amplitude spectrum
phase spectrum

Normalization of Spectral Analyses

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Abstract

Units matter, and having correct ones is crucial to interpretation of spectral analyses. Here we outline the normalization used by `rlpSpec`, namely the power spectral density, and compare it to other quantities commonly encountered in spectral analysis.

Contents

1 Background

There can often be confusion about the different quantities used in spectral analysis [1], partly due to myriad nomenclature within the incredibly vast literature on the subject. Regarding nomenclature: Phrases including "amplitude spectrum", "energy spectral density", "power", "power spectra", and even "spectra" all mean *something*, but are rarely equivalent.

Let us, for the sake of brevity, assume we are in the time domain, and we are considering a discrete stationary signal f of length N, having Fourier transform $\mathfrak{F}\{f\}$ which is complex, and represented by$F$. The **amplitude spectrum** of this transform pair is simply the amplitude of F, or mod$\{F\}$; we will denote this as $S^{(\mathrm{A})}$. The pair's corresponding **phase spectrum** is the phase angle of F, or arg$\{F\}$, denoted by $S^{(\phi)}$.

How do we interpret the quantities

Table with equivalent expressions

[1] This post to `R-help` illustrates the confusion common in spectral analyses:
`http://r.789695.n4.nabble.com/Re-How-do-I-normalize-a-PSD-td792902.html`

Table 1: Representors of various spectral quantities.

Expression	Representing	Equivalent expression
f	stationary timeseries	
F	Fourier transform of f	$\mathfrak{F}\{f\}$
$S^{(\mathrm{A})}$	**amplitude spectrum** of F	$\lvert F\rvert$ or $\mathrm{mod}\{F\}$
$S^{(\phi)}$	**phase spectrum** of F	$\arg\{F\}$
S	**energy spectral density** of $S^{(\mathrm{A})}$	
S	**power spectral density** of $S^{(\mathrm{A})}$	

2 A from-scratch example: White noise.

A straightforward way to understand normalization in spectral analysis is to analyze a real, stationary series which is normally distributed with known variance, $x = \mathcal{N}(\mu, \sigma^2)$. A fundamental result found in many texts on spectral analysis is

$$\mathrm{var}\{x\} \equiv \sigma_x^2 = \int_{-1/2}^{1/2} S(f)df \tag{1}$$

which says if we integrate the power spectral density over all frequencies we can obtain the process variance. If we have a $\mathcal{N}(0,1)$ process, and assume the sampling interval is once per second, we should expect a flat spectrum of 2 units^2/Nyquist across all frequencies $[0, 0.5]$ so that the area under the spectrum is equal to one.

We first generate a series, and find its Fourier transform[2].

```
> set.seed(1234)
> N <- 256
> x <- rnorm(N, mean = 0, sd = 1)
> xv <- var(x)
> X <- fft(x)
> class(X)

[1] "complex"

> length(X)

[1] 256
```

We immediately find the amplitude and phase response:

```
> Sa <- Mod(X) # Amplitude spectrum
> Sp <- Arg(X)  # Phase spectrum
```

[2] A proper Discrete Fourier Transform (DFT) must be normalized by the length of the series; however, most DFT programs (including `stats::fft`) eschew this normalization for efficiency's sake.

followed by the energy spectral densities[3]

```
> XC <- Conj(X)
> all.equal(Se <- Sa**2, Se_2 <- Mod(XC * X), Se_2R <- Mod(X * XC))
```

```
[1] TRUE
```

The single-sided power spectral density (PSD) estimates follow, once we set the Nyquist frequency, defined as half the sampling rate[4].

```
> fsamp <- 1  # sampling freq, Hz
> fNyq <- fsamp/2   # nyquist
> Nf <- N/2
> nyfreqs <- seq.int(from=0, to=fNyq, length.out=Nf)
> S <- Se[1:Nf] * 2 / N   # Finally, the PSD!
```

```
> plot(nyfreqs, S, type="h", xlab="Nyquist frequency", ylab="units**2 / freq")
> mSn <- mean(S)
> polygon(c(0,fNyq,fNyq,0,0), c(0,0,mSn,mSn,0), lwd=2, lty=2, border="red")
```

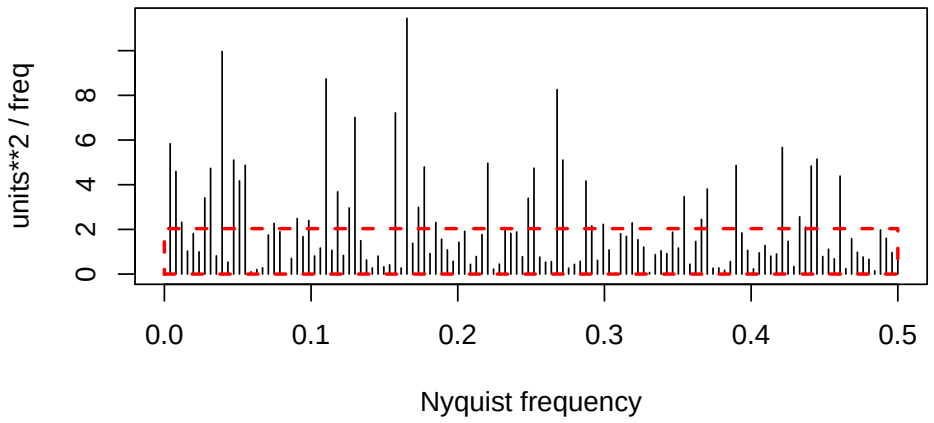


Figure 1: Power spectral density estimates for a single realization of a $\mathcal{N}(0,1)$ process in linear units. The dashed rectangle encompasses the area under the mean spectral level, used to find the integrated spectrum.

[3]Note the equivalence between the complex conjugate based estimates.

[4] Although the PSD of a white noise process is not strictly bandlimited, we will use it to demonstrate differences in normalization.

Figure 2 plots the PSD of our white noise series; it also shows the mean value of the PSD, from which we can test ourselves for proper normalization: an estimate of the integrated spectrum should roughly equal the known variance.

```
> test_norm <- function(sval, nyq, xvar){svar <- sval * nyq; return(svar/xvar)}
> print(xv_1 <- test_norm(mSn, fNyq, xv))
```

```
[1] 0.9933334
```

```
> xv_2 <- sum(S)/Nf * fNyq / xv  # an alternate test
> all.equal(xv_1, xv_2)
```

```
[1] TRUE
```

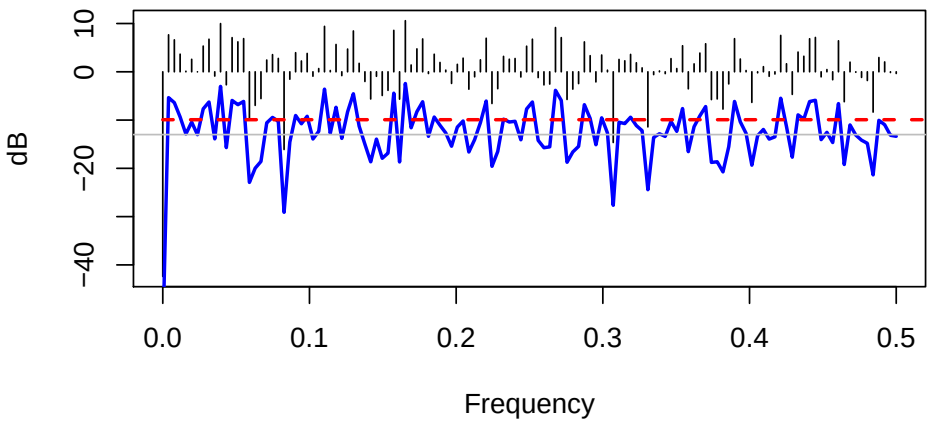
But what if the sampling frequency `fsamp` changes? An obvious change will be the actual Nyquist frequency, which means the variance normalization-test will fail if the PSD estimates are not re-scaled. We simply re-scale the frequencies and PSDs with the sampling rate to obtain the properly-normalized spectra.

```
> fsamp <- 20
> fNyq <- fsamp/2
> freq <- fsamp*nyfreqs
> Snew <- S / fsamp
```

To compare the scalings it will be useful to show the spectral values in decibels (relative to units^2/frequency):

```
> dB <- function(y) 10*log10(y)
> plot(nyfreqs, dB(S), type="h", xlab="Frequency", ylab="dB")
> lines(nyfreqs, dB(Snew), col="blue", lwd=2)
> mSn <- mean(Snew)
> abline(h=dB(1/fsamp), col="grey")
> lines(c(0,fNyq), rep(dB(mSn),2), lwd=2, lty=2, col="red")
> # test variance
> test_norm(mSn, fNyq, xv)
```

```
[1] 0.9933334
```



3 Comparisons between estimators

We wish to compare the normalizations used by other PSD estimation programs; these are summarized in 2.

Table 2: A comparison of functions comparable to `rlpSpec`, excluding extensions which only estimate raw-periodograms.

Function	Namespace	Sine m.t.?	Adaptive?	Reference
`mtapspec`	`RSEIS`	Yes	No	Lees and Park (1995)
`spectrum`	`stats`	No	No	R Core Team (2012)
`spec.mtm`	`multitaper`	Yes	Yes	Rahim and Burr (2012)
`SDF`	`sapa`	Yes	No	Percival and Walden (1993)

3.1 `stats::spectrum`

`spectrum` is a wrapper which calls the appropriate spectrum estimator. For our examples we compare to `spec.pgram`. Using default settings `spec.pgram` assumes the sampling frequency for the input series is 1, and normalizes accordingly. Sampling information used be included by creating a `ts` object from the series prior to spectrum estimation:

```
> fsamp <- 20
> xt <- ts(x, frequency=fsamp)
> pgram20 <- spec.pgram(xt, pad=1, taper=0, plot=FALSE)
> pgram01 <- spec.pgram(ts(xt, frequency=1), pad=1, taper=0, plot=FALSE)
```

The first order question is obviously whether these spectra pass variance-normalization tests, which they do not, but only by a factor of two (too small):

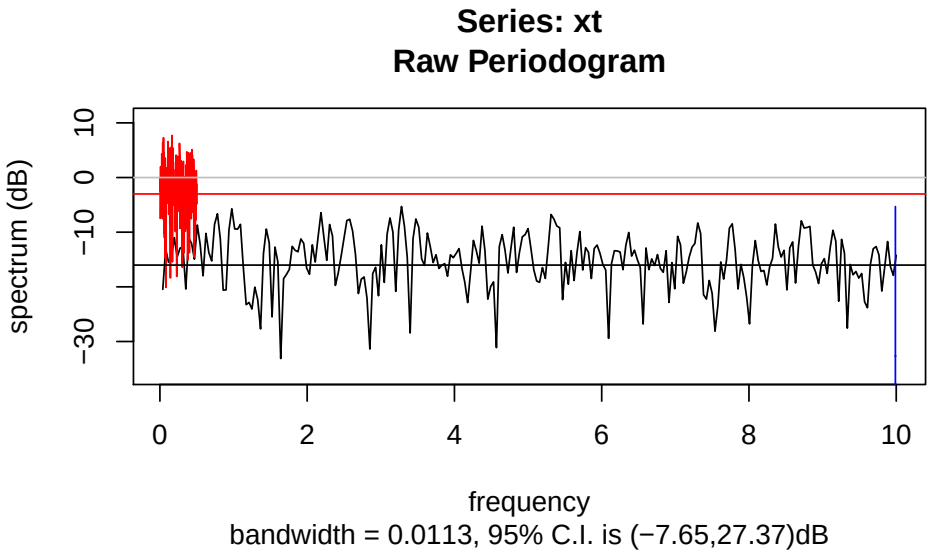
```
> test_norm(mean(pgram01$spec), 0.5, xv)

[1] 0.4845341

> test_norm(mean(pgram20$spec), 10, xv)

[1] 0.4845341

> plot(pgram20, log="dB", ylim=36*c(-1,.3))
> plot(pgram01, log="dB", add=TRUE, col="red")
> abline(h=dB(c(1, 1/2/1, 1/2/20)), col=c("grey","red","black"))
```



But why? The program assumes normalization for complex series: Spectra returned for real data are deficient by a factor of two. Consider the following example:

```
> psd1 <- spec.pgram(x, plot=FALSE)
> psd2 <- spec.pgram(xc<-complex(real=x, imag=x), plot=FALSE, demean=TRUE)
> mean(Mod(xc))

[1] 1.116888

> mean((psd2$spec / psd1$spec))

[1] 2
```

This means that unless we are interested in analyzing complex timeseries, we need only multiply by two for properly normalized spectra using `spectrum`, assuming the sampling information is included in the input series.

3.2 stats::spectrum

Included in the core distribution of R is `stats::spectrum`, which accesses `stats::spec.ar` or `stats::spec.pgram` for either parametric and non-parametric estimation, respectively. The user can optionally apply a single cosine taper, and/or a smoothing kernel. Our method is non-parametric; hence, we will compare to the latter.

```
> spec.pgram(X, pad=1, taper=0.2, detrend=FALSE, demean=FALSE, plot=FALSE)
```

However, the logical arguments `detrend` and `demean` to `psdcore` are passed to `spec.pgram`; they are, by default, both TRUE.

As a matter of bookkeeping, we must deal with the working environment accessed by `rlpSpec` functions. Specifically, we should ensure `psdcore` does not access any inappropriate information by setting `refresh=TRUE`. We can then re-calculate the multitaper PSD and the raw periodogram with `plotpsd=TRUE`. The results are shown in Figure **??**.

3.3 multitaper::spec.mtm

3.4 SDF::sapa

References

Lees, J. M. and Park, J. (1995). Multiple-taper spectral analysis: A stand-alone C-subroutine. *Computers & Geosciences*, 21(2):199–236.

Percival, D. and Walden, A. (1993). *Spectral analysis for physical applications*. Cambridge University Press.

R Core Team (2012). *R: A Language and Environment for Statistical Computing*. R Foundation for Statistical Computing, Vienna, Austria. ISBN 3-900051-07-0.

Rahim, K. and Burr, W. (2012). *multitaper: Multitaper Spectral Analysis*. R package version 1.0-2.

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