

NUMERICAL TECHNIQUES FOR NONLINEAR BEAM-BASED ALIGNMENT

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Abstract

Two techniques to perform Beam-Based Alignment are presented. These techniques are intended for the difficult case arising in circular accelerators characterized by a non-linear dependence of the Response Matrix on misalignments of the magnetic sources, where the standard approach fails. The developed algorithms have been successfully used to reconstruct misalignments in the transverse position of the quadrupoles installed in the main rings of the DAΦNE collider.

INTRODUCTION

We call Beam-Based Alignment (BBA) any procedure aiming at determining the misalignment of the magnetic elements in a particle accelerator, exploiting the effects those misalignments induce on the beam dynamics. Such effects are usually encoded in a Response Matrix (RM) specific for the class of elements taken into account. The standard BBA approach [1] [2] consists of a linear modelization of the dependence of the RM entries on the misalignments and then in the inversion of such model. In order to improve numeric stability, a Singular Value Decomposition (SVD) can be applied to the linear dependence of the misalignments on the RM allowing a cut on the largest singular values.

This approach is very effective in the case of linear accelerators and circular with regular lattices with widely spaced, loosely coupled magnetic elements, but it performs poorly when compact circular accelerators are concerned. In fact the magnet proximity and multi-turn effects introduce significant higher-order dependencies that render the linear modelization ineffective. We analyze the case of the DAΦNE rings [3] [4], in which both conditions the presented conditions occur and linear BBA is not applicable.

We propose two nonlinear BBA algorithms. The first is intended to deal with situations in which nonlinearities are expected to compromise the standard approach, but are still treatable with correcting tweaks. We will refer to it as *Surrogated Beam-Based Alignment*. The second one is an approach that, at the expense of the computational cost, is able to reconstruct misalignments in situations of strong nonlinearity. We shall refer to it as the *Sushi Algorithm*.

In both cases we will treat the accelerator model as an *oracle* that, given a set of misalignments, will predict the resulting RM. In the presented situation we want to reconstruct the transverse misalignment of the DAΦNE positron ring quadrupoles. The oracle is implemented via a series of MadX simulations [5]: in order to compile the RM, 42 quadrupole currents are varied with a 2 Ampere kick and then, in correspondence of the 47 beam position monitors,

the difference in transverse beam position orbit is measured. Despite of the specific simulator adopted in this specific study, the aim of this work is to provide black-box techniques that will work independently of the specific simulation technique chosen - given that the oracle is sufficiently adherent to the real beam dynamics.

SURROGATE BEAM-BASED ALIGNMENT

As anticipated we treat the accelerator physical model as an oracle that, given a misalignment for each magnetic component of the machine, is able to predict the resulting RM. In this perspective the BBA task becomes equivalent to a numerically stable inversion of this black-box, which is to say to determine which set of misalignments provides the response matrix lying closer to the experimentally measured one. We shall assume that evaluation of a single simulated RM presents a fairly high computational cost, e.g. a dozen of seconds on a state-of-art personal computer.

Surrogate BBA consists in approximating the oracle with a function allowing an analytic or a simple numerical inversion, which we call the *surrogate function*. The surrogate function should be at the same time closely matching the original oracle, fast to compute and easy to invert. Thus it should be selected specifically for each case.

Surrogate BBA proves to effectively deliver the desired results for the MadX model of the DAΦNE positron ring in the October 2013 run configuration, while standard techniques fail. In this specific case misalignments are expected to range in the order of $\approx 100 \mu\text{m}$. Under this hypothesis adding the quadratic terms to the linear model provides a suitable surrogate function that differs from the original oracle less than a part in 10^3 in Fröbenius norm. Namely, letting \mathbf{y} be a vector enlisting the transverse misalignments of the quadrupoles, and $M_{ij}(\mathbf{y})$ the corresponding RM obtained through the oracle, then we use as the surrogate function $\tilde{M}_{ij}(\mathbf{y})$ a sort of second order Taylor expansion in \mathbf{y} :

$$M_{ij}(\mathbf{y}) \approx K_{ij}^{(0)} + K_{ij}^{(1)} \cdot \mathbf{y} + \frac{1}{2} \mathbf{y} K_{ij}^{(2)} \mathbf{y} \equiv \tilde{M}_{ij}(\mathbf{y}). \quad (1)$$

We found by numeric inspection that for misalignments up to $\approx 100 \mu\text{m}$ we have

$$\frac{\|\tilde{M}(\mathbf{y}) - M(\mathbf{y})\|}{\|M(\mathbf{y})\|} \lesssim 10^{-3}. \quad (2)$$

The surrogate function coefficients $K_{ij}^{(0)}$, $K_{ij}^{(1)}$ and $K_{ij}^{(2)}$ are obtained by sampling the oracle over a *halo* (a sample set) of misalignments and then performing a best linear fit of $\tilde{M}(\mathbf{y})$ to $M(\mathbf{y})$, in the specified case we used a halo of 14 Ksamples. Although the number of coefficients of the $K_{ij}^{(2)}$ in our

case range in the order of tens of millions, the model can be fitted separately for each RM entry ij , reducing the fit cost to the inversion of a single $14K$ by $14K$ matrix. By carefully selecting the sampled halo points, the fit matrix can be rendered sparse; in our case we achieved a 98% sparsity making negligible the overall fit cost.

Let M_{exp} be the experimental RM measured on the collider. We are bound to find the value of \mathbf{y} that minimizes the quality function:

$$\|\tilde{M}(\mathbf{y}) - M_{exp}\|^2. \quad (3)$$

This minimization cannot be performed in closed formula, but can be easily achieved numerically, provided that an effective algorithm is used. The best way we found to obtain such minimization is to use a quasi-Newton iterative method, with both the gradient and the Hessian matrix of the function computed in closed formula, mixed with a chain of prospecting algorithms.

To describe the action of the prospectors, let \mathbf{y}_i be the i -th partial result of the minimization algorithm. The n -th level prospector will step in every $2^n \cdot k$ iterations, with $k \in \mathbb{N}_0$, substituting to $\mathbf{y}_{2^n \cdot k}$ the value of \mathbf{y}_* in the set

$$\{ t \cdot \mathbf{y}_{2^n \cdot (k-1)} + (1-t) \cdot \mathbf{y}_{2^n \cdot k} \mid t \in \mathbb{R} \} \quad (4)$$

which minimizes $\tilde{M}_{ij}(\mathbf{y}_*)$.

Since in our case any restriction of the quality function (3) along a specific direction results in a quartic polynomial whose coefficients can be computed in closed formula, the minimizations required by the prospectors can be provided quickly and in closed formula too.

Surrogate BBA in the illustrated case proved to be numerically stable and provided two solid digits in the inversion. The algorithm was tested against matrices generated through the oracle with small random noise added to them, simulating experimental measurement errors, and it was shown that these errors do not get amplified significantly by the inversion algorithm.

THE SUSHI ALGORITHM

Finding a suitable surrogate function becomes a nontrivial task when in the range of the expected misalignments a series expansion cannot provide an adherent approximation of the oracle. We found that this is indeed the case of the DAΦNE electron ring in the February 2014 configuration, as simulated with MadX. Again we will try to reconstruct the transverse misalignment of the ring quadrupoles, but this time we expect them to be in the order of $\approx 500 \mu\text{m}$. Since even with smaller misalignments ($\approx 100 \mu\text{m}$) higher order terms kick in making quadratic surrogacy unfeasible, either a different surrogate function or a radically dissimilar approach needs to be employed.

Choosing the second path we developed what we called the *Sushi* algorithm. The main idea consists in defining a hypervolume in the misalignment space in which the solution is expected to be and then, subsequently, to exploit occasional

correlations to *cut out* sections of this hypervolume until the desired accuracy is obtained; pictorially resembling in our view the art of raw fish slicing in Japanese cuisine.

Before we illustrate the core of the algorithm we will introduce a form of preprocessing of the RM entries that heavily reduces the computational cost of the algorithm and provides a slight increase in numerical stability. Since there is no guarantee that the characterization we observed in the RMs has a general validity this preprocessing step can be skipped and the whole RM can be employed to feed the *Sushi* algorithm.

Response Matrix Preprocessing

Statistic analysis of the RMs obtained through the simulator showed strong linear correlations between many of the RM entries. To characterize such dependency we have ran the oracle on 20 thousand randomly chosen misalignments in the range of interest.

For each ordered pair of RM entries we computed a least square linear fit of one entry as a function of the other; then we defined a distance between RM entries as the least χ^2 in the two fit possibilities. We then subdivided the response matrix entries in families using a clusterization algorithm - each family containing entries which are all approximately linearly proportional - then from each family we extracted a representative. Namely, the representative is the entry that minimizes the maximum distance with any other member of its family.

Fit results showed that the complete RM is well approximated by a linear combination of the representative entries. We call the linear space generated by these linear combinations the *generatrix* subspace. Common sense suggests that restricting our analysis to these representatives of the RM entries will reduce computational costs without significantly reducing the information content with respect to the complete RM. Therefore it is convenient to modify the experimental RM so that it will lie on the *generatrix* subspace: this can be achieved by performing a linear fit to deduce the values of the representatives that best characterize the experimental RM, which is equivalent to say that we project the RM on the *generatrix* subspace. After precomputing the linear fit matrix, this projection reduces to a simple matrix multiplication, which can be included in the oracle black-box.

In our case we used a number of families equal to four times the number of degrees of freedom of the misalignment we want to reconstruct (i.e. eight-fold the number of quadrupoles in the ring). This proved to be a suitable choice, since in this way the representatives are able to characterize the RMs with a tolerance inferior to 1 part in 10^3 in norm, while reducing the number of entries of the response matrix by a factor 10; since part of the *Sushi* algorithm scales with the cube of the RM entry count, this results in a significant speedup. The procedure provides also good numeric stability on the projected matrix: since the *generatrix* subspace is heavily less dimensional than the whole RM parameter space, a random variation added to a RM will be nearly nor-

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mal to the *generatrix* and most of the error will cancel out in the projection.

The Algorithm Core

Sushi is an iterative algorithm that characterizes the *partial solution* of a BBA problem with a probability distribution function (p.d.f.) on the possible misalignments and that repeatedly performs a bayesian update of the p.d.f., narrowing it in order to determine with greater precision the location of the solution.

The p.d.f. describing the partial solution is defined as the product of uni-variate gaussian distributions (each with a specified mean and variance), one for each of the misalignment we need to reconstruct. At the beginning of the computation a *prior* distribution derived by general knowledge of the experimental apparatus is provided to the algorithm. For example, in our case we started from a multivariate gaussian p.d.f. for the misalignments, centered in $\mathbf{y} = \mathbf{0}$ and with uniform width $\sigma = 500 \mu\text{m}$.

At each algorithm step two random sets of misalignments are drawn using the p.d.f. adopted at the current step. The oracle is ran on these misalignments producing two datasets that we will call α and β ; each point p in both these datasets consists in pair $(\mathbf{y}_p, \mathbf{M}_p)$, i.e. a misalignment together with the corresponding RM. The α dataset is used to obtain a linear model for the misalignment and the β dataset to estimate the variance of the resulting p.d.f., as we now clarify.

We use the *alpha* dataset to find the best linear dependence of the misalignments, \mathbf{y}_p , as a function of the RM, \mathbf{M}_p . Namely, writing

$$\mathbf{y}_p = \mathcal{F} \cdot \mathbf{M}_p + \mathbf{e}_p \quad (5)$$

we want to find the *fit matrix* \mathcal{F} which minimizes the sum of the residues squared $\sum_p \|\mathbf{e}_p\|^2$.

A new proposed p.d.f. for the next iterative step is then computed. The mean value of the new gaussian p.d.f. is given by $\boldsymbol{\mu}_* \equiv \mathcal{F} \cdot \mathbf{M}_{exp}$. The variance for each misalignment is determined by applying the fit matrix to the entire β dataset and computing the residues by subtracting the reconstructed misalignment ($\mathcal{F} \cdot \mathbf{M}_p$) from the one provided to the oracle when the β dataset was computed (\mathbf{y}_p). We suggest the use of quantiles to determine the width of the resulting distribution, since the nonlinear behaviour of the oracle can force other estimators to converge very slowly and requires the use of unnecessarily large sample spaces. Moreover we'd like to stress that it is mandatory that dataset β is completely independent from dataset α : if we used the points from dataset α to compute the variance of the p.d.f., this would give rise to spurious correlations, spoiling the correctness of the procedure.

The proposal p.d.f. is then merged with the prior distribution. This can be done in two ways: the prior distribution can be replaced by the proposed distribution, or a bayesian merge can be performed. In the second case, denoting with

μ_i and σ_i the mean and variance estimated at the i -th step (for each misalignment), and with μ_* and σ_* the ones extracted from the α and β datasets, we adopt the following formula:

$$\mu_{i+1} = \sigma_{i+1} \cdot \left(\frac{\mu_i}{\sigma_i} + \frac{\mu_*}{\sigma_*} \right) \quad \sigma_{i+1} = \left(\frac{1}{\sigma_i} + \frac{1}{\sigma_*} \right)^{-1} \quad (6)$$

Both approaches have their advantages. The former is more mathematically sound and provides more cautious statements on the location of the solution, but might stall if the prior distribution width is overestimated. The latter will force the algorithm to converge and will avoid stalling, but will produce wrong results if the problem is intrinsically insolvable.

Cut on Singular Values

We found that the algorithm core might require modifications in order to avoid numeric instability, and to better account for the measurement errors that the experimental determination of the RM inevitably entails. Specifically, at each step we have to factor with SVD the fit matrix \mathcal{F} and remove the higher singular values to provide numerical stability.

The mean values $\boldsymbol{\mu}_*$ for the misalignment p.d.f. is obtained by applying the fit matrix, partially deprived of its singular values, to the experimental matrix; the variances $\boldsymbol{\sigma}_*$ are extracted in the same way as above delineated.

With these precautions we have shown that *Sushi* algorithm can reconstruct misalignments up to $\approx 500 \mu\text{m}$ even when a random gaussian error is added to the machine model.

CONCLUSIONS

We have shown how to perform non-linear BBA by inverting multidimensional non-linear functions, method that, as far as we know, has never been tested before. However the numerical techniques here presented are general and can be applied to any multi-dimensional inversion problem. Moreover we developed the *Sushi* algorithm which turned out to be able to solve an inversion problem that we found to be intractable with any other numerical method known to us.

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