ROBUST EMITTANCE EVALUATION FROM COMPLEX TRANSVERSE PHASE SPACES

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Abstract

We present a novel procedure to analyze the transverse phase space of low energy electron bunches, close to a beam waist, in order to retrieve a sound estimate of its emittance. The procedure consist in a genetic code and a non linear fit applied in cascade, the first feeding the parameters starting values of the former. This allows us to cleanse the phase space from noise, separate the core charge from the halos and distinguish between bunch components undergoing different dynamics, such as cross over or the double emittance minima effect. Our procedure performs a rough longitudinal beam tomography, based on dynamical considerations, using transverse data. The application of the procedure to some experimental data is shown.

INTRODUCTION

The phase-space analysis nowadays is a very important matter in the outlook of LINAC accelerators dedicated to modern Free Electron Laser (FEL). Due to the utmost importance of the emittance in the production of FEL radiation, many laboratories all around the world have developed devices and software to better estimate and analyze this beam parameter from experimental data.

At SPARC lab in Frascati (Italy) [1] a movable emittance meter [2] has been designed and built to monitor the projected phase space and the projected emittance in the drift region downstream the RF-Gun and before the subsequent accelerating structures (booster). Such a device is of paramount importance to study a process named emittance compensation, whose theoretical description was reported by Serafini and Rosenzweig [3]. Given an electron beam largely dominated by space charge forces, instead of emittance pressure (quasi-laminar regime), the contributes of the bunch's internal forces and external fields – from RF focusing gradient and solenoid magnetic field – cause slice envelope oscillation, producing projected emittance oscillations, often referred to as plasma oscillation. A convenient damping of these oscillations at the end of the acceleration process allows to attain the maximum beam brightness at the entrance of the undulator. This kind of damping can be achieved by a very careful matching of the bunch envelope with the beam optics. Consequently a complete characterization of such emittance oscillations is needed.

Here we present an innovative method able to analyze and characterize, in a very detailed way, transverse phase space images of quasi-laminar beams. The method originates from the joint use of two existing tools, named GMESA [4] and NoLFiPS [5], and works on the subsequent basis: emittance oscillations are pointed out by a misalignment of the slices phase space projections. Such beams can be represented by the sum of many sub-beams with equal or different densities. Each sub-beam draws concentric ellipses in the phase space, with various slopes and covering areas of various intensities. The whole beam has an associated emittance that is proportional to the total union area of all such ellipses. Therefore the global geometric emittance can be evaluated by finding the union of ellipses boundaries while its rms value is retrieved from the charge distribution enclosed in such boundaries. The analysis method starts with a noise cleaning performed by a Genetic Algorithm (GA) [6,7], that prepares the phase space image to be fitted with a non-linear function composed by the sum of two elliptic shaped exponential function. The fitted phase space enables to divide the traces of different slices and produce an estimate of emittance due only to the core of the bunch.

NOISE CLEANING BY GENETIC ALGORITHM

The phase spaces obtained at SPARC, here analyzed, are the result of data coming from the emittance meter device, where a slit array generates beamlets visible on a screen [2]. The measured beamlets consist in a signal superimposed to a high degree of noise. A first image elaboration allows to remove much of the noise and an appropriate interpolation produces the whole phase space images [8]. At the end of the process, the phase-space generated is an intensity distribution where a weak – but none negligible – background noise is present.

A deeper phase-space noise cleaning is performed by using the code GMESA, Genetic Multiple Ellipse Slice Analysis. The strength of the code lies in representing the beam as composed by sub-beams of different density and in giving an analytical description of the real beam, retrieving the Twiss parameters of the relative elliptical distributions.

Genetic algorithms are particularly suitable to solve problems that have nonlinear features and where it is not possible to consider each parameter as a variable that can be fixed independently from all the others. The projected phase space representation of a real beam by the union of N analytical ellipses is not an easy task; it has been estimated that a good representation needs N=8. This involves the computation of 26 parameters: the two common centroids and the 24 Twiss parameters of the ellipses. The code needs as input the portion of the bunch charge to be cut. The remaining charge defines many density contours and the code has to find the best set of the 26 parameters that best describe the real beam.

One set of 26 parameters is considered like a chromosome and every single parameter of the chromosome is considered a gene. The code starts generating a first random population of 24 chromosomes and each random chromosome represents a possible solution of the. After creating the first population, the genetic optimization process begins. This means that 24 chromosomes generate a new population of 24 son chromosomes by a crossover of the single individuals in an iterative way, from generation to generation. The crossover of chromosomes is performed two by two, exchanging stochastically their genes and considering also a random mutation operator that introduces new features into the optimization process.

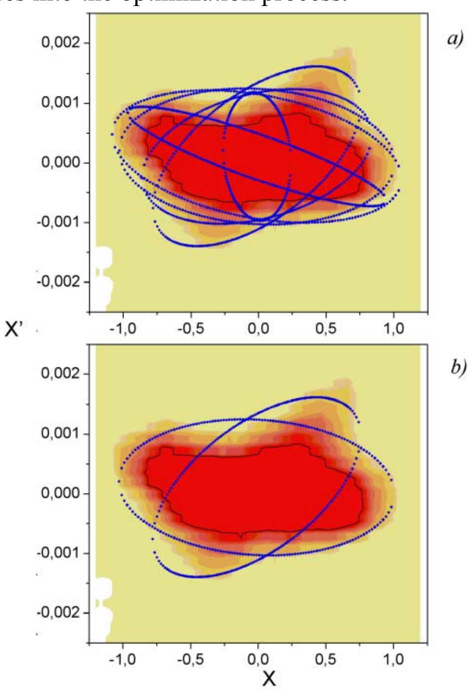

Figure 1: (*a*) Agreement between the genetic solution and the real bunch distribution. (*b*) The two main analytical ellipses, delimiting the background noise from the bunch distribution.

The evolution toward better individuals is driven by a fitness function $F_{fitness}$ that evaluates the performance of each chromosome and allocates a larger reproductive opportunity to the best ones. Each generation is never worse than the preceding one because the best chromosome is always reproduced in the successive generations.

The probability that a couple of different chromosomes produces, by crossing, an individual of the new generation is:

$$P_{ij} = \frac{F^i_{fitness} \cdot F^j_{fitness}}{\sum_{i,j} F^i_{fitness} \cdot F^j_{fitness}} \quad , \qquad (1)$$

The fitness function is defined as:

$$F_{fitness} = \frac{I}{A_d} \qquad (2)$$

where I is the charge enclosed by the union of the ellipses, while A_d is the total area.

Fig. 1(a) shows the genetic solution with eight ellipses and a 5% charge cut superimposed to the projected distribution of the real bunch. They are in very good agreement. Fig. 1 (b) shows the two ellipses that enclose most charge, representing the expected result, delimiting the background noise and permitting to proceed with the analysis.

For sake of clarity it is important to explain that phase-spaces here analyzed can be well-represented by the union of two elliptical distributions that should represent approximately all the bunch charge. Only in a much more accurate description could be considered more than two ellipses; here it is not necessary.

NON-LINEAR FITTING

The second part of the phase space analysis consist in a non-linear fit of the charge density distribution enclosed by the two main ellipses.

The most important element in this step is the fitting function. By a visual inspection of the reconstructed transverse phase spaces [8], the charge distribution seems either to decrease linearly from its maximum or appears as a sum of two parabola like shapes, one on top of the other. From a theoretical point of view the density distribution could drop to zero faster than a Gaussian because of its initial uniform charge distribution at the cathode. We decided than to use a fit function of the form:

$$f(\theta,\varphi,\underline{\Sigma},\underline{\sigma}) = Q_1^2 e^{-r(\theta,\Sigma_1)-r^2(\theta,\Sigma_2)-r^4(\theta,\Sigma_4)} + Q_2^2 e^{-r(\varphi,\sigma_1)-r^2(\varphi,\sigma_2)-r^4(\varphi,\sigma_4)}, \qquad (3)$$

where

$$r(\alpha,s) = \left[\left(\frac{(x-x_0)\cos\alpha}{s_x} + \frac{(x'-x'_0)\sin\alpha}{s_{x'}}\right)^2 + \left(\frac{(x'-x'_0)\cos\alpha}{s_x} + \frac{(x-x_0)\sin\alpha}{s_{x'}}\right)^2\right]^{\frac{1}{2}}. \qquad (4)$$

This function, being the sum of two exponentials with different orientations, can cope with the different dynamic obeyed by the core portion of the bunch and the tail area, yielding some information on the charge content of both portions. Notice that we did not add a baseline term because it has already been subtracted in raw instrumental data elaboration [8].

A total of 18 parameters must be fitted using the least squares method. Since the results of such kind of fittings heavily depend on the initial parameters' values, both in convergence speed and final correspondence between the fit and the experimental data, a sensible choice of starting values is essential.

For the 12 scale parameters, we choose to select the two ellipses produced by GMESA as explained earlier and, assuming a Kapchinskiy-Vladimirskiy distribution, halve both the semimajor and semiminor axes [9]. Four values are then retrieved, so we set the starting values of all the

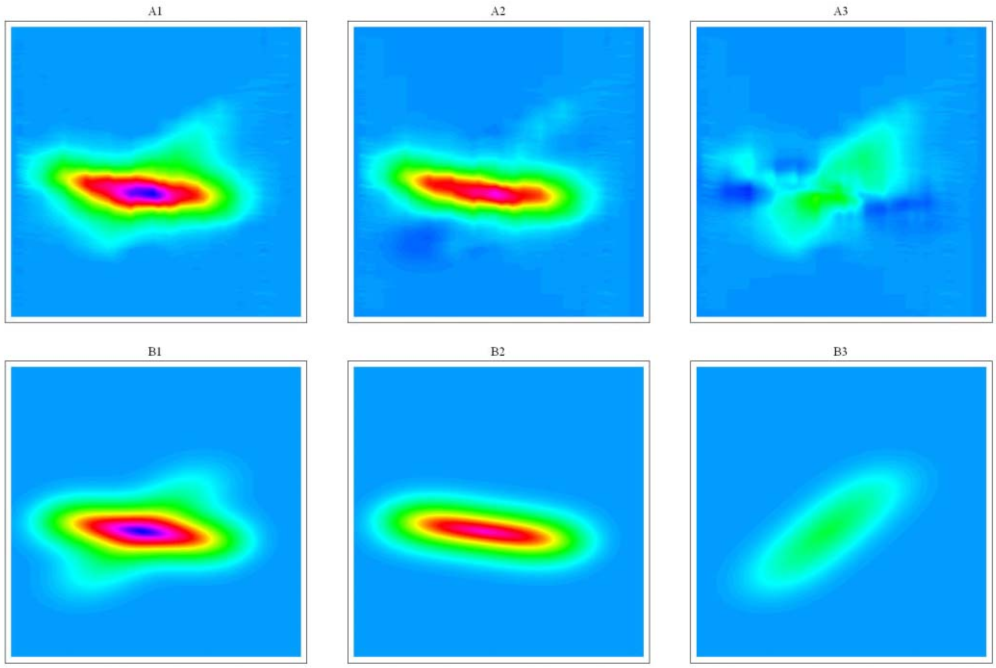

Figure 2: Analysis of a transverse phase space: A1 is the experimental phase space; B1 is the fitted complete phase space; A2 is the cleaned core portion of the beam, obtained by computing A1-B3; B2 is the fitted core, i.e. equation (3) with Q2 = 0; A3 is the cleaned secondary portion, obtained by computing A1-B2; B3 is the fitted secondary beam, i.e. equation (3) with Q1 = 0.

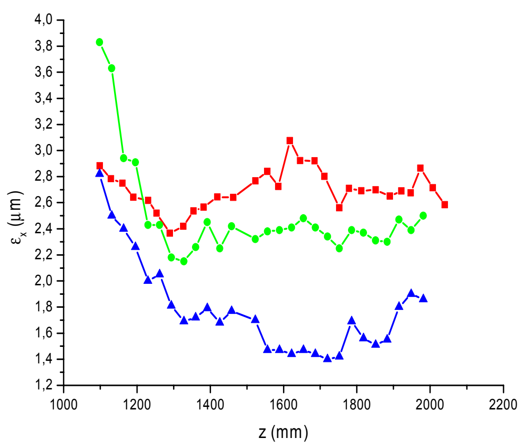

Figure 3: Emittance calculated from raw phase space images (red), full fit (green) and the fitted core portion only (blue).

scale parameters for the same direction equal (i.e. $\Sigma_1 = \Sigma_2 = \Sigma_4$, $\Sigma'_1 = \Sigma'_2 = \Sigma'_4$ and so on). Although the assumption of uniformity is not satisfied, its prescription is only used to infer a starting value for the scale parameters of the fitting function, not the final one. The two angles between the directrix of each ellips and the *x* axis are taken directly from GMESA, while the two weights Q_1 and Q_2 are proportional to the charge held by each ellipse, so that $Q_1^2 + Q_2^2$ is equal to the total charge held by the ellipses. Finally the starting values for x_0 and x'_0 are set equal to their respective values returned by GMESA.

Fig. 2 shows the results of the fitting process and the separation performed between the two beam components. Fig. 3 displays the emittance curves for raw images, full fit and beam core fit. Notice that the total fit emittance is higher than the experimental one, for low values of *z* because the raw data were cut in the acquisition process, due to the size of the beam; notice also that the emittance oscillations disappear in the lower curve, since this effect is give by the interplay of both beam components.

REFERENCES

[1] D. Alesini et al., Nucl. Instrum. Methods Phys. Res., Sect. A 507, 345 (2003).
[2] L. Catani et al., Rev. Sci. Instrum. 77, 093301 (2006).
[3] L. Serafini and J. B. Rosenzweig, Phys. Rev. E 55, 7565 (1997).
[4] A. Bacci (to be published).
[5] A. R. Rossi (to be published).
[6] L. Davis, Genetic Algorithms and Simulated Annealing. London, U.K.: Pittman, 1987.
[7] K. A. DeJong, "An analysis of the behavior of a class of genetic adaptive systems," Ph.D. dissertation, Univ. Michigan, 1975.
[8] A. Mostacci *et al.*, Rev. Sci. Inst. 79 (2008) 1.
[9] T. Wangler, "RF Linear Accelerators", John Wiley & Sons, New York, 1998, p. 265.