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Spectral matching in time domain: a seismological and engineering analysis.

Maria Lancieri, Paolo Bazzurro and Oona Scotti

ABSTRACT

The time domain spectral matching is the most commonly used technique in earthquake engineering to obtain accelerograms whose response spectrum is compatible with a smooth target spectrum, be it a poly-line design spectrum or a hazard spectrum. These accelerograms are used for assessing the response of structures, usually beyond their linear elastic regime. Although this practice is widespread, there is an ongoing debate on whether these matched accelerograms are legitimate substitutes for real ones and on whether they produce biased structural response estimates.

To help shed some light on this debate, we addressed two main questions:

1. How does the matching process modify the time-frequency properties of a real accelerogram?
2. How can one devise a rigorous benchmark to test the performances of spectral matched accelerograms?

We implemented a non-conventional strategy using the jagged spectra of real accelerograms for a given earthquake scenario as targets. This allows establishing a benchmark by which both seismological and engineering points of view can be addressed. Given the non-stationarity of the accelerometric signals, we used the time-frequency Stockwell transform to compare pairs of accelerograms to characterize in both time and frequency the changes induced by the matching process and to investigate the characteristics of an accelerogram causing the peaks of the response of a nonlinear single degree of freedom oscillator.

On the seismological side, we found that the spectral matching generates spectrum-compatible accelerograms with the same dominant frequency of the S-waves of the target and that the matched accelerograms have, on average, higher coda amplitudes with respect to the natural records with the same spectrum, over a time window of 5 s.

On the engineering side, the most important finding regards the large dispersion of peak responses to accelerograms with the same spectrum. Caution should therefore be applied in using very few spectrum-compatible records for practical applications.

Introduction

The development and refinement of spectrum compatible accelerogram generation techniques has been the object of many discussions, as four decades of bibliographic evidence on the topic attests (Rizzo et al., 1975, Kaul 1978, Silva and Lee, 1987, Preumont 1984, Lilhanand and Tseng 1988, Abrahamson 1992, Mukherjee and Gupta 2002, Suarez and Montejo 2007, Hancock et al. 2006, Pousse et al. 2006, Al Atik and Abrahamson 2010, Laurendeau et al. 2012, Zentner 2013, Alexander and al. 2014, Adekristi and Eatherton 2016, among many others).

Historically, the concept of response spectrum was formulated in the early 1930s (Biot 1932, Benioff 1934); the basic idea was that seismic ground acceleration is made up of "exceedingly variable oscillatory movements" and, in order to reduce such variability, the authors suggested defining a spectrum to describe the maximum response of pendula, or single-degree-of-freedom linear oscillators. By design, the response spectrum gives information on the maximum ground motion amplitude at any given frequency, in terms of acceleration, velocity or displacement, but ignores the phases. In the following years, its definition was refined (Housner 1941, Hudson 1956) and it became the standard tool for analyzing the strong motion records properties in relation to the structural behavior of simple linear oscillators that are of particular interest in modal analysis (Housner and al. 1953, Alford et al. 1953, Hudson 1962). In the 1970s, the time history analysis of equipment and structural components was increasingly put into practice in the design of nuclear

power plants. As a consequence, the development of accelerograms compatible with smoothed response design spectra became a necessity. The generation of spectrum-compatible accelerograms is not a trivial task since the response spectrum, unlike the Fourier spectrum, is not a transform. The implication of this is that for any given accelerogram, while it is always possible to compute its response spectrum, there is an infinite number of accelerograms with which it is compatible. Since the concept of an "inverse response spectrum" is meaningless, researchers have developed many different methods to generate spectrum compatible accelerograms. They range from pure synthetic accelerograms that are given by the superposition of sinusoids with a random phase (Gasparini and Vanmarcke, 1976), to the modification of recorded accelerograms via spectral matching techniques.

Spectral matching techniques are based on the idea of modulating the energy content of a recorded ground motion so that its response spectrum matches a target. Conceptually, there are two main strategies to accomplish this. The first is based on the modification of the signal in the frequency domain (Preumont 1984, Silva and Lee, 1987) by adjusting the Fourier spectrum as a function of the ratio between original and target spectra. This strategy is quite intuitive, but it is equivalent to repeatedly superimposing the original accelerogram harmonic motions with uniform amplitude over the entire time window (Lilhand and Tseng 1988). Thus, in general, this method provides unrealistic waveforms because it preserves neither the causality nor the non-stationary behavior of the original seismic signals. The second strategy consists of modifying the original accelerogram in the time domain by adding wavelets (Kaul 1978, Lilhand and Tseng 1988, Abrahamson 1992, Al Atik and Abrahamson 2010) until the desired response spectrum is obtained. This time-domain spectral matching technique assumes that the peak response of a single-degree-of-freedom (SDOF) oscillator of a given frequency that occurs at a specific time t_{max} is mostly sensitive to the accelerogram in the neighborhood of t_{max}. Therefore, the original accelerogram (commonly called seed accelerogram) is modified by superimposing wavelet functions, each centered at t_{max}, whose amplitude and phase are designed to manipulate the SDOF oscillator response precisely at t_{max} in such a way that the discrepancy of the oscillator response to the amplitude of the target spectrum at

that frequency is kept within a pre-specified tolerance. Each wavelet whose duration depends on its frequency produces localized perturbations in the accelerogram. The advantage of working in the time domain is that the non-stationary behavior of the accelerogram is retained. In addition, the wavelet function proposed by Al Atik and Abrahamson (2010), unlike the Lilhand and Tseng (1988) original version, generates velocity and displacement time histories that have no low-frequency bias. For these reasons, the time-domain spectral matching technique is widely used because it provides, quickly and easily, more "realistic" non-stationary accelerograms. The interested reader can find a more detailed discussion on the time-domain matching technique in the relevant literature (Hancock et al. 2006; Seifried 2013).

The end users of these waveforms, namely engineers, use matched accelerograms for assessing structural response during specific applications but, in general, they trust the work done by the seismologist and do not question their legitimacy. To engineers, the sanity check that matched accelerograms must pass to be legitimate is confined to the response they cause to the structures of interest. If matched accelerograms produce unbiased structural responses when compared to those of "equivalent" real records, engineers fully embrace them. The acceptance of matched records is driven by practicality since their use dramatically decreases the number of response analyses necessary to estimate structural responses within a given level of accuracy. However, if the response of such records is biased, engineers may still use them for the reasons stated above, but they may have to statistically correct the responses for the induced level of bias.

The presence of bias in structural response has been a matter of debate for almost two decades. On one hand, some authors (Carballo and Cornell, 2000; Bazzurro and Luco, 2006; Schwab and Lestuzzi 2007; Huang et al., 2008) identified a systematic bias in the estimation of mean nonlinear structural response induced by matched records. This is especially true for highly non-linear structural responses. On the other hand, other studies (Shome et al., 1998, Hancock et al., 2008; Iervolino et al. 2010; Heo et al., 2010) claim that structural response caused by matched

accelerograms has no (or negligible) bias.

Answering the "bias issue" is not trivial since many factors come into play, namely the degree of non-linearity of the structure, the matching strategy, the use of fully synthetic accelerograms, and the amount of modification caused to their original intensity measures (IMs) by the spectral matching if recorded data are used as seeds. Supporters of the spectral matching (Watson-Lamprey and Abrahamson, 2006; Hancock et al., 2008; Grant, and Diaferia, 2013) argue that if the matched signals are characterized by IMs that are similar to that of the real accelerogram used as seed (typically Arias Intensity, duration, and so on), then matched accelerograms do not bias the structural response. Implicit in this reasoning is the assumption that only a naïve application of the matching procedure produces records that may induce bias in structural response. Iervolino and coauthors (2010) raised a central point to this debate around biased response. One must then question whether using the response of real records as a benchmark to validate the performance of matched accelerograms as done in many studies is appropriate. Indeed, assessing the "equivalence" between the matched and real records is not straightforward. The degree of statistical equivalence of the response is often based on few proxies that do not reveal the whole complexity of a seismic signal, a complexity that could have an impact on the non-linear behavior of a structure that experiences it.

Matched accelerograms are only used for engineering purposes, and their seismological features have never been thoroughly investigated. Of course, the matched accelerograms are characterized by smooth spectra whereas recorded time histories have spectra whose jaggedness is related to the complexity of the source process, wave propagation in crustal medium and the response of the shallower soil layers beneath the seismic station. From a seismological viewpoint, however, despite the "quasi-empiric" appellative given by Silva and Lee (1987), the nature and the characteristics of matched accelerograms compared to those of real ones are in fact barely known.

In this paper, we propose an unconventional strategy to create a set of matched waveforms with the two-fold objective of understanding their features vis-à-vis those of real records and, to a limited extent, of testing whether these records produce an unbiased structural response, and if so, why. Instead of matching the spectra of real records to a target smooth spectrum, as routinely done, we matched them to jagged target spectra of real records. The advantage of this strategy is that each target spectrum corresponds to its natural accelerogram. This correspondence allows establishing a real benchmark to which both seismological and engineering point of views can be considered.

More specifically, wearing a seismological hat, we will make a direct investigation of many accelerograms matched to the same jagged spectrum. Our goal is to assess and characterize the common features, if any, shared by original and matched accelerograms. With this aim we propose an original method, based on the Stockwell transform (Stockwell et al. 1996) that allows comparing two non-stationary accelerograms and, thus allows one to understand how the accelerogram is modified by each step of the iterative matching procedure.

Wearing an engineering hat, we instead quantify the differences between the values of a set of standard Intensity Measures (IMs) of the target and matched accelerograms. Finally, we go beyond linear SDOF responses and start to address the engineering concerns by comparing the response and respective damage states caused by original and matched time histories of a nonlinear SDOF oscillator. Using a small subset of accelerograms with the same response spectrum, we use the Stockwell transform to qualitatively identify the accelerogram's features that cause different structural responses.

The Jagged Spectrum Matching Process

Database

The first step is the selection of a sufficient number of accelerograms to allow a robust statistical inference. Selecting many records from past earthquakes from a large magnitude, M, and source-site distance, R, bin would unnecessarily complicate the analysis since the accelerograms would be

too different in terms of both amplitude and duration. Therefore, we chose a narrow, well-populated M-R bin with moment magnitude ranging from 5.8 to 6.6 and hypocentral distance from 10 to 30 km (Figure 1a). In total, we extracted 226 "raw", uncorrected accelerograms from the Southern California Earthquakes, the Euro-Mediterranean (Ambraseys et al. 2004) and Orfeus databases. The M-R scattergram and histogram of the selected suite of records is plotted in Figure 1a. We then applied a baseline correction (based on Paolucci et al. 2011) to each accelerogram in order to remove any residual displacement after a double integration of the accelerometric signal.

Tuning RSPMatch

In this paper, we use the RSPMatch code (Al Atik and Abrahamson 2010), the most commonly used code for signal matching in the time domain. The spectra are matched in the frequency range 0.1 – 35 Hz. The matching procedure here is performed in 4 passes, each of which modifies the accelerogram progressively over 4 frequency ranges: [1-35] Hz, [0.5-35] Hz, [0.3 - 35] Hz, and [0.1-35] Hz. Concerning the matching procedure, as alluded to in the introduction, we used each one of the 226 response spectra as a target for the matching while utilizing the remaining 225 accelerograms as seeds for the matching (Figure 1b). For the sake of conciseness, in the following we will refer to the real accelerogram corresponding to the target spectrum as the "target accelerogram". This exercise is repeated for all 226 records in the bin, hence generating 226 "matched families" for a total of 50858 matched accelerograms. Therefore, each one of the 226 families of records has one real accelerogram and 225 spectrum matched time histories, all of which have the same response spectrum within a given tolerance.

The used wavelet is the "improved tapered cosine" introduced by Al Atik and Abrahamson (2010).

The value of the tolerance parameter is set by the user as a function of the desired degree of similarity between the target and the matched spectrum. The value of the tolerance parameter and the number of iterations, which influence the convergence time of each RSPMatch run, were selected after performing a battery of preliminary tests done on 10 target spectra. This exercise

resulted in setting a 15% tolerance and 20 iterations as a good compromise between accuracy and practicality.

A final comment on the RSPMatch matching criteria adopted in this study concerns the tuning of the convergence damping parameter that specifies the fraction of adjustment made to the acceleration time series at each iteration (for details, see Al Atik and Abrahamson 2010). In standard applications, where the seed is matched to a smooth target spectrum, the matching process is parameterized to minimize the differences between the seed and the matched records (looking at values of quantities, such as Arias intensity and duration) (Grant and Diaferia 2013, Seifried and Baker 2016). With this aim, some authors explicitly tune the convergence damping parameter to 0.7 or even to lower values (Seifried 2013). In our non-canonical application, we are not interested in keeping the similarities between the seed and the matched accelerograms. We are rather interested in obtaining matched and target spectra (and possibly time histories) that are as close as possible. For this reason, during the matching exercise, we used the default value of 1 for the convergence damping parameter.

Qualifying the matched spectra

Since RSPMatch so far is often used by engineers to match smoothed spectra, before pursuing our study we need to investigate whether it works as intended for matching jagged spectra as well.

The successful matching criterion used by the RSPMatch code is based on whether at each frequency the maximum absolute distance between the ordinates of the target and matched spectra is within the set tolerance. The code performs a discrepancy check on a frequency-by-frequency basis, and if the maximum discrepancy value at anyone frequency is greater than the tolerance set by the user, the matching is declared unsatisfactory, no matter what frequency or how many frequencies violated this condition.

For example, Figure 1c shows the matched spectra that were labeled as successfully matched by RSPMatch while Figure 1d displays the spectra labeled as unmatched even though the discrepancy

between matched and target spectra are noticeable only at very low and very high frequencies that are irrelevant for driving the response of most structures.

A more comprehensive view of the achieved quality of the matching for all the records as a function of frequency is given in Figure 2. For each of the 226 matched accelerograms families the median misfit between the target spectrum and the 225 matched spectra has been computed at each frequency (169 points logarithmically spaced) in the 0.1-35 Hz range as follow:

$$Misfit(f) = \frac{1}{226}\sum_{i=1}^{226}\frac{SA_i^{Matched}(f) - SA_i^{Target}(f)}{SA_i^{Target}(f)}$$

Positive misfits indicate that target spectra amplitudes are higher than the matched. For each frequency in the range, Figure 2 shows the number of families with median misfit value expressed in terms of tolerance percentage. The darker bins mean that more than 209 families have a median misfit equal to zero, while the light grey means that less than 20 families have a median misfit less than 10%; it can be seen that for the large majority of accelerogram families the median misfit is centred on zero, except at higher frequencies (f > 25 Hz) where there is a mild median negative bias of about 2%.

From an inspection of Figures 2 we can conclude that all the families of matched records have a median misfit lower than 10% and that spectra of families of matched records are tightly packed around the target value at each frequency. Very few exceptions are observed at the very low and very high frequencies that are inconsequential for the response of most structures. Therefore, we assume that all the accelerograms are successfully matched for the purposes of this work.

Time-Frequency Analysis of Time Histories Matched to Jagged Spectra

Comparison of two non-stationary time histories

The response spectrum does not reflect the complexity of accelerograms. As stated in the introduction, even if the matched accelerograms have the same response spectrum of the target, the accelerograms themselves are different. In this section, we propose a pure seismological method to assess the differences and/or the similarities between two accelerograms sharing the same spectrum.

For stationary time histories, their comparison is easily carried out by performing time cross-correlation or the spectral correlation expressed as the ratio between the squared cross-spectral density, and the product of the auto spectral density of the two signals (Norton and Karczub, 2003).

Seismic signals, however, are not stationary, and for this reason the comparison needs to be performed in the time-frequency domain. The Stockwell-Transform (Stockwell et al. 1996), which is called here *S*-transform for short, is thus a well-suited tool as it provides a time-frequency representation of the signal. The S-transform can be interpreted as an extension of the continuous wavelet transform with Gaussian windowing, as the mother wavelet with a non-null average, and dilation factor equal to the inverse of the frequency (Simon et al. 2007, Ventosa et al. 2008). The *S*-transform, $S(t,f)$, is defined as:

$$S(\tau, f) = \int_{-\infty}^{+\infty} h(t) \frac{|f|}{\sqrt{2\pi}} e^{-\frac{(\tau-t)^2 f^2}{2}} e^{-i2\pi f t}\, dt$$

Where $h(t)$ is the time-series (namely, the accelerogram in this application), f the frequency and t the time. The integral of the *S*-transform along the time axis is simply the Fourier transform of the time-series $h(t)$, and therefore $S(t,f)$ can be interpreted as a power density spectrum unrolled along the time axis.

By definition, the *S*-transform gives the Fourier spectra computed on Gaussian windows centered at each time sample and, therefore, the spectral correlation can then be obtained by looking at the coherence of the *S*-transforms along the time axis. Such a strategy is inspired by the advanced

signal comparison techniques based on local cross-correlation that are mainly used in the domain of full wave tomography (Hale 2006).

In mathematical terms, the forward 1-Dimensional coherence (1DCoh) product of the *S*-transforms is expressed as:

$$\forall\ \Delta t\ \in \left[0, \frac{t_{max}}{\Delta t}\right]$$

$$1DCoh = S_{Match}(t,f)\ \times\ S_{Target}(t+\Delta t,f)/\max|S_{Match}(t,f) \times S_{Target}(t+\Delta t,f)|$$

while

$$\forall\ \Delta t\ \in \left[0, \frac{t_{max}}{\Delta t}\right]$$

$$1DCoh = S_{Match}(t+\Delta t,f) \times S_{Target}(t,f)/\max|S_{Match}(t+\Delta t,f) \times S_{Target}(t,f)|$$

is the backward 1-dimensional coherence image; where S_{Match} and S_{Target} are the *S*-transforms of the matched accelerograms. The S-transform product is computed in the complex domain. Theoretically, Δt should be the sampling interval of the accelerogram, which here is 0.005 s, but in practice, this short Δt would make the calculation too long. For this reason, we set Δt has equal to 0.2 s. The result of the coherence analysis is a time-frequency coherence image obtained plotting the absolute value of the S-transform product. A coherence score is attributed as a function of the maximum reached by the absolute value of the coherence product.

An example is given in Figure 3 where the "target" (Figure 3a) and the matched (Figure 3b) accelerograms are plotted along with their S-transforms (Figure 3c, Figure 3d), the coherence image is given in Figure 3e. The areas of the S-transforms in darker tones have higher amplitudes and can be interpreted as amplitude bursts. The target and the matched accelerograms are both characterized by the presence of an amplitude burst occurring at around 5 s and centered at 2.7 Hz, which is a feature that the S-transform coherence clearly highlights. However, the matched accelerogram differs from the target one mostly because of a longer coda characterized by 3 amplitude bursts

centered at around 3 Hz. We also remark the presence darker stripes located in the 5 – 10 s time window and spanning a large frequency range up to 25 Hz.

Looking at this example we can claim that in this case, the matching process generates an accelerogram having an amplitude burst centered on the same frequency of the amplitude burst of the target accelerogram. In other words, in this particular case, the S-waves (S is for secondary) of the matched and the target accelerograms have both the same dominant frequency. However, note that in this example the codas of matched accelerograms have a longer duration and higher amplitude compared to the coda of the target accelerogram.

The question now is to understand how general these two observations are.

Analysis of time histories matched to the same jagged spectrum

To give an exhaustive answer to this question we should perform the same analysis for all the 50850 waveforms but this exercise is not feasible since the S-transform coherence analysis is time consuming. Hence, we limited the analysis to a subset of five families of matched accelerograms (limiting the number of analysis to 1125 S-transform coherence analysis) chosen to be different from one another. The five families were selected on the basis of the characteristics of the "target" accelerograms, namely different S-wave dominant frequencies, different S-transform shapes (a single burst, multiple bursts), and different Husid duration. The S-wave dominant frequencies of the target histories are 1.50, 3.53, 5.64, 5.95, and 9.0 Hz; they correspond to the values where the maxima of the S-transform amplitudes are located.

To answer whether the dominant frequency of seed and target accelerograms is about the same in all cases in Figure 4 we plot the distribution of the frequencies where the coherence between the target and the matched accelerograms S-transform reach its maximum. In all the examined cases, indeed the maxima of coherence images are centered at the dominant frequency of the target S-wave and the coherence scores are always larger than 0.75. Moreover, this observation is independent of the coherence score. This test shows that the matching process shifts the S-wave

dominant frequency of the seed accelerogram in the same neighborhood of the S-wave dominant frequency of the target accelerogram. In other words, a process driven by the response spectrum induces some similarity in the Fourier spectra (recall that the S-transform is a Fourier transform unwrapped along the time axis) of the matched and the target waveforms. Therefore, even if the matched accelerograms differ from one another, they show common features related to the Fourier spectral content of the target.

We can conclude that, at least for this earthquake scenario and for this subset of 1125 waveforms, the S-waves of the matched and target accelerograms have approximately the same dominant frequency.

The second question was: "do the matched accelerograms have longer coda compared to the target ones in all cases?" To answer this, we compared the target matched accelerogram codas by calculating the ratio of accelerogram envelope.

The performed analysis is based on the following steps:

1. We manually picked the instant, t_{coda}, corresponding to the beginning of the coda of each target/seed accelerogram pair (an example is shown in Figure 5a);
2. We compute the envelope of the target and all the matched waveforms defined as the amplitude of the Hilbert transform of the accelerogram (Figure 5b, the envelope of the matched accelerograms are plotted as density of points);
3. We assume that the matching process does not change the value of the t_{coda} and, therefore, the t_{coda} of the seed accelerogram is attributed to the matched waveform;
4. We align the target and the matched accelerogram at the manually picked t_{coda} values;
5. For each target-matched accelerogram pair, we compute the average coda envelope ratio (*ER*) over 1 second non-overlapping time-windows. This operation both allows

smoothing the ratio value and also reduces the impact of the possible t_{coda} picking errors (Figure 5-c). The quantity *ER* is defined as following:

$$ER = \int_{T}^{T+1} \frac{|\mathcal{H}(m(t))|}{|\mathcal{H}(T(t))|} dt$$

where $|\mathcal{H}(m(t))|$ is the amplitude of the Hilbert transform of the matched accelerogram and $|\mathcal{H}(T(t))|$ is the amplitude of the Hilbert transform of the target accelerogram

6. We repeat the same operation for all the matched families. We set to zero the t_{coda}, and we plot as density of points the ER values computed in six time windows following the t_{coda} (Figure 5d).

To enhance the coda amplitude amplification/reduction, the *ER* distribution in Figure 5d is plotted on a logarithmic base 2 scale. We remark that, in all the six time windows, the *ER* values are greater than 1 (0 in log2 scale) for the large majority of data, indicating that the coda amplitude is usually (but not always) amplified. In particular, the *ER* distributions are centered at two (1 in log2 scale) in the first three seconds after t_{coda} indicating that, on average, the coda amplitude of the matched accelerograms is twice that of the target waveforms. In the following time windows, the *ER* distributions are more scattered and the average ratio is close to 1.4 (0.5 in log2 scale).

This result can be interpreted in two different ways: matched accelerograms usually have higher coda amplitudes than the target accelerograms or, matched accelerograms usually have longer strong-phase duration than the target accelerograms. As will be shown in Section *"Statistical Analysis of Time Histories Matched to Jagged Spectra: Intensity Measures"*, the analysis of the Husid duration leans towards this latter interpretation.

Analysis of the matching process using S-transform

In this subsection, we address the question of the origin of the similarities and differences present in target and matched time histories. As an illustrative example, we thus examine here the different

332 iterations of the RSPMatch matching process for the same accelerogram pairs considered in Figure
333 3.

334 Before delving into the details of the matching iterative process, it is worth recalling that:

335 - the response spectrum is defined as the peak response to the accelerogram of a series
336 of linear elastic single-degree-of-freedom (SDOF) harmonic oscillators, each characterized
337 by a fundamental frequency and damping (often 5% of critical);
338 - the "time domain" matching method assumes that the time at which the SDOF
339 oscillator peak response occurs (hereinafter TPR) does not change as a consequence of the
340 iterative wavelet adjustment;
341 - RSPMatch modifies the seed accelerograms superimposing wavelet functions
342 centered at TPR, whose amplitude and phase are designed to manipulate the SDOF
343 oscillator response.
344 - The time-frequency content of the cosine wavelets (We show the improved tapered
345 cosine used by RSPMatch in the supplementary material) is a direct consequence of the
346 Gabor's principle, asserting that the spreads in the time and frequency measurements must
347 define a rectangle in Fourier space whose area is at least 1. If the wavelet has a long duration
348 the spread will be higher in time domain (this is the case of the 2 Hz wavelet in the top right
349 panel in SM), while if the wavelet has a short duration the spread will be higher in the
350 frequency domain (this is the case of the 20 Hz wavelet in the bottom right panel in SM).

351 The spectral matching process is presented in Figure 6 where we look simultaneously at the
352 response spectra adjustment (Figure 6a), the corresponding S transform modification (Figure 6b),
353 and the accelerogram evolution (Figure 6c). Figure 6a displays the target, seed and matched spectra.
354 The matching procedure here is performed in 4 passes, each of which modifies the accelerogram
355 progressively over 4 frequency ranges: [1-35] Hz, [0.5-35] Hz, [0.3 - 35] Hz, and [0.1-35] Hz (a1-
356 a4). Looking at Figure 6a (top panel), the spectrum of the seed is below the target up to 4 Hz, at

higher frequencies the target and the seed spectra have comparable amplitudes. Note that for passes 2,3 and 4 the updated input seed spectrum is the response spectrum of the accelerograms obtained as the output from the previous pass.

As far as the S-transform features, for both target and seed the highest amplitude bursts visible on the S-transform (Figure 6b) correspond to the S-waves on the time histories (Figure 6c), as already shown in Figure 3. The S-wave dominant frequencies (the center of the amplitude burst) are located between 5-10 s and centered on 2.7 Hz for the target and between 3 and 7 s and centered around 4 Hz for the seed. The TPR values are plotted with empty circles as a function of the fundamental frequency of the corresponding SDOF (Figure 6b). We remark that many TPR values are around the time of the amplitude burst corresponding to the S-waves. This observation is valid for the 225 time histories. Therefore, for the investigated scenario, the response spectrum is controlled by the S wave amplitudes in a frequency range of 2 – 8 Hz. After the first pass (Figure 6b) the wavelets passing through the TPR lying on the S-phase seed shift the amplitude burst center from 4 to 2.7 Hz, closer to the target dominant frequency. In particular, we remark that the TPR located between 3 and 7 s, are now more spread in time. This step is at the origin of the similarity highlighted in Figure 3 and Figure 4.

At lower frequencies (< 1 Hz), the response spectrum amplitude is controlled by the coda of the accelerograms for both target and seed cases, as shown by the location of TPR values. During the first pass of the matching a lower frequency coda appears (indicated by the black arrows on Figure 6b and Figure 6c), having generally higher amplitudes than the seed. The coda amplitude and shapes are adjusted in the subsequent passes, as apparent by inspecting the corresponding accelerograms (Figure 6c).

The low-frequency content is adjusted by the RSPMatch code with the insertion of many low-frequency cosine wavelets (characterized by a longer duration and a spread along the time axis of the S-transform,) in the coda of the accelerogram. The consequence of such an adjustment is that

the coda amplitude of the matched record is higher than the seed, over a time window of 5 s (Figure 6c). A systematic analysis of the seed coda amplification induced by the spectral matching process (see Appendix C) shows that, in general, this trend takes place over an average time window of 3 seconds.

Concerning the frequencies higher than 10 Hz, we observe that the TPR values of the seed accelerogram of all the SDOFs with fundamental frequency greater than 7 Hz (with the exception of 10 Hz) are aligned at 4.8 s (Figure 6b). This implies that, during the matching process, many high-frequency wavelets are injected at the same instant. The amplitude of such wavelets is relatively small since the target and seed spectra are close. Nevertheless their superposition originates the high-frequency (above 10Hz) low amplitude stripes visible on the matched accelerogram.

Thanks to the S-transform analysis we were able to trace the modification induced on the seed by the matching process, and to explain the origin of the similarities between matched and target accelerograms. The question arising now is if and how the changes induced by the spectral matching process impact the response of structures subject to matched records compared to the response of natural records with the same target spectrum.

Time-Frequency Analysis of the Response of a Nonlinear Spring

A comprehensive response to this question can only be given after the analysis of responses of many structures with different geometries, and material laws have been investigated. In this paper, we start addressing this question by considering a nonlinear SDOF system with an initial fundamental frequency of 1 Hz. For this purpose, we selected the “spring 1a” SDOF system in the FEMA P440A document (Applied Technology Council, 2009), which is intended to model the behavior of a typical gravity frame system (e.g., steel) commonly found in US buildings. The force-displacement backbone curve yields at a normalized base shear of 0.25 and a drift of 0.5% and includes a strength drop at a normalized base shear of 1 and drift of 2.5%. This drop terminates with a horizontal plateau with a residual strength of 55% of the ultimate capacity starting at a drift of 4%

and extending to an ultimate deformation capacity of 7%. Figure 7 shows the backbone capacity curve of the spring with its degrading hysteric behavior obtained by subjecting it to the 1 Hz sinusoidal acceleration time history with increasing amplitude shown at the top of the figure. The spring response is characterized by cyclic strength and stiffness degradation.

We analyze now the spring response and its relationship with the input accelerogram using the S-transform technique. An example is given in Figure 8 where one of the 226 real accelerograms used as input is represented by its response spectrum, its accelerogram and the corresponding S-transform (with a zoom between 0 and 1 Hz). The accelerogram's features are visually compared with the time history of spring drift, Θ, along with its S-transform and the response hysteretic behavior expressed in terms of normalized base shear versus drift.

The spring reaches the max of 4% drift at around 7 s (vertical lines on the subplot), when an energetic pulse centered at 1 Hz occurs in the accelerogram as clearly visible in the S-transform. The spring oscillates around its linear fundamental frequency of 1 Hz up to this burst of amplitude. After this instant, the spring enters the nonlinear response regime and its oscillation frequency shifts to 0.4 Hz because of the stiffness degradation observed in the hysteretic curve.

In Figure 9 we move a step forward in our analysis by considering two additional accelerograms this time matched to the response spectrum of the accelerogram shown in Figure 8. The two matched accelerograms have different duration, different number of amplitude bursts arriving at different times (cd. Figure 9e and Figure 9f).

Although they have essentially the same response spectra, matched accelerograms induce very different SDOF responses (cf. Figure 9i, 9k, 9m and Figure 9j, 9l, 9n). In the case of the first matched accelerogram, the spring responds similarly to the target accelerograms (Figure 9m). At the occurrence of the amplitude pulse at 1 Hz the spring reaches the maximum drift (of about 6%) (Figure 9i) and immediately after its dominant oscillator frequency decreases to 0.4 Hz (Figure 9k). The response to the second matched accelerogram, however, shows a different, more intriguing

behavior (Figure 9j, 9l, 9n). The spring responds to the first amplitude pulse visible in the accelerogram S-transform at around 7 s (dashed line in Figure 9j

) and reaches a drift higher than the 2.5% at which the ultimate base shear of the spring is attained in the capacity curve. Then a second pulse of higher amplitudes occurs at 12 s; the spring response reaches 4% drift, its strength is reduced to 55% (Figure 7) of its base shear capacity and its fundamental frequency drops from 1 Hz to 0.4 Hz. Finally, a third small pulse centered at 0.4 Hz occurs at 16 s and, although its amplitude is not large it is sufficient to lead the structure to its ultimate 7% drift capacity.

From this example, we learn that the two matched accelerograms are both different than the target. But for the first accelerogram, these differences do not radically change the SDOF response, whereas the second accelerogram shows a more aggressive behavior. The level of aggressiveness of matched accelerograms is not easily generalizable. In Appendix C we present an example of two accelerograms matched to another target spectrum where one of the accelerograms is less aggressive than the target.

Of course, these considerations apply to the response of this specific SDOF spring whose force-deformation backbone curve is characterized by an abrupt strength drop after the yielding.

The most interesting result is that time histories that are matched to the same spectrum (in this case the jagged one of a real record) can cause widely different responses to the same structure. This result suggests caution in selecting only a few matched records to test the fitness for purposes of an existing structure or of a newly designed one. Also, and perhaps even more importantly, with the knowledge of the nonlinear behavior of the structure that the matched time histories are intended to test, the seismologist could, using the S-transform technique adopted here, easily identify and cherry pick accelerograms that are either benign or aggressive *for that specific structure*. The spectral analysis findings discussed here could be used judiciously to help selecting a pool of records that are consistent with the target but are statistically balanced between aggressive and

benign behavior for the structure at hand. This arbitrariness, however, could potentially be misused, if so desired.

Statistical Analysis of Time Histories Matched to Jagged Spectra: Intensity Measures

The S-transform analysis presented in the previous paragraphs is a useful tool to look in detail at the characteristics of both the accelerograms and of the induced drift. However, this is a time-consuming procedure not suitable for a comprehensive statistical analysis of the entire data-set. A simpler way to address the question about the degree of similarity between the matched and the target accelerograms is to carry out a statistical analysis of the similarity of an ensemble of IMs whose values are extracted from both the natural target record and from the 225 matched records for all the 226 permutations. The IMs considered here are:

1. Peak Ground Acceleration, defined as $PGA = \max|h(t)|$, where h(t) is the ground acceleration expressed in g;
2. Arias Intensity (Arias, 1970) $AI = \frac{\pi}{2}\int_0^T h(t)^2 dt$ where T is the whole ground motion duration;
3. Husid duration (defined as the duration time interval between 5%- 95% of AI) (Husid 1969);
4. Standardized CAV (EPRI 2006) defined as the integral of the absolute value of the ground acceleration over non-overlapping time windows of 1s with acceleration greater than 2.5% of g, that is $SCAV = \sum_{i=0}^{N} H(h(T_i) - 0.025)\int_{t=Ti}^{t=Ti+1} |h(t)|dt$ where H is the Heaviside (or unit step) function equal to 0 if h(T) < 0.025g and to 1 elsewhere;
5. Housner Intensity $HI = \int_{0.1s}^{0.5s} PSV(\tau)d\tau$ where PSV is the pseudo spectral velocity and τ is the oscillator period;
6. Spectral intensity $SInt = \int_{0.1s}^{2.5s} PSA(\tau)d\tau /$ where PSA is the pseudo spectral acceleration.

For each considered IM, the distribution of IM values computed on the 226 seed ground motions (real data) is compared separately with each one of the 226 IMs distributions computed using the matched data. Such a comparison was done for all the 226 matched families, but for the sake of synthesis Figure 10a displays only 19 distributions randomly selected among the 226 available. Nevertheless, the trends and the properties shown by this subset are fully representative of those of all the other families of matched ground motions. The IM distributions are graphically represented by boxplots, which provide a representation of distribution features such as width, symmetry, median, and other quantiles. The box limits shown here are the 25th and 75th quantiles of the distribution, the whiskers located at the top and bottom of the box span the distribution over 2.7 standard deviations (this range encloses a probability of about 99.3%), and finally the black horizontal line in the middle of the box is the median value. By comparing the box sizes, it is possible to conclude that for all the investigated IM that do not explicitly depend on the duration of the record the variability of the IM is indeed strongly reduced by the spectral matching, as intended. For example, the PGA values of seed data vary between 0.04 g and 1.6 g (corresponding to -1.4 and 0.2 log10(PGA) values in Figure 10a), while the box plots of the 19 matched families are tightly compressed around their median values, and the boxes are reduced to a line with whiskers, in some cases only barely visible. As mentioned and as expected, the conclusion above does not hold for the Husid duration, because the matching does not significantly affect the duration of the seed record (see Appendix C for a detailed discussion), and only partially holds for AI and SCAV because these two IMs are dependent, although less directly, on the duration of the record.

It is, however, more interesting and instructive to compare the median values of each IM computed for the matched families with the corresponding value of the target ground motion. This value is plotted as a dot in Figure 10a, Figure 10e, Figure 10g, Figure 10i, Figure 10k. The median values of peak ground acceleration (PGA), Housner Intensity and Spectral Intensity of the matched accelerograms are close to the corresponding values of the target record. Again, this is to be

expected since these IMs are directly or indirectly targets for the matching procedure and do not depend explicitly on the duration of the record.

The Husid Duration is the only investigated parameter that after the matching still shows median values close to the median value computed on the seed ground motions and a certain variability (as shown by wide boxes Figure 10c). Moreover, the median duration of the matched families differs from the duration value of the target ground motion (except for few families, as discussed in the following). All these observations lead to conclude that the Husid Duration is the least modified IM by the matching process (in this case the coda ratio distributions are mainly centered on 1, recall Figure C1 in Appendix C)

The distributions of Standardized CAV and Arias intensity (Figure 10e and Figure 10g) can be better interpreted by looking jointly at the PGA and Husid distributions since they are expressed as the integral over time of quantities derived from the ground motion amplitude (Figure 10a and Figure 10c). If the median PGA is close to the target value (the box and the dot are close), but the Husid duration is higher than the target value (the box is above the dot as, e.g., in the first box in Figure 10a) then Arias and Standardized CAV have median values higher than the "target" value. In the second highlighted case, the matched ground motions have median PGA and Husid duration close to the "target" values and both Standardized CAV and Arias intensity distributions have median values close to the target.

Finally, a more comprehensive visualization of the discrepancy between IM values of target and matched accelerograms is provided in Figure 10b, Figure 10d, Figure 10f, Figure 10h, Figure 10j, Figure 10l. This figure shows, for all the considered IMs, the distribution of the difference between the median value computed for each one of the 226 families of matched time histories (namely the center of the box plot in Figure 10a, Figure 10c, Figure 10e, Figure 10g, Figure 10i, Figure 10k) and the IM value of the target accelerogram of that family (the dot in Figure 10a, Figure 10c, Figure 10e, Figure 10g, Figure 10i, Figure 10k). The asymmetric tail of the histograms related to Arias

intensity, Standardized CAV, and Husid duration clearly shows that the values of these IMs estimated from the matched records tend to be higher than the values from the target record. The systematic over-estimation of these IMs is apparently induced by the matching procedure. The PGA distribution has a short-left tail (Figure 10b), however, the 87% of the differences are within the ±15% range delimited by the vertical dashed lines, and only the remaining 13% is smaller than -15%. The differences between the values of Housner and Spectral Intensities of matched and target accelerograms are instead minimal (Figure 10k, Figure 10l), since these quantities are directly related to the response spectra matched by the procedure. For these two IMs the histograms of the differences are plotted here only as sanity checks.

The statistical comparisons between the distributions of differences between Intensity Measures (IMs) of matched and target accelerograms show high similarities for those IMs (e.g., PGA, Housner Intensity and Spectral Intensity) that are not heavily dependent on duration. On the contrary, the distributions of Husid Duration, Standardized Cumulative Absolute Velocity (SCAV) and Arias Intensity (AI) are skewed to the left, implying that these IMs tend to have higher values for matched than target accelerograms. This result supports the seismological observations on coda amplification of the matched time-series (Figure 5). We also know that such a coda can determine a more aggressive (Figure 9n) or more benign (Figure C2n) behavior on a SDOF response, but we did this exercise on only a few examples so far. In the following, we will perform a systematic investigation to statistically characterize the behavior of the entire matched accelerograms dataset, with respect to the studied SDOF response.

Statistical Analysis of the Response of a Nonlinear Spring.

Taking advantage of a large number of matched waveforms, we compute the distribution of differences, $Max\ \Theta_{Matched} - Max\ \Theta_{Target}$, of the spring maximum drift induced by the entire ensemble of matched accelerograms and that of the target accelerogram (Figure11a). This distribution has a median value equal to zero and the interquartile range (IQR defined as $Q_{84} - Q_{16}$)

is 0.7% wide. This result indicates that, at least for this spring, there is no evidence that the matched time histories induce structural responses that are either more benign or more aggressive than those of target accelerograms.

However, for a deeper understanding of what makes a matched accelerogram either more aggressive or more benign for the considered spring we categorized the *target accelerograms* into four classes based on the severity of their maximum spring responses: *yielding class* (between 0.5% and 2.5% drift), *strength drop class* (between 2.5% and 4% drift), *plateau class* (between 4% and 7%), and *ultimate class* (equal to 7% drift). (See Figure 7 for the definition of the four response severity classes).

Figure11 shows the histograms of the drift misfits of time histories matched to target accelerograms whose responses belong to the yielding class (Panel b), to the strength drop class (Panel c), to the plateau class (Panel d) and the ultimate/collapse class (Panel e).

If the response spectrum matching operation does not introduce biases in this spring's response and if we assume that the response spectrum is everything that matters for estimating nonlinear structural response (which, of course, is not entirely true), then the drifts related to the target accelerograms and the drifts related to the matched accelerograms should belong to the same response severity class (Table1). This is the case for the "yielding target accelerograms" (Figure11b), in which the median and the average values of the drift misfits are equal to 0 and the IQR is of the order of 0.4%. All the matched accelerograms induce a response that is below yielding (see Table 1). This is expected since the spring behaves linearly for all the matched accelerograms and for linear responses the spectrum is all that matters.

A different behavior, however, is observed when the response of the spring enters the nonlinear regime. For the matched time histories whose target belongs to the strength drop class (Figure11c), the median drift difference equals to 0% and the IQR is on the order of 1.4%. Among the matched time histories, 1088 are associated with a linear behavior (visible as a histogram on the left tail of

the distribution), 1558 matched time histories induce a more severe response and drive the spring to the plateau segment of the capacity curve (see histogram in the right tail), and finally 164 time histories drive the spring to its ultimate 7% drift (see histogram on the far-right tail).

The most scattered distribution of drift difference is the one corresponding to matched accelerograms whose target accelerograms push the spring into the plateau part of the backbone curve (Figure11d). This plateau class is composed of 8775 matched waveforms (corresponding to 39 target time histories) with a median difference in spring response equal to -0.4% drift and IQR on the order of 2.5%. Among the matched waveforms, 18 induce a spring response within the yielding segment (visible as a histogram on the far-left tail of the distribution), 2455 induce a drift within the strength drop segment (histogram on the left tail), and 909 lead the spring to its ultimate drift (see histogram on the right tail). Looking at the overall statistic for the plateau class (Table 1), almost 40% of the matched accelerograms cause responses that are either less severe (28% in strength drop and 0.2% even in the linear range) or more severe (10% in ultimate) than that of the target time histories.

Finally, the ultimate/collapse drift class (Figure11e) contains 15300 (corresponding to 68 target time histories) with an asymmetric distribution characterized by a tall bin centered on zero (the median is equal to zero and IQR is on the order of 0.1%). The left tail composed of 2366 accelerograms driving the spring within the plateau segment of the capacity curve and 73 accelerograms with drift belonging to the drop strength segment of the capacity curve.

In synthesis, from Figure11 we can conclude that:

1. Two time histories with the same response spectrum can cause completely different nonlinear responses in the same structure. The distribution of the maximum induced drifts, which is structure-specific, can be very wide when the target spectrum is high enough that the matched time histories cause, on average, a maximum response in the nonlinear range.

2. We observe no distinct bias in the nonlinear response of matched time histories for

this spring. Given that this spring has a brittle behavior (essentially a strength reduction factor, *R*, equal to 1.0), this result is consistent with the findings of others (e.g., Bazzurro and Luco, 2006, Luco and Bazzurro, 2007, Seifried and Baker, 2016) that used, as conventionally done, a smoothed target spectrum rather than the jagged target spectrum used in this study.

This analysis shows that the benign or aggressive behavior of a matched accelerogram does not depend only on the features produced by the spectral matching (like the coda amplification or IMs left tails), but also on the characteristics of the structure that experiences them. This observation confirms for records matched to jagged spectra the findings in Bazzurro and Luco (2006) that accelerograms matched to a smoothed spectrum (or any accelerogram, for that matter) cannot be labeled as "aggressive" or "benign" without considering a particular structural vibration period and specific yield strength and cyclic behavior of the structure. Of course, this conclusion needs to be pursued beyond the studied SDOF.

Conclusions

This work represents a first step towards resolving the ongoing debate on whether the matched accelerograms are legitimate substitutes for real ones and on whether they produce biased structural response estimates. Presently the debate suffers from the following caveats (i) selected real accelerograms are used as the seed for the matching, which modifies their seismological characteristics and thus may systematically change the structural response (i.e., induce bias) (ii) beyond yielding, the structural response is no longer controlled only by the spectral amplitude of the input ground motion (see Seifried and Baker 2016 for an in-depth discussion) and (iii) other quantities that are not explicitly matched by the procedure may have an impact on the response.

To overcome such limitations, we established an “unconventional” engineering benchmark, comparing and contrasting the seismological characteristics of a set of matched and recorded accelerograms sharing the same real “jagged” response spectrum. The study is based on 226

accelerograms, corresponding to a scenario centered on magnitude 6.2 and a source-to-site distance of 20 km. Iteratively, 225 accelerograms were made spectrum compatible with the response spectrum of the remaining one using a matching procedure that operates in the time domain. The 226 permutations generated more than 50,000 matched waveforms that constitute the basis for our statistical study.

The seismological conclusions of the papers concern the similarities of matched and real accelerograms that shared the same target spectrum. To compare two accelerograms we introduced and employed a new method; that is based on the analysis of the coherence of S-transforms along the time axis. We found that amplitude bursts injected in the matching procedure control the spectrum response shape in the 2-10 Hz frequency range, at least for the accelerograms of the investigated scenario. This suggests that spectral matching generates accelerograms with the same dominant frequency (in the 2-10 Hz range in our scenario) of the S-waves of the target accelerograms. However, although the S-waves of target and matched accelerograms have common features, matched accelerograms show, on average, higher coda amplitudes over a time window of 5 s; this discrepancy can be ascribed to the longer duration of low-frequency wavelets inserted by the matching procedure. This is also seen in the statistical analysis of the Intensity Measures (IMs), where the IMs dependent on duration (e.g., Husid duration, SCAV, Arias intensity) show positively biased central metrics.

Moving towards the engineering side of the study we focused our efforts on studying the effects of spectrum matching on the response of a SDOF oscillator with a brittle nonlinear behavior. We looked both at the dispersion and at the bias of structural responses to matched records.

The most interesting result is that accelerograms matched to the same spectrum can cause structural responses that are widely different from one another and also widely different than the response of the real record that shares the same response spectrum. In other words, in a pool of accelerograms matched to the same spectrum some can cause drifts associated to moderate damage while some can

cause drifts associated to collapse. More specifically, based on a few examples, we observed that matched accelerograms having a longer coda can be either more aggressive or gentler to the specific SDOF system than the real one. To draw a clear-cut conclusion on the possible response bias of this SDOF spring, a statistical analysis of the results showed that no appreciable bias in the response of accelerograms (compared to the case of real records) when matched to the jagged spectra of real records. These results may not hold for other nonlinear SDOF oscillators but was somewhat expected for this one since it has a strength reduction factor essentially equal to unity. However, more investigations using additional nonlinear SDOF and multi-degree-of-freedom structures are needed to shed more light on the issue of bias possibly induced by spectrum-compatible records matched to jagged (or smooth) spectra.

We believe, however, that some of the results and the tools developed in this study using such an atypical approach are also applicable to the conventional case of accelerograms matched to smoothed spectra. In particular using the tools proposed here, a seismologist could identify the features that make accelerograms compatible to smoothed spectra either benign or aggressive for the structure of interest. Therefore, given the limitations to using very few matched records in practical applications, these tools may help seismologists in judiciously choosing an appropriate balance of benign and aggressive signals for engineering purposes. Hence, we recommend that a seismologist is first supplied by the engineer, at the bare minimum, with a nonlinear SDOF representation of the structure so that the record selection is not done blindly. These recommendations derive naturally from the results of this work but it is our intent to confirm them by carrying out a specific study based on accelerograms matched to conventional smooth hazard/design spectra.

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Data and Resources

The accelerograms used in this paper are issued from the Southern California Earthquakes (CESMD –strongmotioncenter.org, last visit June 2014), the Euro-Mediterranean (Ambraseys et al. 2004) and Orfeus (https://www.orfeus-eu.org/data/strong/ last visit June 2014) databases.

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The structural analysis has been performed using Open System for Earthquake Engineering Simulation (McKenna et al. 2000). The FEMA P440A single degree of freedom model has been kindly provided by Dimitrios Vamvatsikos.

The figures have been prepared using Matplotlib 2.1.1 (Hunter, 2007)

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TABLE

Table 1: overview of the SDOF responses caused by matched accelerograms.

	# Target	#Matched	Yielding	Strength-Drop	Plateau	Ultimate
Yielding	76	17100	17100(100%)			
Strength-Drop	43	9675	1088 (11.2%)	6865(70.9%)	1558(16.2%)	164(1.7%)
Plateau	39	8775	18 (0.2%)	2455 (28%)	5393(61.4%)	909 (10.4%)
Ultimate	68	15300		73(0.5%)	2366(15.5%)	12861(84%)

List of Figure Captions

Figure 1 Panel a: Magnitude-Distance scatter plot (grey dots) overlapped with the histogram of the distance (grey bars). Panel b: 226 response spectra (grey lines), the black dashed line is a randomly selected spectrum used as "target" for illustrative purposes. Panel (c): response spectra matched within the 15% tolerance (black lines), the black dashed line the target plotted. Panel (d): response spectra with a misfit greater than the 15% tolerance.

Figure 2: Distribution of the median misfit for each matched family as a function of frequency in the whole 0.1 -35 Hz range.

Figure 3 Target accelerogram (a) and matched time history (b) plotted along with their S-transform (c and d, respectively). The target and matched S-transforms coherence image as a function of frequency and time (e) is represented using a sequential palette, with boundaries varying from 0 (clear) to 1 (darker). The white star shows the time-frequency location where the maximum value of coherence product occurs.

Figure 4 Distribution of the frequency where the coherence product between the S-transforms of matched and target histories reaches the maximum value. The values in the legend indicate the different maxima values, where 1 stands for high coherence between the S-transforms (as the case shown in Figure 3) and a value lower than 0.6 stands for a low coherence. The dashed vertical line indicates the frequency of the maximum S-transform amplitude on the target accelerogram.

Figure 5 (a) example of a target accelerogram (black line), the envelope is traced as a continuous line, the vertical line is the time when the coda starts. b: the envelope of the target accelerogram is plotted as a solid line, the envelopes of the accelerogram matched to this time histories are plotted as density of points. Panel c: ratio between the matched and the target envelopes plotted with the same palette of panel b, the horizontal dashed lines are the ratio values averaged on non-

overlapping time windows with a duration of 1 second. Panel d, 2D histogram of the envelope ratio values computed for all the matched-target data pairs (50850) the palette indicates the percentage of pairs in each cell. For the sake of clarity, the plot neglects the cell with less than 2% of data. The 1D histograms are computed in each time-window of 1 s and they are plotted as well. The bins height is related to the background tone, the corresponding % are described in the legend.

Figure 6 Time-frequency analysis of the RSPMatch matching process. *First column* (a) from top to bottom: the four passes of the spectral matching seen on spectrum response with details on line types given in the legend. *Second column* (b): target and seed S-transform amplitude followed by the S-transform evolution of the four passes of the seed time history processed by the spectral matching software. Details on palette and markers are given in the legend. *Third column* (c): target and seed time histories followed by the intermediate time histories produced by the spectral matching software. The accelerogram after the fourth and last iteration is the one whose spectrum successfully matches the target.

Figure 7 Top: 1 Hz acceleration sinusoid with amplitude increasing at each cycle from 0.008 to 0.12 g with increments of 0.01g per cycle. Such a sinusoid is used as acceleration input to the spring 1a FEMA model. Bottom: Force-deformation backbone curve of the spring 1a model shown as base shear normalized by the base shear at yielding versus drift ratio.

Figure 8 Overview of the features of one of the 226 real target waveforms and the corresponding spring response. From the top to the bottom: response spectrum, accelerogram, accelerogram S-transform zoomed between 1 and 5 Hz, accelerogram S-transform zoomed between 0 and 1 Hz; drift time-history, drift S-transform, and spring cyclic behavior. The solid vertical line indicates the occurrence time of the maximum lateral drift. Details on the S-transforms scales are given in the legend.

Figure 9 Comparison between two accelerograms matched to the target spectrum of the accelerogram shown in Figure 8 and the corresponding spring responses. Each column has the same

743 structure utilized in Figure 8; details on graphic features are reported in the legend. The instant
744 where the spring reaches a drift higher than 2.5% is plotted as a dashed line on panels (f), (h) and
745 (l).

746 Figure 10 On the left, comparison between the IM values derived from target records and matched
747 records for 19 families randomly selected from the pool of 226. The panels on the right show, for
748 each IM, a histogram of the difference between the median values of the IM measure of the 226
749 matched families and the corresponding IM value of the target accelerogram. The Legend explains
750 the different symbols.

751 Figure11 Histograms of the differences between the drift of the accelerograms matched to the target
752 spectrum ("matched drift") and the drift of the target accelerograms. (a) Drift misfit for all the
753 matched accelerograms. Drift misfit (filled histograms) for matched accelerograms whose seed
754 accelerogram generated a drift belonging to the *yielding (b)*, *strength drop, plateau,* and *ultimate*
755 *classes.* The overlaid histograms refer to drift misfits of matched time histories belonging to classes
756 that are different from that of the seed. Spring capacity curve are also shown on the right side; the
757 segment corresponding to the seed class response is highlighted. The Legend explains the different
758 symbols.

759 Figure A1 Improved cosine wavelets, as implemented in RspMatch 2009, for frequencies spanning
760 form 0.5 Hz to 20 Hz along with the corresponding S-transforms.

761 Figure B1 See Figure 5 legend for the description of graphic features

762 Figure C1 See figure 8 legend for the description of graphic features.

763 Figure C2 See figure 9 legend for the description of graphic features

APPENDIX C: Analysis of the matching effect on the seed waveform

The subsidiary question arising from the analysis of matched coda with respect to the target (Figure 5 in section 3.3) is whether the spectral matching systematically amplifies the seed accelerogram coda amplitude. To give a quantitative answer we compared a seed accelerogram with the 225 accelerograms obtained by matching it to different target (Figure A1a, A1b and A1c). Such a comparison, which is based on the ratio between the accelerogram envelopes, is done according to the following steps:

- Given a seed accelerogram $S(t)$, we computed its envelope defined as the amplitude of the Hilbert transform $|\mathcal{H}(S(t))|$) (Fig A1a).
- We manually picked the beginning of the coda accelerogram (t_{coda}) by a visual inspection of the accelerogram and of the envelope (e.g., see vertical line in Fig 6).
- We selected the 225 matched accelerograms ($M_i(t)$, with i ranging from 1 to 225, having the same seed accelerogram $S(t)$ and we compute their envelope $|\mathcal{H}(M_i(t))|$
- We attribute the same t_{coda} to all the matched signals.
- We normalized the accelerogram amplitudes to the same PGA value. This is a necessary step since the target spectra have different amplitudes. We look at the relative amplitudes of coda with respect to PGA.
- We aligned the seed and all the matched accelerograms with respect to t_{coda}.

A visual comparison of the envelope amplitudes is given in Figure A1b. After t_{coda}, the envelopes of matched accelerograms have scattered amplitude (plotted as density of curves) implying that the shape of the seed accelerogram coda has been modified. The following step quantifies such a coda modification by computing the ratio between envelopes. Figure A1c displays the envelope ratio as a function of time, where the ratio curves are plotted as density of points. The envelope ratio is

mainly equal to one before the coda, starts to increase at the end of the strong phase and then reaches high values (as high as 10 in the example in the figure) on the coda.

In order to reduce the effect of the possible errors in picking the t_{coda}, and to smooth the local oscillations of the envelope ratio curve, we computed the average envelope ratio (*ER*) over a moving and not-overlapping time-window of 1 s.

$$ER = \int_{T}^{T+1} \frac{|\mathcal{H}(m(t))|}{|\mathcal{H}(s(t))|} dt$$

ER values are plotted as horizontal dashed lines in Figure A1c.

Finally, we extended this analysis to the whole data set of 50850 waveforms. In Figure A1d the distribution of the average enveloped ratio is plotted as a 2D histogram. The density of points in each histogram cell is expressed in percentage of waveforms. Note that to make the figure more readable the histogram cells with less than 2% (almost 1000 waveforms) are neglected.

We observe that the *ER* values are scattered in the first 2 seconds of the coda and that the distributions are centered at 2 (1 in log2 scale). In the following seconds the ER distributions are centered on 1 (0 in log2 scale) instead. Therefore, we conclude that the matching process modifies the relative PGA coda ratio in the first 2 s of signal and, on average, enhances the coda amplitudes by a factor 2. Afterwards the amplitude modifications are not significant.

Appendix C: S-transform analysis of a matched accelerogram less aggressive than the target

We analysed in detail the response of the SDOF spring to three different accelerograms with the same jagged spectrum. Figure C1 refers to the target accelerogram, which drives the SDOF to collapse, whereas Figure C2 presents the results of two accelerograms whose spectrum is matched to that of the accelerogram in Figure C1. The first matched accelerogram (Figure C2 left column) because of longer coda is gentler than the second matched one (Figure C2 right column). Indeed, in the former case the accelerogram larger amplitudes (and the relative energy) are distributed over longer time windows in the frequency range of interest and, as a consequence, the SDOF enters in the hysteretic loop but never reaches the ultimate drift. On the contrary, both the target accelerogram Figure C1 and the second matched accelerogram (Figure C2 right column) both have a single amplitude (and energy) burst, which is sufficient to abruptly send the SDOF to the ultimate drift capacity.