

LINAC ALIGNMENT AND FREQUENCY TOLERANCES FROM THE PERSPECTIVE OF CONTAINED EMITTANCES FOR THE G/NLC[†]

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Abstract

The next generation of linear colliders will consist of several tens of thousands of accelerating structures and this will entail inevitable errors in the dimensions and alignments of cells and groups thereof. These errors result in a dilution of the beam emittance and consequently a loss in overall luminosity of the collider. For this reason it is important to understand the alignment tolerances and frequency tolerances that are imposed for a specified emittance budget. Here we specify an emittance dilution of no more than 10% of the injected nominal value of 20 nm.rads and we track the progress of the beam down the linac whilst accelerating structures (and sub-sections thereof) are misaligned in a random manner. Random frequencies are also incorporated in the misalignment analyses. Tolerances are specified for both frequency errors and misalignment errors.

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INTRODUCTION

The main X-band linacs of the G/NLC (Global/Next Linear Collider) [1] are required to sustain an unloaded gradient of 65 MV/m (with a loaded gradient of 55 MV/m) and be able to accelerate 192 bunches of charged particles for almost 14 km. In order to prevent breakdown occurring in the accelerating structures, surface cleanliness, surface electromagnetic fields and several other parameters have been carefully studied and the breakdown events have been reduced to manageable rates [2].

It is also important to minimize the wakefield left behind each accelerated bunch in the train as cumulative BBU [3] or severe emittance dilution [4] will occur. The wakefield is reduced by almost 2 order of magnitude at the first trailing bunch by detuning the cell frequencies such that the characteristic modal frequencies add destructively [5]. However, soon thereafter the wakefield re-coheres and further down the train succeeding bunches would experience a wake large enough to drive a BBU instability. This is prevented by coupling out the wake from each cell to four waveguide-like manifolds [6] that lie co-linear with the axis of the accelerating structure. This method of wakefield damping has been successful in reducing the wakefield for earlier structures [7].

However, the latest structures, motivated by electrical breakdown considerations [2], are a factor of 3 shorter than the original DDS series [5]. Reducing the accelerating structure's length increases the dipole wakefield mode spacing and hence reduces the effectiveness of the overlapping of neighbouring modes. For this reason we interleave the modes of neighbouring structures and effectively fill-in the space between modes

in a single structure. The focus herein is on the G/NLC baseline design structure H60VG3S17. This accelerating structure is 60 cm in length and consists of 55 cells with an initial fundamental group velocity of 0.03c. The average iris to free space wavelength is 0.17.

The final emittance of the beam can be diluted by a beam injected off axis (injection offset) and by misalignment of cells. Space considerations prevent the former being presented. However, we refer the interested reader to [8] for some details on the remarkably loose frequency tolerances for a beam subjected to an injection offset.

Here we investigate the emittance growth due to long-range transverse wakefields for misaligned cells in the accelerator structure. We study the case of a beam injected on-axis but with misaligned cells (and groups thereof). In particular, we include frequency errors and calculate their impact on misalignment tolerances.

The paper is organized such that the next section discusses the wakefield of the G/NLC baseline design and the second main section analyzes misalignment tolerances.

TRANSVERSE WAKEFIELDS

The G/NLC baseline design uses four-fold interleaving of the dipole frequencies of accelerator structures [9]. The dominant first dipole band wake [10] that results from this process is illustrated in Fig. 1. For the sake of comparison, the decay in the envelope of the wakefield that occurs due to purely Ohmic damping together with that which occurs due to detuning the cell frequencies is also shown. Detuning the cell frequencies gives rise to destructive interference of the modes and results in the

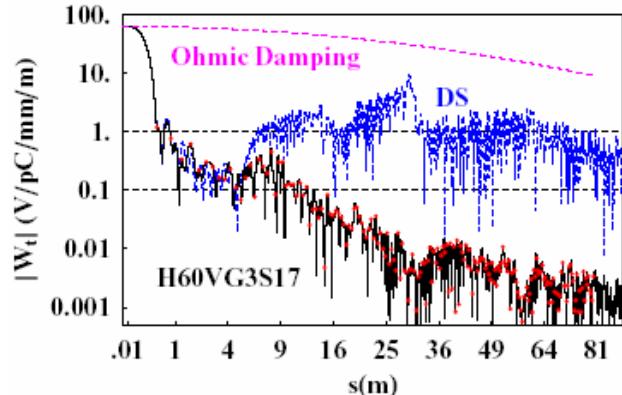


Figure 1: Envelope of the four-fold interleaved long-range transverse wakefield $|W_d|$ for H60VG3S17. The red dots indicate the location of each bunch. Also shown, in blue, is the wake that results from detuning only (DS), and in magenta, the decay of the wake that results from copper losses in the cells (Ohmic damping).

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Gaussian functional fall-off in the envelope of the wakefield for the first few meters, illustrated in Fig. 1. However, eventually the modes recohere. The recoherence position is set by the minimum mode spacing. For this particular accelerator structure the dashed blue curve in Fig. 1 gives a recoherence position of ~ 6.4 m. In H60VG3S17 a portion of the remaining wakefield is coupled out through a slot cut into each cell to four attached collinear waveguide-like manifolds and this reduces the wakefield to below 1 V/pC/mm/m (refer to the black line in Fig. 1).

MISALIGNMENT TOLERANCES

Introduction

Misalignments from cell-to-cell and groups thereof (structure-to-structure in particular) cause a dilution in the emittance of the beam. In addition to cell misalignment errors there are frequency errors that are caused by fabrication errors and by errors in the original design. We constrain the emittance dilution to be no more than 10 % of the injected emittance and we consider the misalignments that are allowable both with and without random frequency errors. To begin, we consider the case excluding frequency errors and we make an analytical estimate for the misalignments. The analytical estimate is compared with tracking simulations performed with LIAR [11].

Analytical estimation of emittance dilution

In order to estimate the growth of the projected emittance $\Delta\epsilon$ of a train of bunches caused by misaligned accelerator structure cells the following formula for the expectation value of [12] is used:

$$\langle\Delta\epsilon\rangle = r_e^2 N^2 \bar{\beta}_0 L_s \langle\Delta S_k^2\rangle \frac{1 - (\gamma_0 / \gamma_f)^{1/2}}{\gamma_0^{1/2} \gamma_f^{3/2}} \quad (1)$$

where r_e is the classical electron radius, N is the number of particles in the bunch, $\bar{\beta}_0$ is the average value of the beta function at the beginning of the linac, L_s is the number of structures in the linac, L_s is the length of the structure, γ_0 and γ_f are the initial and final relativistic factors of the beam. The sum wakefield of the k^{th} bunch is defined in terms of the wakefield at the location of bunch w_k as: $S_k = \sum_{i=1}^k w_i$ and the RMS value by: $S_{\text{RMS}} = \langle\Delta S_k^2\rangle^{1/2}$ where ΔS_k is the difference between S_k and the average value $\langle S \rangle = N_b^{-1} \sum_{k=1}^{N_b} S_k$. Here, N_b is the number of bunches.

Eq. (1) is derived excluding frequency errors and assuming a lattice with the beta function smoothly increasing along the linac as $\beta \propto E^{1/2}$.

For small misalignments, w_i is a linear function of cell offsets, $W_i = \sum_{s=1}^{N_c} w_{is} y_s$ (N_c = Number of cells). The matrix W for the G/NLC structure H60VG3S17 with 55

cells is based on the method in [13]. It has a dimension of $N_b \times N_c$. In our calculation we used $N_b = 192$ for a bunch spacing of 1.4 ns and $N_c = 55$

Eq. (1) is utilized to obtain the RMS alignment tolerances on cells and this is compared with tracking simulations in the next section.

Tracking simulations

The beam is tracked down the complete linac under the influence of misaligned groups of cells and the emittance dilution is recorded. The results of such simulations are illustrated in Fig. 2 where the emittance growth due to

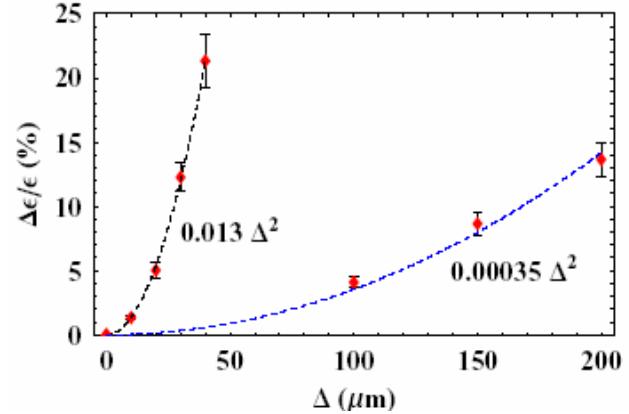


Figure 2: Percentage emittance growth $\Delta\epsilon/\epsilon$ versus RMS offset Δ for both single-cell and single-structure misalignments (illustrated by the black line and the blue line, respectively). The quadratic fit is also shown for each misalignment type. Error bars are for the standard error of the sampled mean.

cell-to-cell and structure-to-structure misalignments are shown. For each point we make 50 tracking simulations and take the mean emittance dilution. There is a clear quadratic dependence on RMS misalignment. We perform similar simulations for groups of cells and extract the RMS offset that allows no more than 10 % dilution in

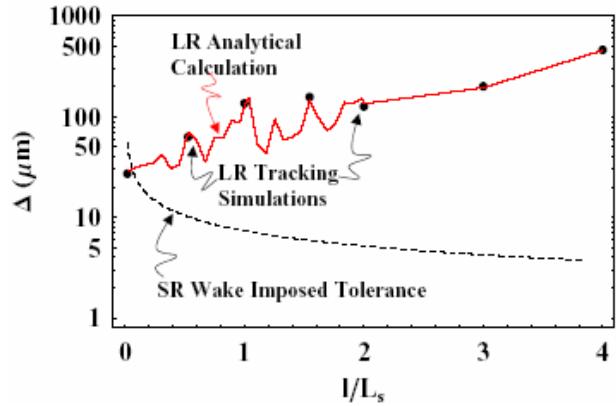


Figure 3: Tolerance Δ for random-random errors versus misalignment length l in units of the structure length L_s (0.60m). The solid red curve shows the result of an analytic calculation for the long-range (LR) wakefield tolerance based on Eq. (1) and the dots are calculated by tracking the beam down complete linac. The dashed line shows the short range (SR) wakefield tolerance.

the beam emittance. The large number of wakefiles are processed with a *Python* [14] code, prior to tracking the beam down the linac. These results are displayed in Fig. 3 together with those obtained from Eq. 1. The agreement is excellent. Also shown is the alignment tolerance that results from the short-range wakefield. This is of the order of 7 μm from one structure-to-the-next and it will be achieved by beam-based alignment (from the dipole signal radiated to the manifolds).

Similar simulations are performed for structure bows and tilts. This results in a random misalignment tolerance of 83 μm for the saggitta of a bowed structure and 0.4 mm.rads for the angular tilt of a structure.

Including random-systematic frequency errors

Frequency errors that are random within a given structure but are repeated from structure-to-structure are referred to herein as random-systematic errors. These errors are unlikely to occur in the fabrication process as it is more likely that errors from structure-to-structure will also be random. Nonetheless, we investigate the tolerances that are imposed for a 10 % emittance dilution for random-systematic errors and these results are presented in Fig. 4. In this simulation frequency errors with an RMS value of 5 MHz have been used. Each of the dashed lines corresponds to a machine made with a given error repeated from structure-to-structure throughout the linac. This type of error can give rise to tight alignment tolerances, since the lowermost line, for example in Fig. 5 specifies a structure-to-structure alignment of $\sim 50 \mu\text{m}$. Thus, in designing and fabricating the structures care must be taken to avoid such systematic errors.

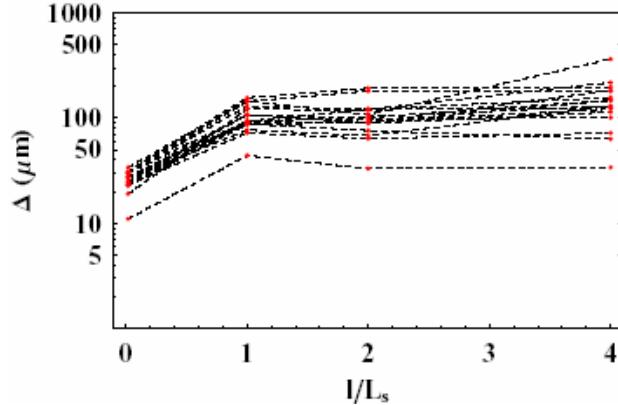


Figure 4: Tolerance Δ for random-systematic errors versus misalignment length l in units of the structure length L_s (0.60 m). The dots indicate the results of the tracking simulation. The tolerance is for long-range wakefields.

Including random-random frequency errors

Errors that are random within a given structure and are randomly distributed throughout the entire linac are considered here. This is representative of tool wear in machining several tens of thousands of structures, for example.

In particular, frequency errors with an RMS value of 3 MHz and 5 MHz are used in the alignment tracking

simulations. The results of these simulations are presented in Fig. 5 where they are compared with the case where frequency errors are excluded. It is clear that the introduction of frequency errors makes the alignment tolerances tighter. For the G/NLC baseline design there

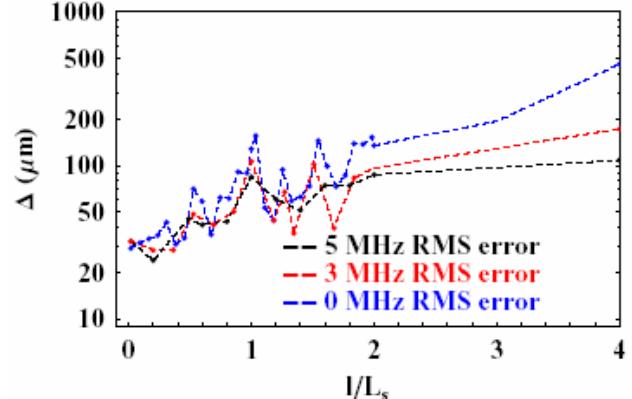


Figure 5: Tolerance Δ for random-random errors versus misalignment length l in units of the structure length L_s (0.60 m). The blue curve and dots are the results of a tracking simulation with no frequency errors included.

are 4 structures per girder so that, with reference to Fig. 5, the girder-to-girder alignment is $\sim 200 \mu\text{m}$ for and $\sim 100 \mu\text{m}$ for frequency errors with an RMS value of 3 MHz and 5 MHz, respectively.

CONCLUSIONS

To operate the collider with reasonable alignment and frequency tolerances we adopt a random-random dipole frequency tolerance of 3 MHz (which is comparable with that on the fundamental mode which is $\sim 1 \mu\text{m}$) [15]. The cell and structure alignment tolerances are then approximately 28 μm and 100 μm , respectively.

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