $\sqrt[d]{n}$, leading to progressively slower convergence as d increases. This is known as *the curse of dimensionality* [27].

3.7 Dimensionally adaptive grid

The tensor product construction is fairly rigid in that it allows for no local refinement; only the per-dimension node counts n_i can be tuned. Such tuning is sometimes referred to as *dimensional adaptivity*, and it can be beneficial. To examine that, let us inspect
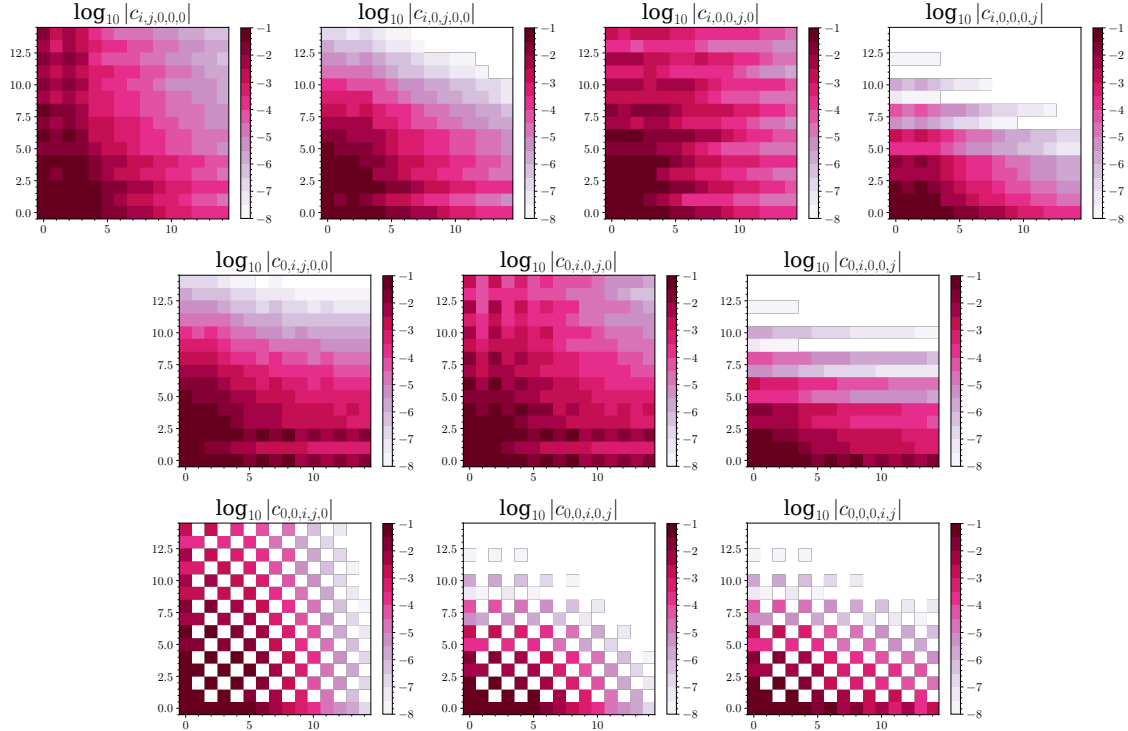
Figure 2: Two-dimensional slices of the 5-dimensional coefficients c corresponding to the decomposition of f_1 into a tensor product of Chebyshev polynomials as given in eq. (3.12). On all plots the horizontal axis is i, the vertical is j.

the coefficients $c_{i_1\ldots i_5}$ corresponding to f_1: their two-dimensional slices are presented in Figure 2. From these we can learn that the coefficients decay much faster in the 5th dimension compared to the rest.

To make use of this insight, let us study Figure 3, where the scaling of c is depicted in each dimension. If we want to sample so that coefficients in each direction are close to each other (to prevent oversampling), we would need to maintain the ratio of e.g.

$$n_1 : n_2 : n_3 : n_4 : n_5 \approx 2 : 4 : 2 : 3 : 1. \tag{3.13}$$

Better results would of course be obtained if instead of a fixed ratio, we would choose the best n_i ratio for each value of n; this, however, can only be done *a posteriori*.

3.8 Discussion

Polynomial interpolation is a well understood interpolation method. It achieves exponential convergence rates for analytic functions in one dimension, and is easy to evaluate accurately via the barycentric formula. It should be considered a safe and dependable default method.

Its performance in multiple dimensions, however, is held back by the tensor product grid construction, that automatically comes with the curse of dimensionality. It is also sensitive to singularities close to the interpolation space: the closer the singularity, the worse the convergence becomes—this is particularly inconvenient for amplitudes, which are
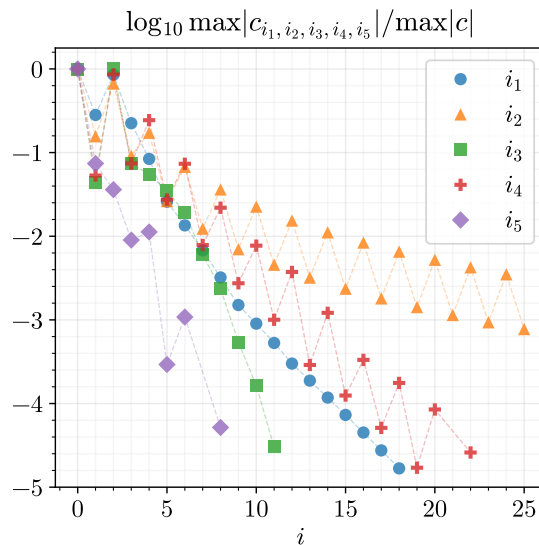
Figure 3: The maximal value of the 5-dimensional coefficients c for f_1 along each of the dimensions, corresponding to the decomposition of eq. (3.12).

very often not analytic at boundaries. Finally, the method is inflexible: the node sets that do not suffer from the Runge phenomenon are quite rigid, and if an interpolant was constructed with n data points, one can not easily add just a few more—the best one can do is to use a nested node set, as in Section 3.3, and roughly double n. Similarly, if an interpolant was constructed on a subset of the full phase space, there is no good way to smoothly extend it to the rest of the phase space by adding new data.

In Figure 4 we present the approximation errors depending on the number of data points n, corresponding to different was to use polynomial interpolation in practice: different sampling schemes, symmetry handling options, and ways to include weights. The "a" method corresponds to interpolating the amplitude a directly, while f corresponds to option 1 from Section 2.4. The methods marked with "half-domain" correspond to option 3 from Section 2.6, while the rest correspond to option 2.

Looking at the results, we can conclude:

- *Should the interpolant be constructed on a or f?* Including the weight w (i.e. option 1 from Section 2.4) helps a lot for very peaky functions (f_5), but seems to slightly hinder others. Possible reason is that w is not analytic at the boundaries, which polynomial interpolation is sensitive to.
- *How should the symmetries be included?* Domain reduction (i.e. option 3 from Section 2.6) significantly helps f_3 and f_4, makes almost no difference for f_1 and f_2, and slightly hinders f_5, for which data duplication (i.e. option 2) is better.
- *Does factoring out the known peaky behaviour from the interpolant help?* Yes, cancelling the $1/\sin^2\theta_H$ factor from the f_5 interpolant brings a modest, but notable improvement. Subtracting this peak could have been even better though.
- *Does dimensional adaptivity help?* It only makes a notable improvement for f_1.

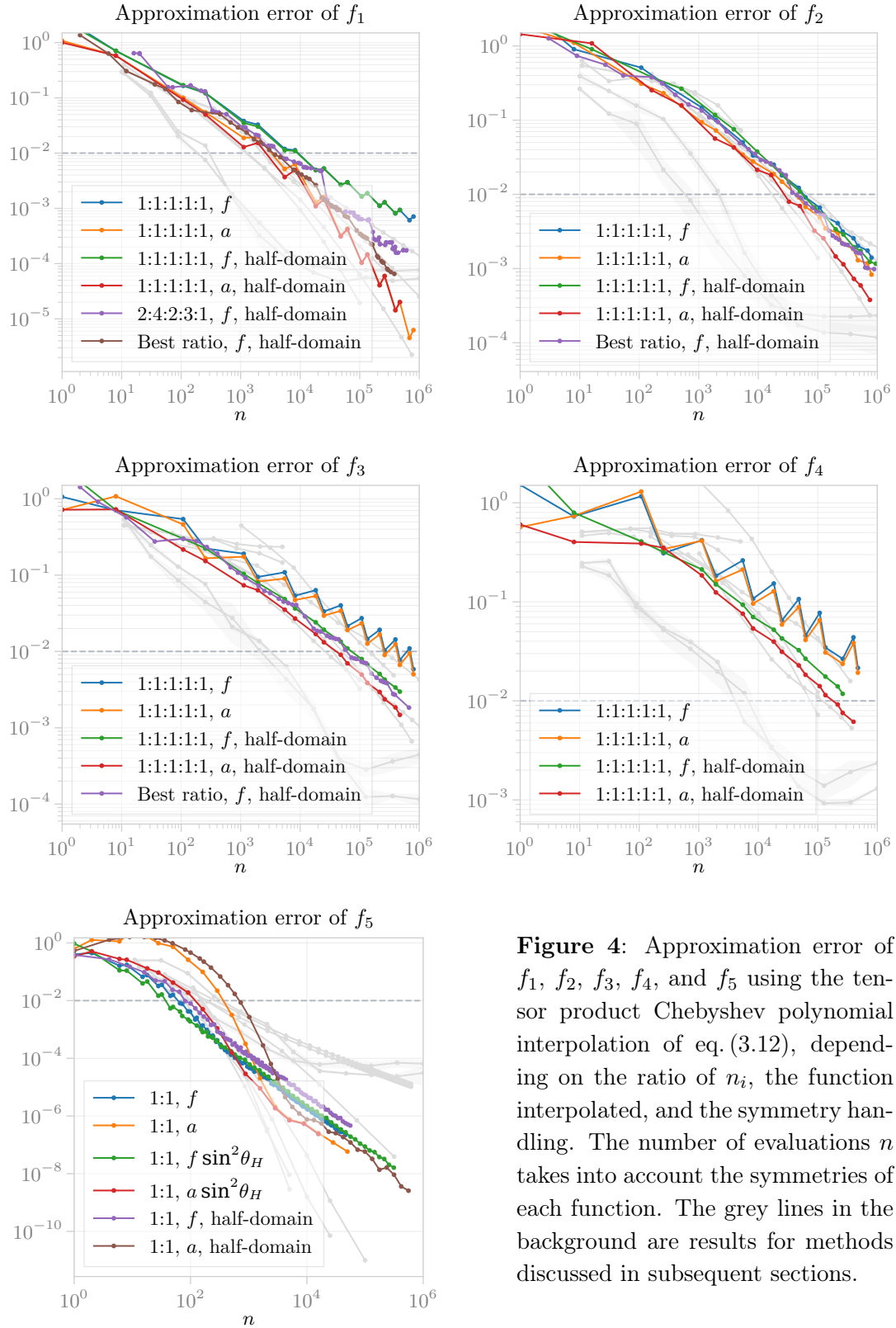**Figure 4**: Approximation error of f_1, f_2, f_3, f_4, and f_5 using the tensor product Chebyshev polynomial interpolation of eq. (3.12), depending on the ratio of n_i, the function interpolated, and the symmetry handling. The number of evaluations n takes into account the symmetries of each function. The grey lines in the background are results for methods discussed in subsequent sections.

4 B-spline interpolation

An alternative way to prevent the Runge phenomenon in polynomial interpolation is to limit the power of the polynomial, and use a basis of splines. A *spline* of degree p is a $p-1$ times continuously differentiable piecewise polynomial. In this section we use *B-splines* (basis splines) [28, 29], which is the standard basis choice for spline interpolation.

B-splines have been applied in engineering applications in the context of the finite element method [30] and in graphics as *non-uniform rational B-splines* (NURBS) [31]. B-splines have also been successfully used for interpolating amplitudes in lower-dimensional cases [32, 33], which makes this a particularly interesting method for us to compare with. Spline interpolation has also been applied in the context of PDF fits [34].

In this section we define the B-spline basis functions and show how to define multi-dimensional B-spline interpolants on tensor product grids. We then present the resulting approximation errors from using uniform B-splines and finish with a discussion of the obtained performance.

4.1 B-spline basis functions

A B-spline basis function of degree p and index i is defined recursively through the Cox-de Boor formula [35, 36]:

$$
\begin{aligned}
N_{i,0}(x) &= \begin{cases} 1 & \text{if } t_i \leq x \leq t_{i+1}, \\ 0 & \text{otherwise}, \end{cases} \\
N_{i,p}(x) &= \frac{x - t_i}{t_{i+p} - t_i} N_{i,p-1}(x) + \frac{t_{i+p+1} - x}{t_{i+p+1} - t_{i+1}} N_{i+1,p-1}(x),
\end{aligned}
\tag{4.1}
$$

where t_i are the coordinates of *knots*—the locations at which the pieces of the piecewise function meet.

Knots define a *knot vector* $\vec{t}$, which is a sequence of $m+1$ non-decreasing numbers $(t_0, \ldots, t_m)$. The knot vector should be chosen such that the resulting B-spline basis spans the space of polynomials. This can be checked via the *local Marsden identity* [37]. In practice it is fulfilled by either using multiple coinciding knots at the boundaries or by extending the range of the knot sequence [38]. The most straightforward choice of knot vector is therefore the uniform construction, with p auxiliary knots placed outside the interpolation domain. The basis functions resulting from such uniform knot vectors for $p = 1, 2, 3$ are shown in Figure 5.

Another common choice is the *not-a-knot* construction, where knots coincide with data points, except at $p-1$ points, which are omitted. Since in the even degree case this results in an odd number of not-a-knots, this knot vector is better defined for odd degree B-splines. Note that the linear case simplifies to the uniform construction since there 0 not-a-knots in this case.

From eq. (4.1) it can be seen that the basis functions are non-negative, form a partition of unity, and have local support. Moreover, thanks to the recursive nature of eq. (4.1), there are efficient algorithms that make B-splines fast to evaluate compared to other spline
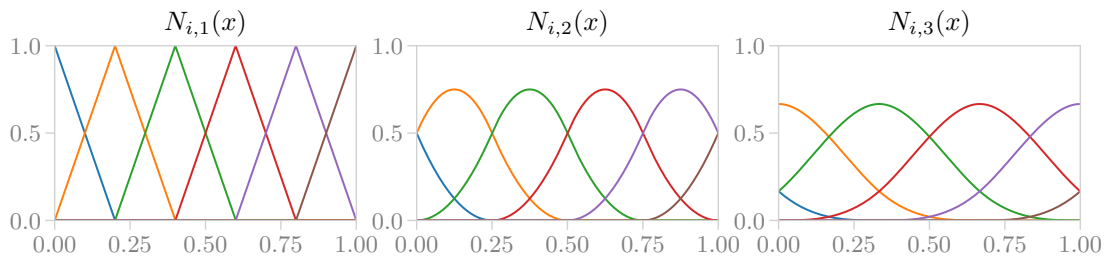
Figure 5: Linear, quadratic and cubic B-spline basis functions from eq. (4.1) with uniform knot vectors, for different i.

functions [39]. This is especially true for B-splines with uniform knot vectors, since the denominators in eq. (4.1) are constant. In the not-a-knot case the knot distances are not all equal, but can be precomputed in advance.

4.2 B-spline interpolants

A one-dimensional B-spline interpolant is a linear combination of $n + 1$ basis functions

$$b(x) = \sum_{i=0}^{n} N_{i,p}(x) \cdot c_i, \tag{4.2}$$

where the c_i are interpolation coefficients sometimes referred to as *control points*. The most straightforward extension to the d-dimensional case is through a tensor product construction

$$B(\vec{x}) = \prod_{j=1}^{d} b_j(\vec{x}_j). \tag{4.3}$$

To fully constrain a B-spline with $n + 1$ basis functions in each direction, $(n + 1)^d$ interpolation nodes are required. The interpolation nodes can partially be selected freely but need to satisfy the Schoenberg–Whitney conditions, which are degree dependent and state that for each knot t_i there must be at least one data point x such that $t_i < x < t_{i+p+1}$. Moreover, the properties of the basis functions imply that a B-spline interpolant is numerically stable [40].

4.3 Discussion

In Figure 6 the performance of B-spline interpolation is compared to the other methods described in this paper. For the 2-dimensional f_5, percent-level accuracy is obtained with $\mathcal{O}(10^2 - 10^3)$ points. For the 5-dimensional test functions, the same accuracy requires $\mathcal{O}(10^4 - 10^5)$ points. In most cases a significant performance gain is obtained by using higher degrees than linear, but beyond cubic splines we see no significant improvements. In a few cases, such as for f_3 and f_4, quadratic splines perform slightly better than cubic splines. The difference between interpolating on the amplitude or directly on the test function is shown for f_1, f_3 and f_5. For f_1 and f_3 it is better to not include the weights during interpolation, while for f_5 it is better to include it except for very large n.

Besides performance there are additional considerations with B-splines and the tensor product construction in general. One problem is that the construction is made impractical due to the fact that the location of knots and interpolation nodes depend on the total number of points. Consider a situation where a B-spline has been constructed with 1000 data points and the subsequent validation indicates that ~ 100 more points are required to achieve the desired precision target. To then construct a new B-spline with 1100 evaluations, the existing 1000 evaluations would have to be discarded, because the inclusion of additional points would slightly shift the placement of the previous nodes. A special case which avoids this problem is when the number of evaluations is exactly doubled, since in the uniform construction this is equivalent to inserting a new knot and data point between each existing one. In the situation described above, constructing a B-spline using 2000 points would then be the most efficient way to proceed. A more consistent way of avoiding this problem is to combine B-splines with some adaptive strategy. We show in Section 5 how this can be done in the context of sparse grids.

Another potential issue with B-splines based on tensor product constructions, is that function evaluations at the boundary are required. This can be challenging for scattering amplitudes since evaluating at the boundaries can be less precise and more time-consuming than in the bulk of the phase space, as observed in e.g. [13]. For such cases, the boundary of the interpolation space can be shifted to a point where the evaluation is reasonable, meaning that the approximation would not cover some parts of the phase space. Alternatively, methods that incorporate extrapolation, such as the modified bases on adaptive sparse grids from Section 5, can be used to alleviate this problem.
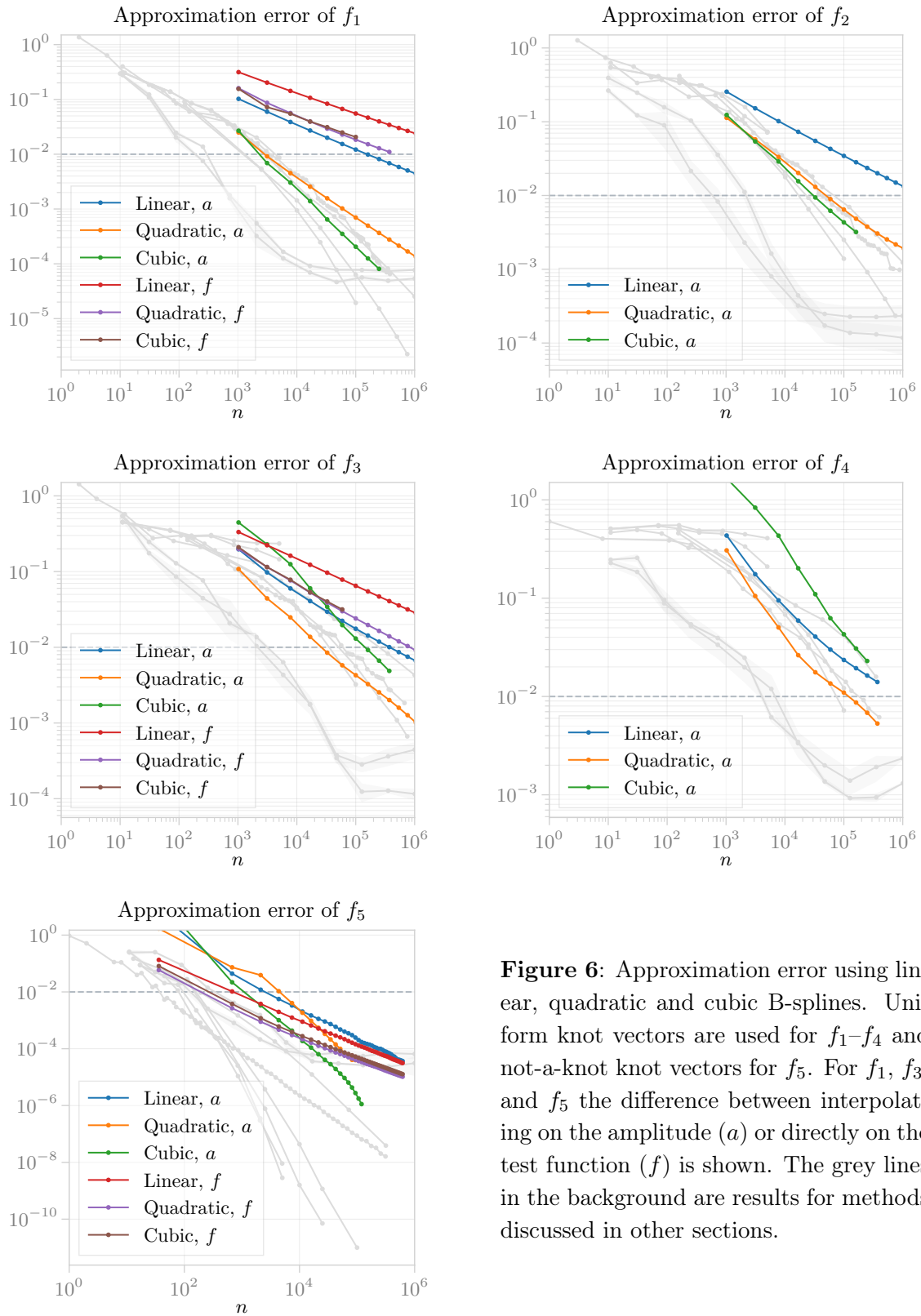
Figure 6: Approximation error using linear, quadratic and cubic B-splines. Uniform knot vectors are used for f_1–f_4 and not-a-knot knot vectors for f_5. For f_1, f_3, and f_5 the difference between interpolating on the amplitude (a) or directly on the test function (f) is shown. The grey lines in the background are results for methods discussed in other sections.

5 Sparse grids

The methods described in the previous sections are based on the tensor product construction of eq. (3.11), which results in a *full grid*. A *sparse grid* construction aims to omit points from the full grid that do not significantly contribute to the interpolant, and in this way alleviate the curse of dimensionality. Such constructions were first described by Smolyak [41] and have since then found use in a wide variety of applications [42–49].

In this section we first introduce sparse grids built on a hierarchical linear basis. Next, we describe how to incorporate spatial adaptivity and upgrade the basis to higher degree polynomials. Finally, we study the impact these constructions have on the approximation quality.

5.1 Classical sparse grids

Sparse grids can be constructed in two main ways, either with the *combination technique* using a linear combination of full grids [50], or through a hierarchical decomposition of the approximation space [45]. In this section we use the latter approach, since it makes it straightforward to incorporate spatial adaptivity.

First, let us restrict to functions that vanish at the boundaries. In this case, a one-dimensional basis can be constructed with rescaled "hat" functions that are centred around the grid points $x_{l,i} = i \cdot 2^{-l}$, $i \in \{0, 1, ..., 2^l\}$:

$$\phi_{l,i}(x) \equiv \phi\left(\frac{x - i \cdot 2^{-l}}{2^{-l}}\right), \qquad \phi(x) \equiv \max(1 - |x|, 0), \tag{5.1}$$

where l is the *grid level*. Since these basis functions have local support, it is possible to define *hierarchical subspaces* W_l through the *hierarchical index* sets I_l by

$$W_l \equiv \text{span}\{\phi_{l,i} : i \in I_l\}, \qquad I_l \equiv \{i \in \mathbb{N} : 1 \leq i \leq 2^l - 1, \ i \text{ is odd}\}. \tag{5.2}$$

The function space of one-dimensional interpolants is then defined as the direct sum of all subspaces up to a maximum grid level k

$$V_k \equiv \bigoplus_{l \leq k} W_l. \tag{5.3}$$

The extension to the multivariate case is via a tensor product construction

$$\Phi_{\vec{l},\vec{i}}(\vec{x}) \equiv \prod_{j=1}^{d} \phi_{l_j,i_j}(x_j), \tag{5.4}$$

with multi-indices $\vec{i} = (i_1, ..., i_d)$, $\vec{l} = (l_1, ..., l_d)$ and d-dimensional grid points $\vec{x}_{\vec{i},\vec{l}} = (x_{l_1,i_1}, ..., x_{l_d,i_d})$. Similarly to the one-dimensional case, the hierarchical subspaces are defined to be

$$W_{\vec{l}} \equiv \text{span}\{\Phi_{\vec{l},\vec{i}} : \vec{i} \in I_{\vec{l}}\}, \qquad I_{\vec{l}} \equiv \{\vec{i} : 1 \leq i_t \leq 2^{l_t} - 1, \ i_t \text{ is odd}, \ 1 \leq t \leq d\}. \tag{5.5}$$
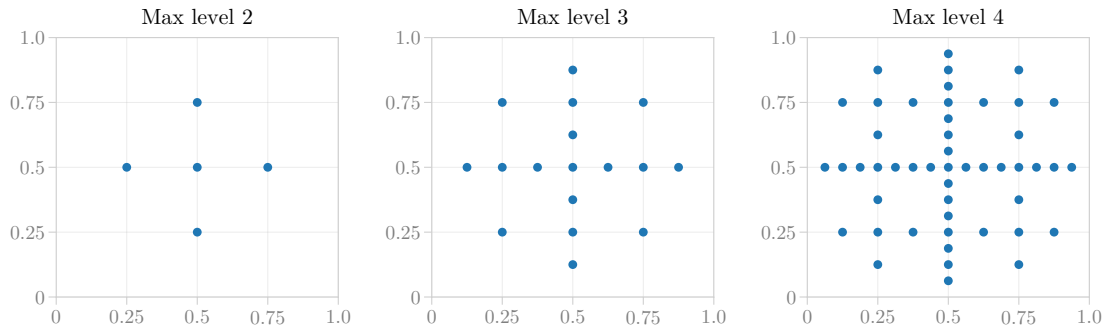
Figure 7: Sparse grid structure in two dimensions for $k = 2, 3, 4$.

Grid type	$\mathbf{d} \backslash \mathbf{k}$	2	4	6	8	10
Full	$d = 2$	25	289	4225	$6.6 \cdot 10^4$	$1.1 \cdot 10^6$
	$d = 5$	3125	$1.4 \cdot 10^6$	$1.2 \cdot 10^9$	$1.1 \cdot 10^{12}$	$1.1 \cdot 10^{15}$
Sparse	$d = 2$	5	49	321	4097	$9.2 \cdot 10^3$
	$d = 5$	11	315	5503	$6.1 \cdot 10^4$	$5.5 \cdot 10^5$

Table 1: Number of grid points from the full and sparse constructions, for dimensions 2 and 5.

A multidimensional full-grid function space V_k^F can now be naively constructed with the direct sum

$$V_k^F \equiv \bigoplus_{|\vec{l}|_\infty \leq k} W_{\vec{l}}, \tag{5.6}$$

where $|\vec{l}|_\infty = \max(l_1, \ldots, l_d)$. The mechanism of the sparse grid is to instead limit the selection of subspaces according to

$$V_k^S \equiv \bigoplus_{|\vec{l}|_1 \leq k+d-1} W_{\vec{l}}, \tag{5.7}$$

where $|\vec{l}|_1 = l_1 + \cdots + l_d$. This avoids including basis functions that are highly refined in all directions simultaneously, which is what causes the number of grid points to explode in high dimensional cases.

Figure 7 shows nodes of the resulting two-dimensional sparse grids for $k = 2, 3, 4$. Table 1 shows the difference in the number of grid points between sparse and full constructions, for dimensions 2 and 5. Of course, omitting grid points can never increase the approximation quality, but the aim is to achieve a close approximation quality, while omitting most points. For sufficiently smooth functions, it is known that the asymptotic accuracy of a full grid interpolant scales with the mesh-width $h_k = 2^{-k}$ as $\mathcal{O}(h_k^2)$, while for a sparse grid it decreases only by a logarithmic factor to $\mathcal{O}(h_k^2 (\log h_k^{-1})^{d-1})$ (see [45]).
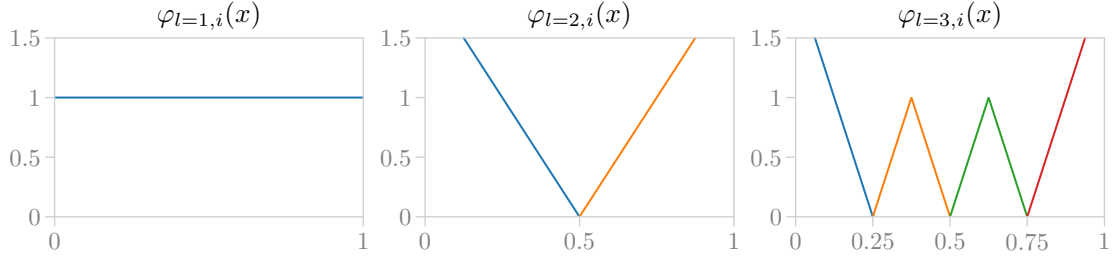
Figure 8: Modified linear hat-basis for sparse grid levels $l = 1, 2, 3$ and different i.

5.2 Boundary treatment

Since the basis functions of eq. (5.1) do not have support at the grid boundaries, we can, so far, only handle target functions that vanish at the boundary. There are two main ways to incorporate boundary support into sparse grids. One possibility is to add boundary points to the grid [45], but for even moderately high dimension this causes the number of points to increase significantly, and defeats the main purpose of the sparse construction. The other option is to use so-called *modified* basis functions [45] that linearly extrapolate from the outermost grid points:

$$\varphi_{l,i}(x) \equiv \begin{cases} 1 & \text{if } l = 1 \wedge i = 1, \\ \begin{cases} 2 - 2^l \cdot x & \text{if } [0, \frac{1}{2^{l-1}}] \\ 0 & \text{else} \end{cases} & \text{if } l > 1 \wedge i = 1, \\ \begin{cases} 2^l \cdot x + 1 - i & \text{if } x \in [1 - \frac{1}{2^{l-1}}, 1] \\ 0 & \text{else} \end{cases} & \text{if } l > 1 \wedge i = 2^l - 1, \\ \phi_{l,i}(x) & \text{otherwise.} \end{cases} \tag{5.8}$$

Figure 8 shows the modified linear basis for $k = 1, 2, 3$. It is apparent that sparse grids are best suited for functions whose boundary behaviour is less important than that in the bulk to the overall structure. The interpolant is constructed as a linear combination of basis functions in V_k^S according to

$$u(\vec{x}) = \sum_{|\vec{l}|_1 \leq k+d-1} \sum_{\vec{i} \in I_{\vec{l}}} \alpha_{\vec{l},\vec{i}} \cdot \Phi_{\vec{l},\vec{i}}(\vec{x}), \tag{5.9}$$

where the interpolation coefficients $\alpha_{\vec{l},\vec{i}}$ are referred to as *hierarchical surpluses* since at each level they correct the interpolant from the previous level to the target function. They are thus also a measure of the absolute error at each level in each direction, which makes the interpolant $u(\vec{x})$ well suited for local adaptivity. The basis functions $\Phi_{\vec{l},\vec{i}}(\vec{x})$ are constructed from either eq. (5.1) or eq. (5.8) depending on if the target function vanishes at the boundary or not. The process of determining the coefficients $\alpha_{\vec{l},\vec{i}}$ is known as *hierarchization*. This can in principle be done in the same way as for any interpolation method; construct and solve a linear system of equations where the interpolant is demanded to reproduce the target

function at each interpolation node. A more efficient way, however, is available for bases satisfying the *fundamental* property:

$$\varphi_{l,i}\left(2^{-l}i\right) = 1 \quad \text{and} \quad \varphi_{l,i}\left(2^{-l}(i-1)\right) = \varphi_{l,i}\left(2^{-l}(i+1)\right) = 0, \tag{5.10}$$

In this case the coefficients can be calculated on the fly: the grid is initialized by normalizing the first coefficient to the central value $\alpha_{\vec{1},\vec{1}} = f(0.5, \ldots, 0.5)$; points $\vec{x}_{\vec{l},\vec{i}}$ are then added, one at a time, and the coefficients are defined as the corrections

$$\alpha_{\vec{l},\vec{i}} = f(\vec{x}_{\vec{l},\vec{i}}) - \tilde{f}(\vec{x}_{\vec{l},\vec{i}}), \tag{5.11}$$

where $\tilde{f}(\vec{x}_{\vec{l},\vec{i}})$ is the current approximation with the already added points and $f(\vec{x}_{\vec{l},\vec{i}})$ is the true function value.

5.3   Spatially adaptive sparse grids

While the classical sparse grid construction uses significantly fewer points than a full grid, it is completely blind to how the target function varies across the parameter space. In many high dimensional problems, it is typical that some regions are more important than others. This information is exploited by spatially adaptive sparse grids, where the grid points that contribute most to the interpolant are *refined* first (see [45, 51]). Refining a grid point means adding all its neighbouring points at one level lower to the grid.

Determining which points are more important relies on some heuristic criterion. A common strategy is to use the *surplus criterion*, where the point with the largest hierarchical surplus is refined first. This is the *greedy strategy*. Its disadvantage is that it might get stuck refining small regions of the parameter space. To avoid this, in [45] it is proposed to weigh the surplus criterion by the volume of the support of the corresponding basis function, $2^{-|\vec{l}|_1}$, resulting in the *balanced strategy*.

Figure 9 shows the difference between greedy and balanced refinement on a two-dimensional grid. We find that greedy refinement might perform slightly better for our error metric if the structure of the target function is simple enough, while balanced refinement is significantly more reliable for more complicated target functions.

5.4   Higher degree basis functions

The one-dimensional basis of rescaled hat functions in eq. (5.1) is straightforward to implement and avoids the Runge phenomenon due to its piecewise nature. The drawback is that the linear approximations come with low interpolation performance, as we have previously observed in Section 4.

There are many ways to make the extension to higher polynomial degrees. Here we differentiate between two types of basis functions: those that fulfil the fundamental property eq. (5.10) and those that do not.

Fundamental basis functions allow for fast hierarchization and make it easy to construct efficient evaluation algorithms. In addition to the linear basis from Section 5.1 we test the more general polynomial piecewise functions (C0-elements) [45, 52], as well as fundamental B-splines [48]. For these benchmarks we make use of the sparse grid toolbox SG++ [45],
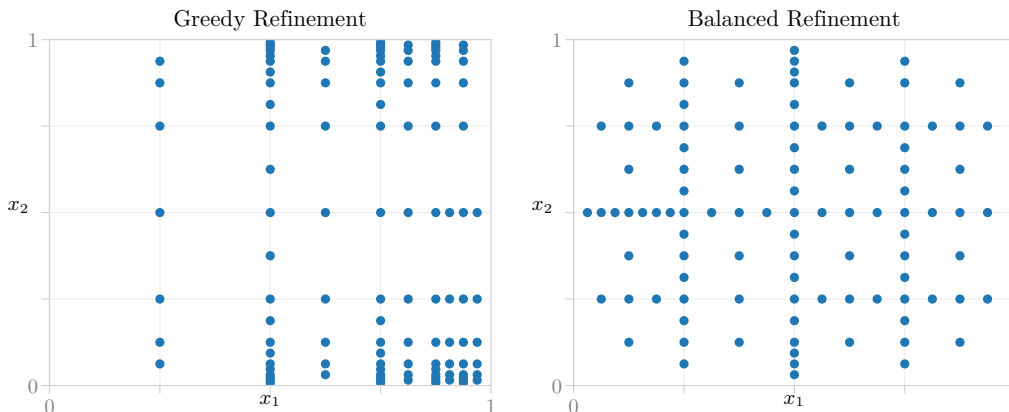
Figure 9: Point distribution from spatial adaptivity with greedy and balanced refinement for the two-dimensional test function f_5.

where both of these basis functions are already implemented. Beyond fundamental basis functions we also investigate extended not-a-knot B-splines as described in [49, 53].

C0 elements

Higher degree polynomials can be defined on the hierarchical structure by using grid points on upper levels as the polynomial nodes [45, 52]. This implies the maximum degree p is bounded by the maximum grid level. For sparse grids without boundaries the relation is $p \leq l - 1$. This can be seen already for the linear case in Figure 8, since on levels 1 and 2 the basis functions are constant and linear respectively. The drawback of this extension is that despite the higher degree, the smoothness is not increased and the interpolant will only be continuous. For this reason these basis functions are usually referred to as C0 elements.

Fundamental B-splines

The fundamental B-spline basis is constructed with the aim of fulfilling the fundamental property of eq. (5.10), while preserving useful properties of B-splines, for example smoothness. The construction is introduced in [48], and it works by applying a translation-invariant fundamental transformation to the hierarchical B-spline basis. Besides fulfilling the fundamental property, this transformation preserves the translational invariance of B-splines which improves performance during evaluation. The modified basis that extrapolates toward the boundaries is defined similarly to the linear case. We refer to [48] for more details on the derivation. For both this and the C0 elements, the implementations in SG++ are used for the benchmarks.

Extended not-a-knot B-splines

In this section we summarize the main equations and statements on extended not-a-knot B-splines presented in [49, 53]. The extension mechanism ensures that polynomials are interpolated exactly, which in many cases increases the quality of interpolation. The basis consists of extended not-a-knot B-splines on lower levels, and Lagrange polynomials on

p	$e_{i,j=0}, \quad i = 1, \dots, p+1$	$e_{i,j=2^l}, \quad i = 2^l - 1 - p, \dots, 2^l - 1$
1	$[2, -1]$	$[-1, 2]$
3	$[5, -10, 10, -4]$	$[-4, 10, -10, 5]$
5	$\begin{cases} [8, -28, 42, -35, 20, -6] & \text{if } l = 3, \\ [8, -28, 56, -70, 56, -21] & \text{if } l > 3. \end{cases}$	$\begin{cases} [-6, 20, -35, 42, -28, 8] & \text{if } l = 3, \\ [-21, 56, -70, 56, -28, 8] & \text{if } l > 3. \end{cases}$

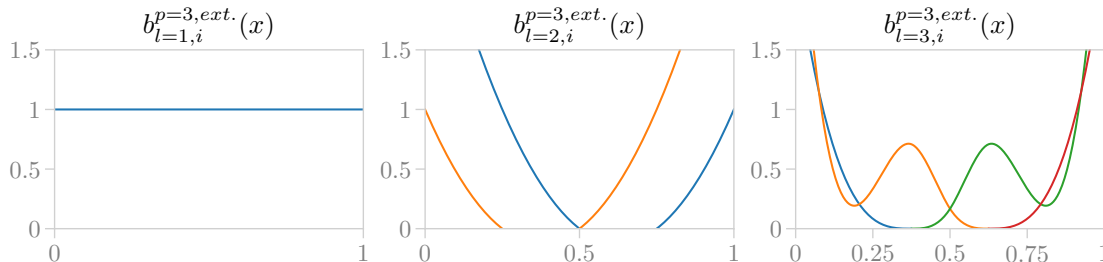**Table 2**: B-spline extension coefficients for the upper and lower boundaries, taken from [53].

Figure 10: Extended not-a-knot cubic B-spline basis functions at sparse grid levels $l = 1, 2, 3$ and different i. At level 1 there are not enough points to define the B-spline and a linear Lagrange polynomial is used instead.

upper levels where there are too few points for the B-spline to be defined. A basis function of odd degree p, level l and index i is defined as

$$b_{l,i}^{p,\text{ext.}}(x) = \begin{cases} b_{l,i}^p + \sum_{j \in J_l(i)} e_{i,j}\, b_{l,j}^p & \text{when } l \geq \Lambda^{\text{ext.}}, \\ L_{l,i}(x) & \text{when } l < \Lambda^{\text{ext.}}, \end{cases} \tag{5.12}$$

where $\Lambda^{\text{ext.}} = \lceil \log_2(p+2) \rceil$, and $e_{i,j}$ are extension coefficients that only depend on the degree. For $p = 1, 3, 5$ these coefficients are listed in Table 2. The $b_{l,i}^p$ are not-a-knot B-splines (see Section 4) and $L_{l,i}(x)$ are regular Lagrange polynomials defined with a uniform knot vector $t = (0, 2^{-l}, \dots, 1)$ as

$$L_{l,i}(x) = \prod_{\substack{1 \leq m \leq 2^l - 1, \\ m \neq i}} \frac{x - t_m}{t_i - t_m}, \quad i = 0, \dots, 2^l. \tag{5.13}$$

The index set $J_l(i)$ defines the extension of the B-spline. It determines to which interior basis functions the boundary basis functions are added. An interior basis function of index i includes the boundary basis function if i is among the first or last $p + 1$ interior indices. Formally the index set is defined as $J_l(i) = \{j \in J_l \mid i \in I_l(j)\}$, where $J_l = \{0, 2^l\}$ and $I_l(0) = \{1, \dots, p+1\}$, $I_l(2^l) = \{2^l - 1 - p, \dots, 2^l - 1\}$ (see [53]). The basis functions described by eq. (5.12) are shown in Figure 10 for the cubic case. The linear case simplifies to the linear hat-basis described in Section 5.1.

5.5 Discussion

In Figure 12 we compare the approximation error from spatially adaptive sparse grids, constructed with balanced refinement, against the other methods described in this paper. A comparison between different refinement criteria is given in Figure 11 for test functions f_1, f_3 and f_5, using the modified linear basis. In some cases the greedy construction is slightly better, but for example the results for f_3 demonstrate the danger of this refinement strategy. The balanced construction results in a much smaller approximation error, which hints at the greedy algorithm getting stuck refining local structures. In practice, it is difficult to predict when refining greedily is better, and in such cases the advantage seems to not be very significant. Moreover, greedy refinement is not very robust against numerical artefacts and noise in the training data. For these reasons we prefer to use some form of balanced refinement, since this is much safer in practice.

We also try to weigh the refinement criterion by the phase-space weight w from eq. (2.29). For f_1 and f_3 this results in a more uniform target function, and the resulting sparse grid becomes similar to the balanced construction without weighting. We therefore see only minor differences in the results from balanced and weighted refinement.

For other basis choices we see significant improvements for all test functions when increasing the degree with the piecewise polynomial and fundamental B-spline bases. With the extended not-a-knot B-splines we see an even better improvement for f_5, but for f_1–f_4 the performance is at best similar to the linear case. In particular for f_3 and f_4 the cubic and quintic cases converge very poorly. This result is unexpected since these bases have been applied to high-dimensional test functions with good results in [53]. We reproduce those benchmarks with our implementation and also cross-check the new results for our test functions with SG++.

The improvements of the spatially adaptive sparse grids over the non-adaptive full grid methods at low amounts of training data are modest. We see in each test function that the scaling is better, however, and that at high amounts of training data the improvements are more significant.

Taking interpolation performance aside, a major advantage of spatially adaptive sparse grids is flexibility. Since it is difficult to predict how much training data is required to reach a certain precision target for an unknown function, it is likely that training data needs to be added iteratively. As is discussed in Section 3 and Section 4, non-adaptive methods are very limited in this regard. A spatially adaptive sparse grid on the other hand is able to add one point at a time, making it possible to validate during construction and in principle stop at exactly the required number of points. If a non-adaptive method is used to reconstruct an unknown function, we are likely to overshoot the required number of points, making the effective number of function evaluations higher than what is represented by these results. The results for the non-adaptive methods at a given training size are therefore the best case scenario, while the sparse grid results are close to what one obtains in practice.
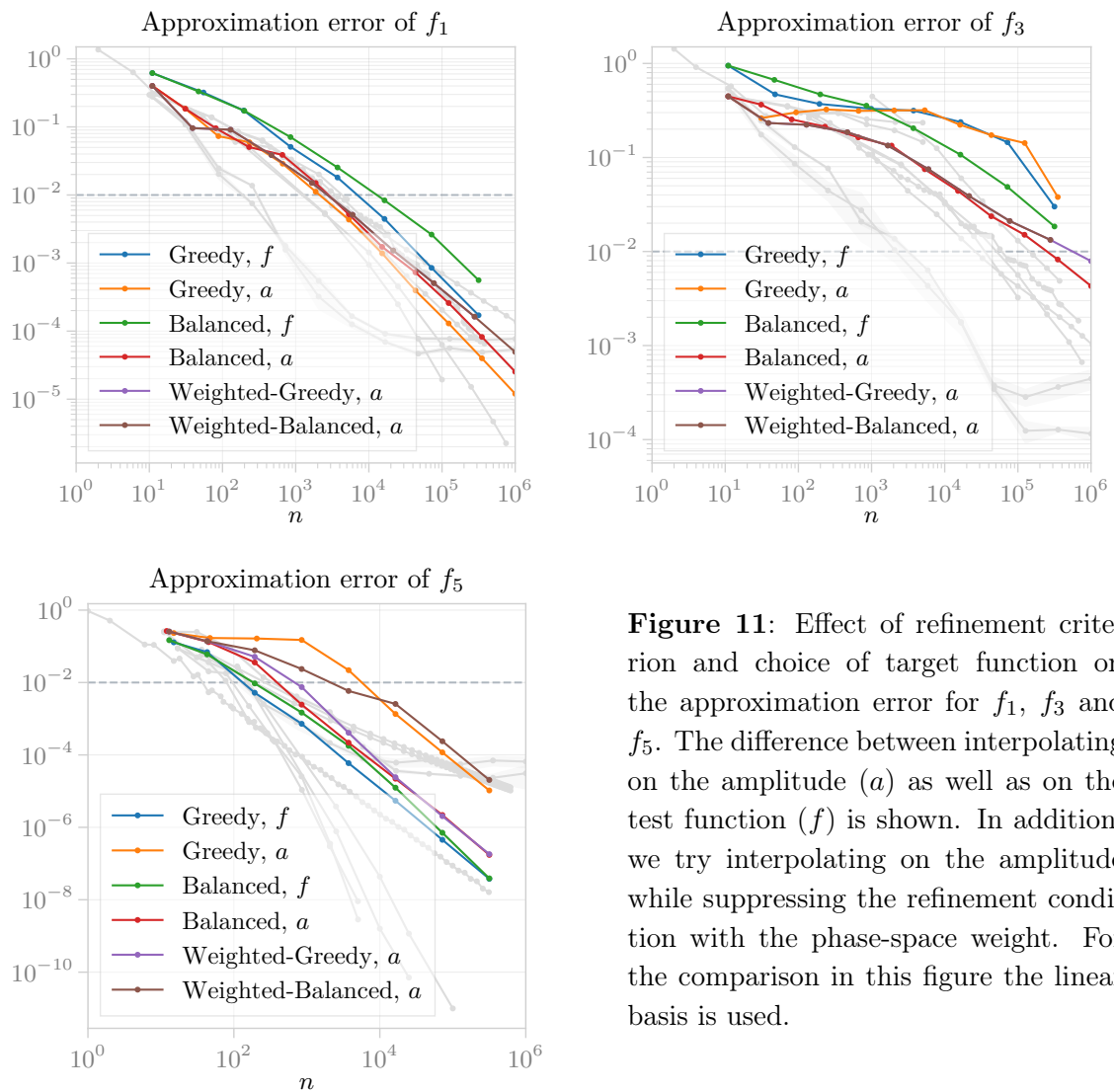
Figure 11: Effect of refinement criterion and choice of target function on the approximation error for f_1, f_3 and f_5. The difference between interpolating on the amplitude (a) as well as on the test function (f) is shown. In addition, we try interpolating on the amplitude while suppressing the refinement condition with the phase-space weight. For the comparison in this figure the linear basis is used.
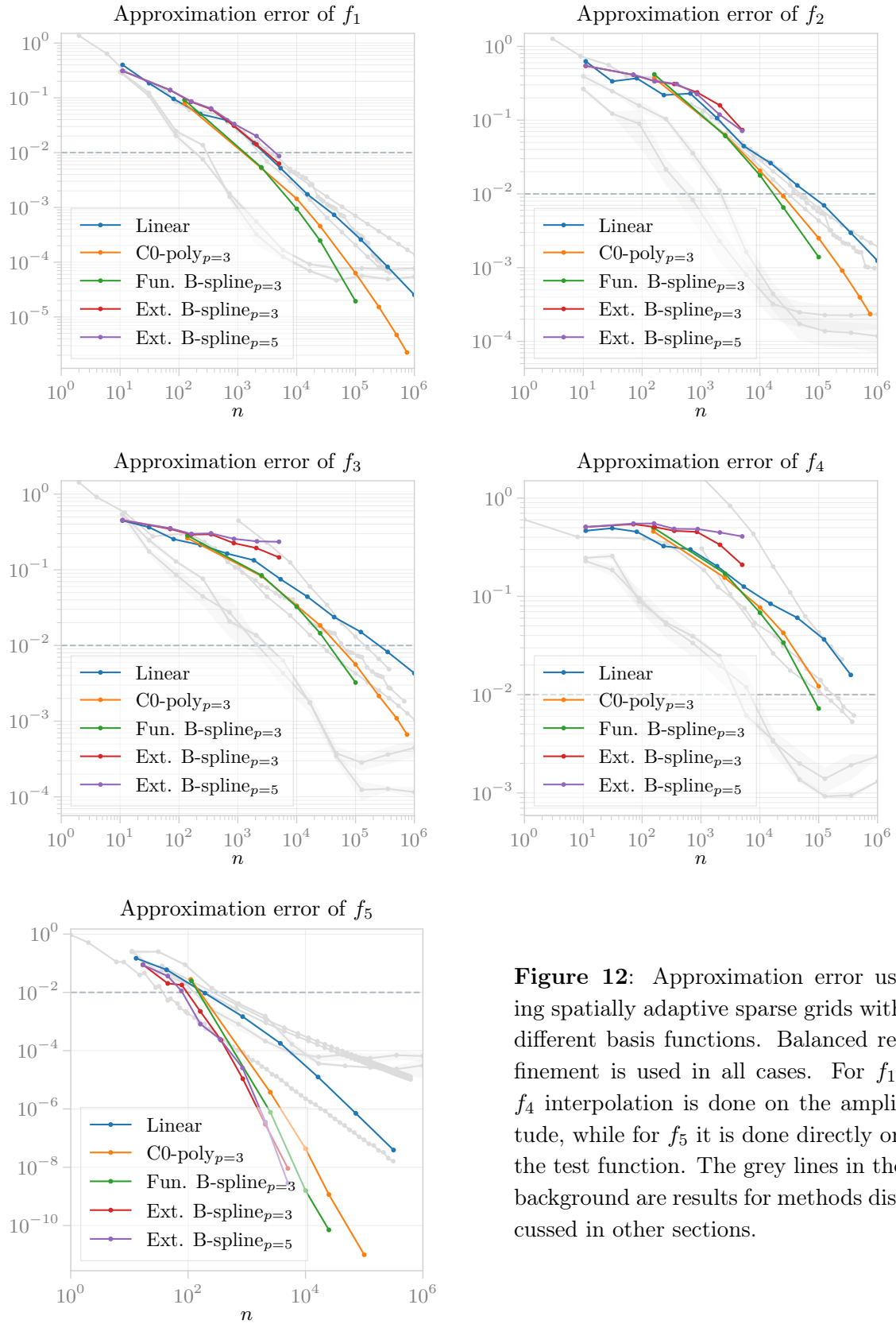
Figure 12: Approximation error using spatially adaptive sparse grids with different basis functions. Balanced refinement is used in all cases. For f_1-f_4 interpolation is done on the amplitude, while for f_5 it is done directly on the test function. The grey lines in the background are results for methods discussed in other sections.

6 Machine Learning Techniques

Machine learning techniques represent a very promising tool for amplitude interpolation [54–59]. These techniques leverage the power of neural networks, approximator functions that are structured as a sequence of operations dependent on learnable parameters. Neural networks can be optimized to approximate any function of a set of inputs to arbitrary precision—given sufficient time and data. This is accomplished by minimizing the *loss function*, which characterizes how close the neural network results are to the desired ones. The optimization of neural network parameters is performed by evaluating the loss function on data subsets or batches and performing gradient descent to minimize the objective in an iterative way. In our case, neural network trainings are framed as regression tasks, where the output of the network is trained to match a target given an input.

The main advantage that this approach puts forward for the interpolation problem is its versatility. Neural networks by default introduce a minimal bias in the interpolants they can represent, so they can easily adapt to a wide variety of target distributions. Additionally, networks are not limited to a single training or dataset for their optimization. This makes them a prime tool for adaptive interpolation, since after an initial training their evaluated shortcomings can be used as a guideline for optimization through subsequent retrainings.

However, neural network based interpolation techniques face a challenge in precision as function complexity grows. Namely, the performance of neural networks steadily decreases with increased particle multiplicity [56] and the inclusion of beyond tree-level contributions [57]. One way to partially mitigate this issue is to incorporate prior knowledge about the amplitude symmetries into the learning task. In our case, we focus on the Lorentz symmetry and work with architectures that are aware of the Lorentz invariance of the amplitudes. This feature is also present in all other interpolation methods discussed in this paper, but there are several ways to implement it on neural networks. We explore two ways of enforcing Lorentz invariance. On the one hand, we train a *multilayer perceptron* (MLP) [60, 61] by feeding it only Lorentz invariant inputs. On the other hand, we use the *Lorentz-Equivariant Geometric Algebra Transformer* (L-GATr) [58, 59], a neural network whose operations are constrained to be equivariant (or covariant) with respect to Lorentz transformations.

To approximate our test functions, we train the networks on a_n as functions of the phase-space points using a *mean squared error* (MSE) loss. We generate the training data points uniformly over the phase space, using a low-discrepancy Sobol sequence. For the testing data points, we use the leading-order-unweighted sampling described in eq. (2.30). Additionally, we also build an extra dataset from unweighted samples for *validation*, a routine checkup that is performed regularly during training to prevent overfitting and select the best performing model constructed during training. The validation set size is always 10% of that of the training dataset until it reaches a size of 4000 points; after that it remains constant for larger training sets.

Targets for tree-level processes are preprocessed with a logarithmic *standardisation*:

$$\hat{a} = \frac{\log(a) - \overline{\log(a)}}{\sigma_{\log(a)}}, \tag{6.1}$$

where $\overline{\log(y_i)}$ and $\sigma_{\log(y_i)}$ are the mean and standard deviation of the amplitude logarithm distributions over the whole dataset. When dealing with f_2 and f_4, this preprocessing is not valid, because a takes negative values. We circumvent this issue by reflecting the amplitude distribution with respect to its maximum value, and then applying the logarithmic standardisation.

As for the inputs, all networks are trained on functions of the four-momenta of the sampled points. We derive the four-momenta for each point from their original parametrization presented in eq. (2.8) and eq. (2.22). When applying this mapping for f_1–f_4, we prepare the $t\bar{t}$ inputs so that the angle φ_t lies only in the range $[0, \pi]$, which allows all neural networks to take advantage of the parity symmetry of these functions.

All networks are trained for 5×10^5 steps with a batch size of 256, the Adam optimizer [62] and a Cosine Annealing scheduler [63] with a maximum learning rate of 10^{-4} when training for the $f_1 - f_4$ test functions and 5×10^{-4} for the f_5 test function. Due to instabilities during training, we refrain from applying early stopping and we perform validation checks every 300 iterations.

6.1 MLP

We use an MLP as the first baseline for this task. The MLP is built as a simple fully connected neural network with GELU activation functions [64]. The inputs for the network are pairwise momentum invariants s_{ij}. Alternative input choices have been tested, including the phase space parameters introduced in eq. (2.8) and eq. (2.22), yielding worse results.

The MLP architecture consists of 5 hidden layers with 512 hidden channels each, amounting to 10^6 learnable parameters. This configuration is chosen as a result of a scan, as the one that performed the best for 10^5 data points. The inputs are preprocessed by taking their logarithms and performing standardization as in eq. (6.1).

6.2 L-GATr

Equivariant neural networks constitute a very attractive option for any problem where symmetries are well defined [58, 59, 65–67]. These networks respect the spacetime symmetry properties of the data in every operation they perform. They do so by imposing the equivariance condition, defined as

$$f\left(\Lambda(x)\right) = \Lambda\left(f(x)\right), \tag{6.2}$$

where x is a network input, f is a network operation and Λ is a Lorentz transformation. By restricting the action of the network to equivariant maps, it does not need to learn the symmetry properties of the data during training and its range of operations gets reduced to only those allowed by the symmetry. This makes equivariant networks very efficient to train and capable of reaching high performance with low amounts of training data.

L-GATr is a neural network architecture that achieves equivariance by working in the spacetime geometric algebra representation [68]. A geometric algebra is generally defined as an extension of a vector space with an extra composition law: the geometric product. Given

two vectors x and y, their geometric product can be expressed as the sum of a symmetric and an antisymmetric term

$$xy = \frac{\{x, y\}}{2} + \frac{[x, y]}{2} \, , \tag{6.3}$$

where the first term can be identified as the usual vector inner product and the second term represents a new operation called the *outer product*. The outer product allows for the combination of vectors to build higher-order geometric objects. In this particular case, $[x, y]$ is a bivector, which represents an element of the plane defined by the directions of x and y.

The spacetime algebra $\mathbb{G}^{1,3}$ can be built by introducing the geometric product on the Minkowski vector space $\mathbb{R}^{1,3}$. The geometric product in this space is fully specified by demanding that the basis elements of the vector space γ^μ satisfy the following anti-commutation relation:

$$\{\gamma^\mu, \gamma^\nu\} = 2g^{\mu\nu} \, . \tag{6.4}$$

This inner product establishes that the vectors γ^μ in the context of the spacetime algebra have the same properties as the gamma matrices from the Dirac algebra. Both algebras are very tightly connected, with the Dirac algebra representing a complexification of the spacetime algebra.

With this notion in mind, we can now cover all unique objects in the spacetime algebra by taking antisymmetric products of the gamma matrices. A generic object of the algebra is called a multivector, and it can be expressed as

$$x = x^S \, 1 + x^V_\mu \, \gamma^\mu + x^B_{\mu\nu} \, \sigma^{\mu\nu} + x^A_\mu \, \gamma^\mu\gamma^5 + x^P \, \gamma^5 \qquad \text{with} \qquad \begin{pmatrix} x^S \\ x^V_\mu \\ x^B_{\mu\nu} \\ x^A_\mu \\ x^P \end{pmatrix} \in \mathbb{R}^{16} \, . \tag{6.5}$$

In this expression, the components of the multivector are divided in grades, defined by the number of gamma matrix indices that are needed to express them. Namely, $x^S 1$ constitutes the scalar grade, $x^V_\mu \gamma^\mu$ the vector grade, $x^B_{\mu\nu}\sigma^{\mu\nu}$ the geometric bilinear grade, $x^A_\mu \gamma^\mu\gamma^5$ the axial vector grade, and $x^P\gamma^5$ the pseudoscalar grade.

Apart from its extended representation power, the spacetime algebra offers a clear way to define equivariant transformations with respect to the Lorentz group on a wide range of geometric objects in Minkowski space. The main consideration is that Lorentz transformations on algebra elements act separately on each grade [58, 69]. As a consequence, any equivariant map must transform all components of a single grade in the same manner and allow for different grades to transform independently.

This guideline allows for an easy adaptation of standard neural network layers to equivariant operations in the algebra. In the case of L-GATr, this adaptation is performed on a transformer backbone. Transformers [70] are ideal architectures to deal with datasets organized as sets of particles, since the attention mechanism can be leveraged to capture

correlations between them in a very accurate way. L-GATr is built with equivariant versions of linear, attention, normalization and activation layers [70, 71]. It also includes a new layer MLPBlock featuring the geometric product to further increase the expressivity of the network. Its layer structure is

$$\bar{x} = \text{LayerNorm}(x)$$
$$\text{AttentionBlock}(x) = \text{Linear} \circ \text{Attention}(\text{Linear}(\bar{x}), \text{Linear}(\bar{x}), \text{Linear}(\bar{x})) + x$$
$$\text{MLPBlock}(x) = \text{Linear} \circ \text{Activation} \circ \text{Linear} \circ \text{GP}(\text{Linear}(\bar{x}), \text{Linear}(\bar{x})) + x$$
$$\text{Block}(x) = \text{MLPBlock} \circ \text{AttentionBlock}(x)$$
$$\text{L-GATr}(x) = \text{Linear} \circ \text{Block} \circ \text{Block} \circ \cdots \circ \text{Block} \circ \text{Linear}(x) . \tag{6.6}$$

All of these layers are redefined to operate on multivectors and restricted to act on algebra grades independently to ensure equivariance. Further details for each of the layers are provided in Refs. [58, 59].

Through this procedure, we build knowledge about the Lorentz symmetry into the architecture, but it can also be used to enforce awareness of the discrete symmetries described in Section 2.6 besides the parity invariance present in f_1–f_4. Being a transformer, L-GATr handles individual particle inputs independently and can enforce any exchange symmetry on individual particles. This is performed in practice by including common scalar labels to every set of particles that leave the amplitude invariant under permutation.

To operate with L-GATr, we need to embed inputs into the geometric algebra representation and undo said embedding once we obtain the outputs. For the interpolation problem, inputs always consist of particle 4-momenta p, which can be embedded into multivectors as

$$x_\mu^V = p_\mu \qquad \text{and} \qquad x^S = x_{\mu\nu}^T = x_\mu^A = x^P = 0 . \tag{6.7}$$

Each particle is embedded to a different multivector, resulting in the inputs being organized as sets of particles or tokens. Each token also incorporates a distinct scalar label as part of the inputs. The value for these labels is selected according to the permutation invariance pattern of each process we study. This ensures that L-GATr also respects any instance of particle exchange symmetry. The token labels are not part of the multivectors, they are fed to the network as separate scalar inputs. Multivectors and scalars traverse the network through parallel tracks, mixing with each other only at the linear layers.

As for the outputs, we make use of a global token, which is introduced as an extra empty particle entry. This extra token holds no meaning at the input level, but at the output level its scalar component represents the estimator for the target amplitude. As for the inputs, in L-GATr we divide them by the standard deviation over each of the particle momenta to prevent violating equivariance.

Our L-GATr build consists of a model with 8 attention blocks, 64 multivector channels, 32 scalar channels and 8 attention heads, resulting in 7×10^6 learnable parameters.

6.3 Discussion

We show the results from both the MLP and L-GATr networks in Figure 13. Both networks manage to clear the percent-level target accuracy on all test functions with a low amount of

training points. Comparing our two architectures, the MLP is the best performer with very small training datasets, whereas L-GATr always takes over in the large training dataset limit. From this pattern we can infer that the MLP is slightly more effective at modelling the amplitude distributions in low data regimes, whereas L-GATr becomes better with more training data thanks to its larger capacity. We also observe a general slowdown in improvement for all networks as we increase the training data.

Comparing with other methods, machine learning algorithms surpass all other interpolation methods in the low data regime for all 5-dimensional test functions, and they are only overtaken in the large data regime. Their improvement with respect to other approaches is the biggest in the case of the higher order correction functions f_2 and f_4, signalling their potential utility for the interpolation of more complex multi-loop amplitudes.

The only front where neural networks underperform is in the case of the f_5 test function. This is the only 2-dimensional function we test, and seeing less benefits from neural networks in lower dimensions should not be surprising.

Another important result that we obtain from this study is that we have the ability to train our neural networks on uniform samples and evaluate them on unweighted samples. If we instead train and evaluate neural networks on datasets produced with a single sampling method we observe only a marginal improvement over the results presented in Figure 13. This is very advantageous for our problem, since that means that we can train our algorithms on datasets produced by naive sampling methods and then evaluate them on physically motivated distributions without a significant performance degradation.

Finally, it is possible to modify the training datasets dynamically to focus on those regions in the target space that are poorly estimated in the initial stages of the training. Such adaptive strategies are hard to balance in practice, since they involve extensive hyperparameter optimization and they are substantially slower than ordinary trainings. For these reasons, we refrain from trying them out in this paper.
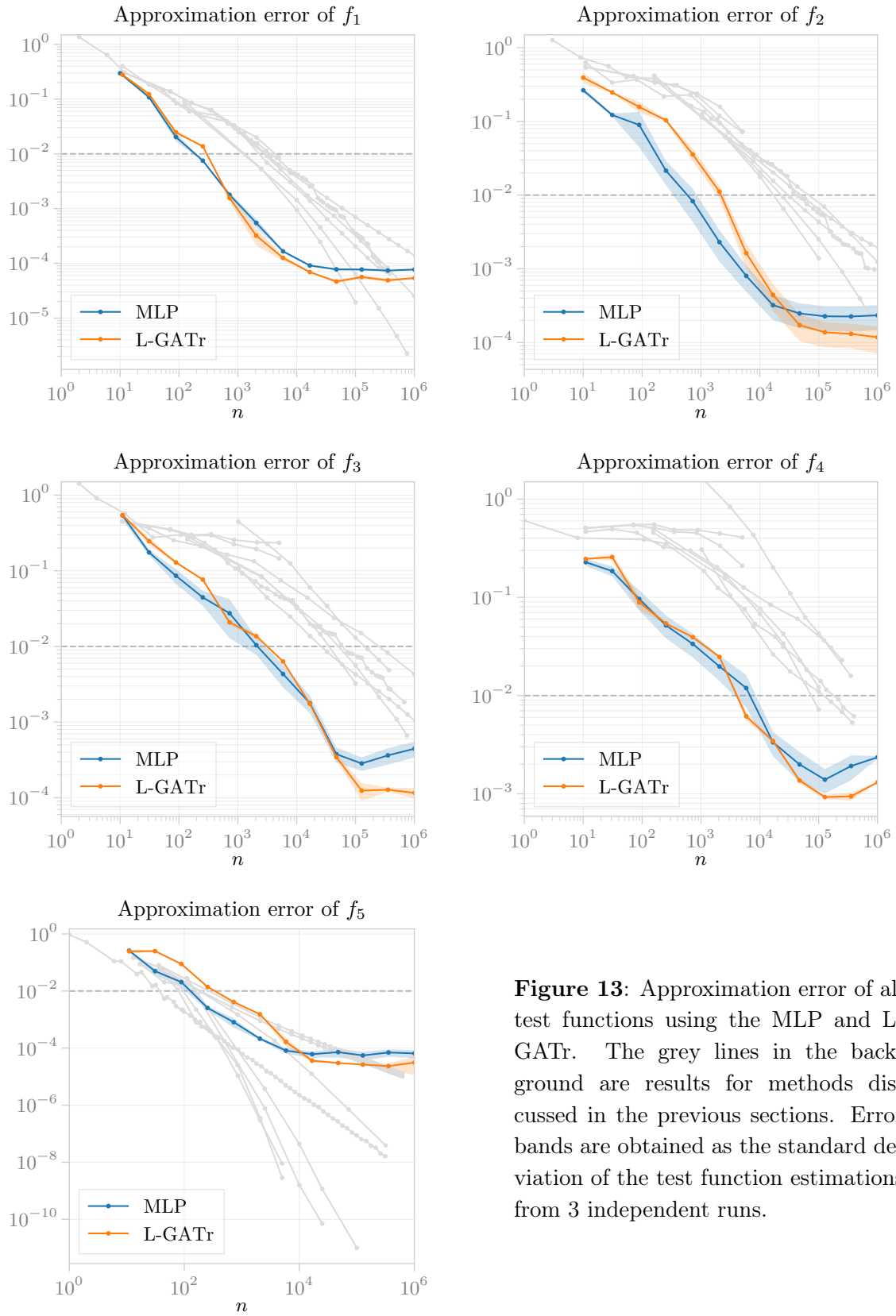
Figure 13: Approximation error of all test functions using the MLP and L-GATr. The grey lines in the background are results for methods discussed in the previous sections. Error bands are obtained as the standard deviation of the test function estimations from 3 independent runs.

7 Conclusions

We have presented a detailed investigation of several frameworks to interpolate multi-dimensional functions, focusing on scattering amplitudes depending on a number of phase space variables. We have used amplitudes related to $t\bar{t}H$ production (5-dimensional phase space, test functions f_1–f_4) and Higgs+jet production (2-dimensional phase space, test function f_5) at the LHC as test functions, and applied various ways of polynomial interpolation, B-spline interpolation, spatially adaptive sparse grids, and interpolation based on machine learning techniques, using a standard multi-layer perceptron and the Lorentz-Equivariant Geometric Algebra Transformer.

Considering that the evaluation of amplitudes is costly, the main performance measure is how the approximation error of the different interpolation methods scales with the number of data points.

To measure the approximation error we notice that loop amplitudes typically have peaks or show a steep rise towards the phase-space boundaries, but the contribution of such regions to physical observables might be small, because it is suppressed by phase-space density or parton distributions. With this in mind, we have used physically motivated error metrics by weighing the approximation errors in certain phase-space regions proportional to those regions' contribution to the total cross section, targeting a precision of at least 1%.

For the 5-dimensional test functions, we find that machine learning techniques significantly outperform the classical interpolation methods, in some cases by several orders of magnitude. For the lower dimensional case, we see that most methods perform well enough, but if very high precision is required, sparse grids are the best choice.

In fact, for all test functions we see that the performance of machine learning approaches starts to stagnate after a certain precision threshold, while classical interpolation approaches scale smoothly. Since this threshold is fairly high, this still leaves machine learning techniques as the best practical choice in high dimensions, but does call for a further investigation.

Another important measure for the usefulness of a particular method is its extendibility. Since it is difficult to predict how much data is needed to reach the desired error target, it is likely that more training data needs to be added between validations. Both the adaptive methods and neural networks provide this option. Spatially adaptive sparse grids are particularly flexible: they allow for the addition of single points at a time and for an assessment of which are approximated the worst, and thus need more points. Neural networks are fairly insensitive to the data point distribution, which allows for more data to be easily added, at the cost of a repeated training. Additionally, several methods based on them provide uncertainty estimates on their predictions, such as Bayesian neural networks [56, 72–75] or repulsive ensembles [76, 77]. These approaches may pave the way forward in validating the reliability of machine learning techniques.

In summary, our investigations show that the construction of multi-dimensional amplitude interpolation frameworks with a precision that is sufficient for current and upcoming collider experiments is feasible and therefore numerical calculations for multi-scale loop amplitudes continue to have a promising future.

Acknowledgements

A Additional details

A.1 Phase space parametrisation for $pp \to t\bar{t}H$

The variables used for test functions f_1 to f_4 originate from a $2 \to 3$ phase space to produce a top quark pair and a Higgs boson, where we use three angular variables and two variables of energy type:

$$d\Phi_{t\bar{t}H} = \frac{1}{2^{10}\pi^4 \hat{s}\, s_{t\bar{t}}} \sqrt{\lambda(s_{t\bar{t}}, m_t^2, m_t^2)} \sqrt{\lambda(\hat{s}, s_{t\bar{t}}, m_H^2)} \times$$
$$\Theta(\sqrt{\hat{s}} - 2m_t - m_H)\Theta(s_{t\bar{t}} - 4m_t^2)\Theta([\sqrt{\hat{s}} - m_H]^2 - s_{t\bar{t}})\, ds_{t\bar{t}}\, d\Omega_{t\bar{t}} \sin\theta_H\, d\theta_H \quad \text{(A.1)}$$

with θ_H being the poar angle of the Higgs boson relative to the beam axis, $d\Omega_{t\bar{t}} = \sin\theta_t\, d\theta_t\, d\varphi_t$ and λ being the Källén function, $\lambda(a, b, c) = a^2 + b^2 + c^2 - 2ab - 2bc - 2ca$, depending on the variables

$$\hat{s} = (p_3 + p_4 + p_5)^2 \, , \ s_{t\bar{t}} = (p_3 + p_4)^2 \quad \text{(A.2)}$$

and the masses. As the production threshold of the $t\bar{t}H$ system is located at $s_0 = (2m_t + m_H)^2$, a convenient variable for a scan in partonic energy is

$$\beta^2 = 1 - \frac{s_0}{\hat{s}} \quad \text{(A.3)}$$

such that $\beta^2 = 0$ at the production threshold and $\beta^2 \to 1$ in the high energy limit. For more details we refer to Ref. [13].

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