Discrete-Time Bases and Filter Banks

Advances Signal Processing Seminar

Stefan Mendel & Franz Zotter

Outline

- Introduction
  - Orthonormality
  - Biorthogonality
- Orthonormal expansions and filter banks
  - Haar expansion
  - Sinc expansion
- Analysis of filter banks
  - Time domain
  - Modulation domain
  - Polyphase domain
  - Relations between time, modulation, and polyphase domain
- Results on filter banks
  - Biorthogonal Relations

1) We introduce the concept of orthogonality, orthonormality, and biorthogonality.

2) We investigate two orhtonormal series expansions in detail. The Haar expansion with maximal time resolution and the Sinc expansion with maxi

3) Analyses of the filter banks in 3 different domains are given. We show time domain, modulation domain, and polyphase domain (and their relatio

4) Finally we compare the results on filter banks and series expansions.

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Orthonormal Expansions

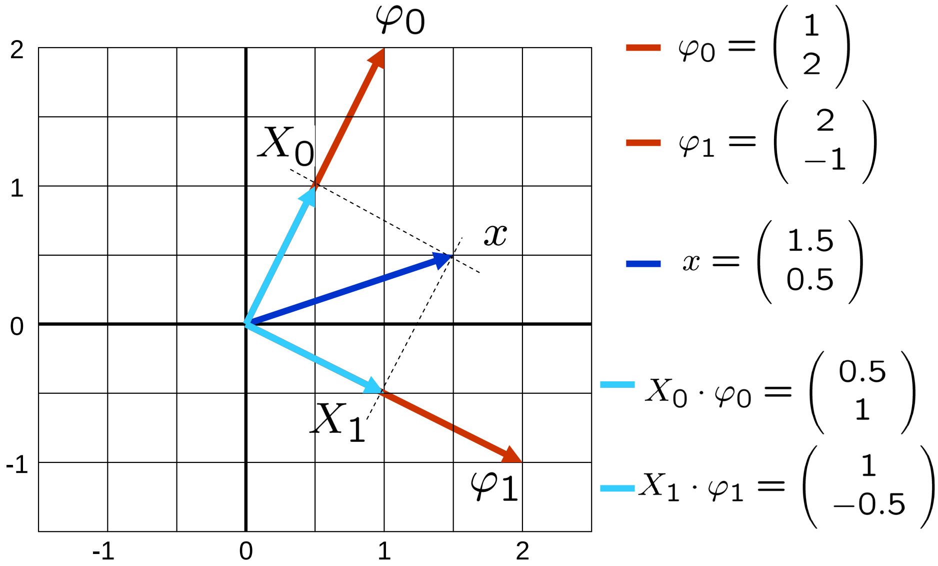
- Sequence $x[n]$ is square-summable $x[n] \in l_2(\mathcal{Z})$
- Expansion $x[n] = \sum_{k \in \mathcal{Z}} \langle \varphi_k[l], x[l] \rangle \varphi_k[n] = \sum_{k \in \mathcal{Z}} X[k] \varphi_k[n]$
- Transform $X[k] = \langle \varphi_k[l], x[l] \rangle = \sum_{l} \varphi_k^*[l] x[l]$
- Orthonormality $\langle \varphi_k[n], \varphi_l[n] \rangle = \delta[k-l]$
- Conservation of energy $\|x\|^2 = \|X\|^2$

Any square summable sequence x[n] can be written as a series expansion, where $\{\varphi_k[n]\}$ are sets of orthogonal basis functions and are complete in the space of square summable sequences $l_2(Z)$.

X[k] is called the *transform* of x[n]. An example for a orthogonal (not orthonormal) expansion is the discrete- time Fourier transform (DFT). To be orthonormal the basis function must satisfy the orthonormality constraint, (orthogonal and normalized to unity).

An improtant property for orthonormal expansions is the conservation of energy.

Orthogonal: Example



An example for an orhogonal expansion. Note that this expansion is not orhtonormal, since the scalar product of $<\varphi_0, \varphi_0> = 5$ and $<\varphi_1, \varphi_1> = 5$ are not normalized to 1.

The transforms X0 is obtained by projecting x on the vector φ_0. The reconstruction is obtained by projecting x on φ_0 which yields $X[0] = <\varphi_0, x>/||\varphi_0|| = 0.5$ since $<\varphi_0, x>=2.5$ and $||\varphi_0||= <\varphi_0, \varphi_0> = 5$.

Biorthogonal Expansion

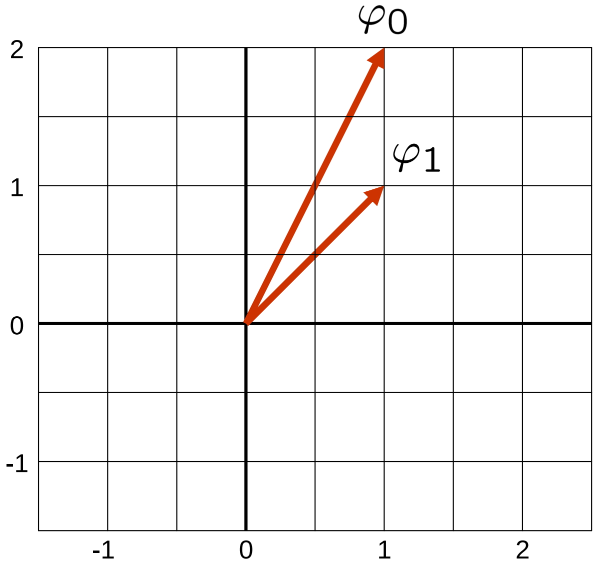
- Expansion
$$x[n] = \sum_{k\in\mathcal{Z}} \langle \varphi_k[l], x[l] \rangle \tilde{\varphi}_k[n] = \sum_{k\in\mathcal{Z}} \tilde{X}[k] \tilde{\varphi}_k[n]$$
$$= \sum_{k\in\mathcal{Z}} \langle \tilde{\varphi}_k[l], x[l] \rangle \varphi_k[n] = \sum_{k\in\mathcal{Z}} X[k] \varphi_k[n]$$

- Transform $\tilde{X}[k] = \langle \varphi_k[l], x[l] \rangle$ and $X[k] = \langle \tilde{\varphi}_k[l], x[l] \rangle$

- Conservation of energy $\|x\|^2 = \langle X[k], \tilde{X}[k] \rangle$

In biorthogonal expansions we have a dual basis with $\{\varphi_k[n]\}$ and $\{\varphi^t_k[n]\}$ where t denotes tilde. These dual bases are used to obtain the transform with $\{\varphi_k[n]\}$ and reconstruct the signal x[n] with $\{\varphi^t_k[n]\}$, or vice versa.

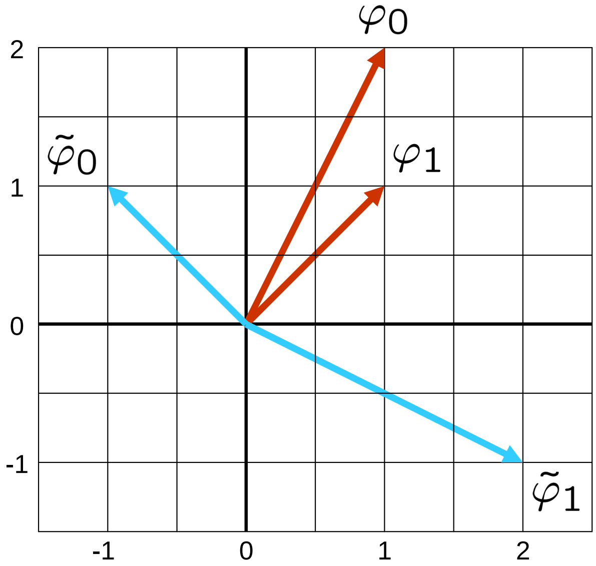
Biorthogonal: Example



$$\varphi_0 = \begin{pmatrix} 1 \\ 2 \end{pmatrix}$$

$$\varphi_1 = \begin{pmatrix} 1 \\ 1 \end{pmatrix}$$

Biorthogonal: Example



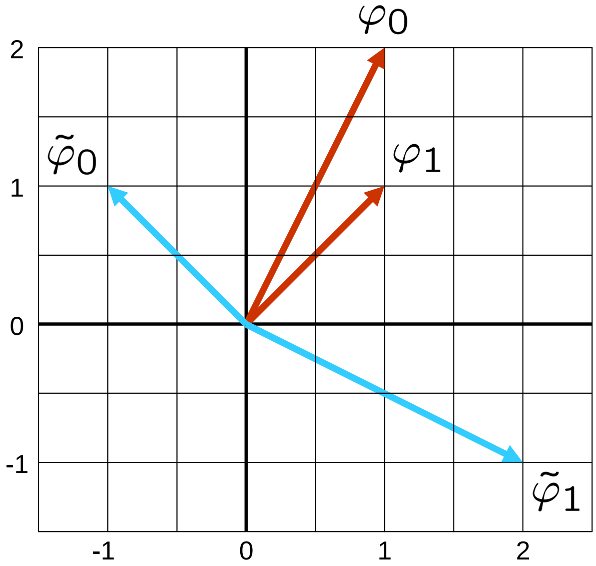
$$\varphi_0 = \begin{pmatrix} 1 \\ 2 \end{pmatrix}$$

$$\varphi_1 = \begin{pmatrix} 1 \\ 1 \end{pmatrix}$$

$$\tilde{\varphi}_0 = \begin{pmatrix} -1 \\ 1 \end{pmatrix}$$

$$\tilde{\varphi}_1 = \begin{pmatrix} 2 \\ -1 \end{pmatrix}$$

Biorthogonal: Example



$$< \varphi_k, \tilde{\varphi}_l > = \delta(k-l)$$

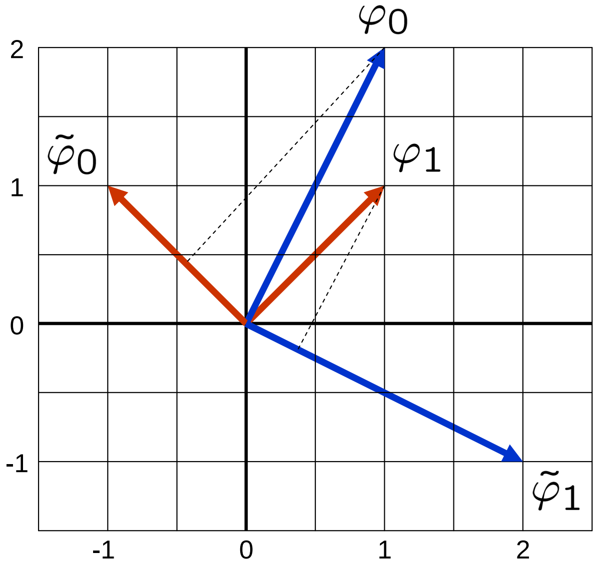
$$< \varphi_0, \tilde{\varphi}_0 > = 1$$

$$< \varphi_0, \tilde{\varphi}_1 > = 0$$

$$< \varphi_1, \tilde{\varphi}_0 > = 0$$

$$< \varphi_1, \tilde{\varphi}_1 > = 1$$

Biorthogonal: Example



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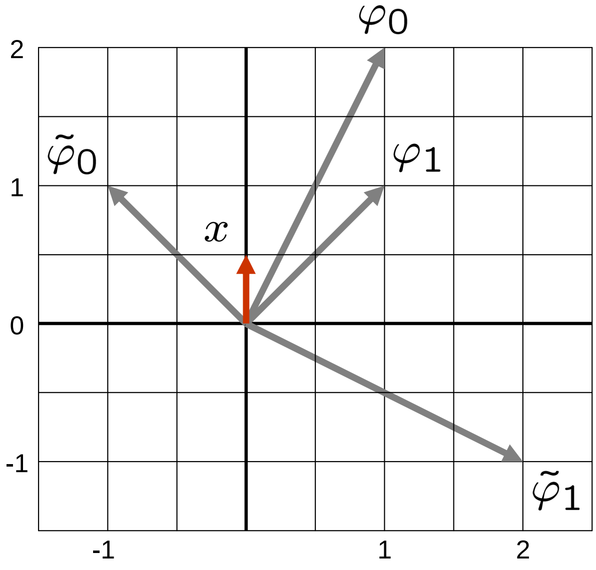
$$< \varphi_1, \tilde{\varphi}_1 > = 1$$

$$\varphi_0 = \begin{pmatrix} 1 \\ 2 \end{pmatrix} \quad \varphi_1 = \begin{pmatrix} 1 \\ 1 \end{pmatrix}$$

$$\tilde{\varphi}_0 = \begin{pmatrix} -1 \\ 1 \end{pmatrix} \quad \tilde{\varphi}_1 = \begin{pmatrix} 2 \\ -1 \end{pmatrix}$$

Biorthogonal: Example Reconstruction



$x = \begin{pmatrix} 0 \\ 0.5 \end{pmatrix}$

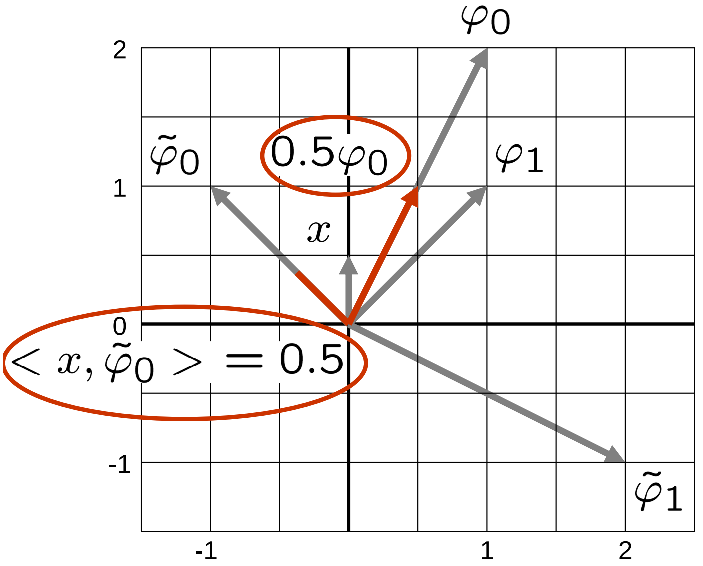
$$x[n] = \sum_{k \in \mathcal{Z}} X[k] \varphi_k[n]$$

$$X[k] = \langle \tilde{\varphi}_k[l], x[l] \rangle$$

$$x[n] = \sum_{k \in \mathcal{Z}} \tilde{X}[k] \tilde{\varphi}_k[n]$$

$$\tilde{X}[k] = \langle \varphi_k[l], x[l] \rangle$$

Biorthogonal: Example Reconstruction



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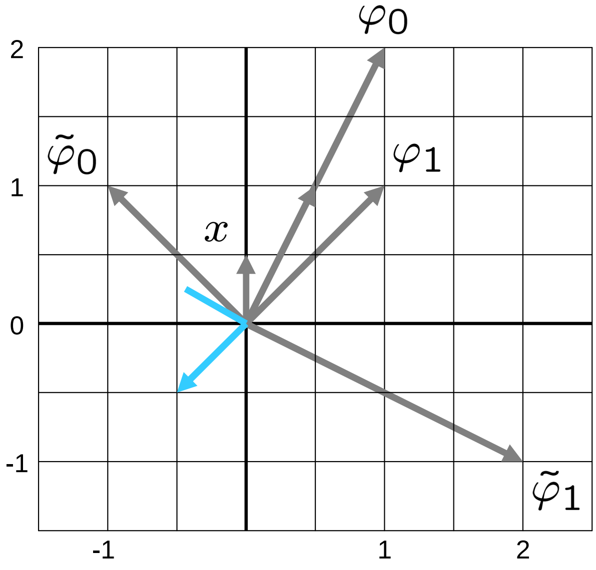
Biorthogonal: Example Reconstruction



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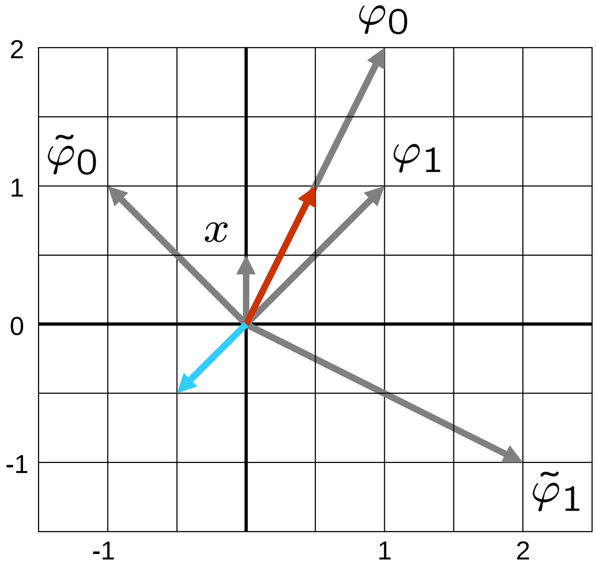
Biorthogonal: Example Reconstruction



$$x = \begin{pmatrix} 0 \\ 0.5 \end{pmatrix}$$

$$x[n] = \sum_{k \in \mathcal{Z}} X[k] \varphi_k[n]$$

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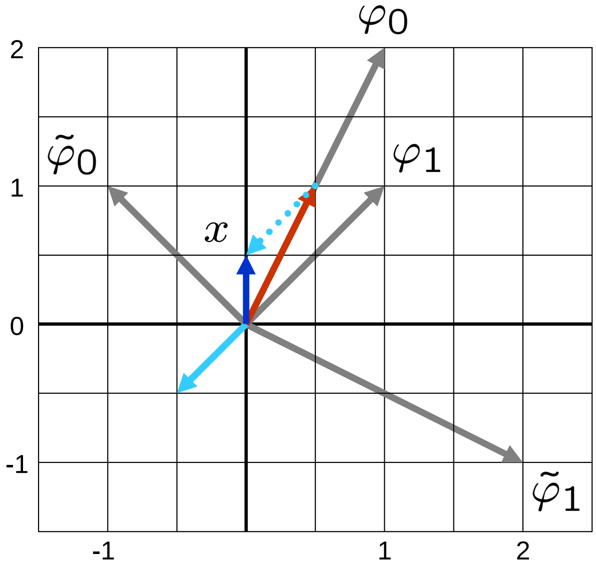
Biorthogonal: Example Reconstruction



$x = \begin{pmatrix} 0 \\ 0.5 \end{pmatrix}$

$$x[n] = \sum_{k \in \mathcal{Z}} X[k] \varphi_k[n]$$

$$X[k] = \langle \tilde{\varphi}_k[l], x[l] \rangle$$

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Haar Expansion

- Basis functions

$$\varphi_{2k}[n] = \begin{cases} \frac{1}{\sqrt{2}} & n = 2k, 2k+1, \\ 0 & \text{otherwise,} \end{cases} \qquad \varphi_{2k+1}[n] = \begin{cases} \frac{1}{\sqrt{2}} & n = 2k, \\ -\frac{1}{\sqrt{2}} & n = 2k+1, \\ 0 & \text{otherwise.} \end{cases}$$

- Time-varying periodic

$$\varphi_{2k}[n] = \varphi_0[n-2k], \quad \varphi_{2k+1}[n] = \varphi_1[n-2k]$$

- Transform

$$\begin{aligned} X[2k] &= \langle \varphi_{2k}, x \rangle = \frac{1}{\sqrt{2}}\Big(x[2k] + x[2k+1]\Big) \\ X[2k+1] &= \langle \varphi_{2k+1}, x \rangle = \frac{1}{\sqrt{2}}\Big(x[2k] - x[2k+1]\Big) \end{aligned}$$

One basis function spanns a subspace that is the coarse or average version of x[n] and the other the difference or added detail. This corresponds to a low and highpass characteristic, but with very poor frequency resolution.

A very important property of the transform is the time-varying periodicity. The even indexed basis functions are translated of each others, and so are the odd indexed ones.

Haar Expansion & Filterbanks

- Filter $h_0[n] = \begin{cases} \frac{1}{\sqrt{2}} & n = -1, 0, \\ 0 & \text{otherwise}, \end{cases}$ $h_1[n] = \begin{cases} \frac{1}{\sqrt{2}} & n = 0, \\ -\frac{1}{\sqrt{2}} & n = -1, \\ 0 & \text{otherwise}. \end{cases}$

$$h_0[n] * x[n]\Big|_{n=2k} = \sum_{l \in \mathcal{Z}} h_0[2k-l]x[l] = \frac{1}{\sqrt{2}}x[2k] + \frac{1}{\sqrt{2}}x[2k+1] = X[2k]$$

$$h_1[n] * x[n]\Big|_{n=2k} = \sum_{l \in \mathcal{Z}} h_1[2k-l]x[l] = \frac{1}{\sqrt{2}}x[2k] - \frac{1}{\sqrt{2}}x[2k+1] = X[2k+1]$$

Filters $h_0[n]$ and $h_1[n]$ followed by downsampling by 2 implement φ_0 and φ_1

$$h_0[n] = \varphi_0[-n], h_1[n] = \varphi_1[-n]$$

We can implement the orthonormal basis functions with FIR filter. Note that these filters are acausal.

The result, that the filter are time- reversed versions of the basis function is intuitive, since filtering, i.e., convolving is the scalar product with the time- reversed filter coefficients.

Time-Domain Analysis

$$
\begin{pmatrix} \vdots \\ y_0[0] \\ y_1[0] \\ y_0[1] \\ y_1[1] \\ \vdots \end{pmatrix}
=
\begin{pmatrix} \vdots \\ X[0] \\ X[1] \\ X[2] \\ X[3] \\ \vdots \end{pmatrix}
=
\begin{pmatrix}
\ddots & & \\
& \begin{matrix} \overbrace{h_0[0] h_0[-1]}^{\varphi_0[n]} \\ \underbrace{h_1[0] h_1[-1]}_{\varphi_1[n]} \end{matrix} & \\
& & \begin{matrix} \overbrace{h_0[0] h_0[-1]}^{\varphi_0[n]} \\ \underbrace{h_1[0] h_1[-1]}_{\varphi_1[n]} \end{matrix} \\
& & & \ddots
\end{pmatrix}
\begin{pmatrix} \vdots \\ x[0] \\ x[1] \\ x[2] \\ x[3] \\ \vdots \end{pmatrix}
$$

Matrix notation.

Reconstruction

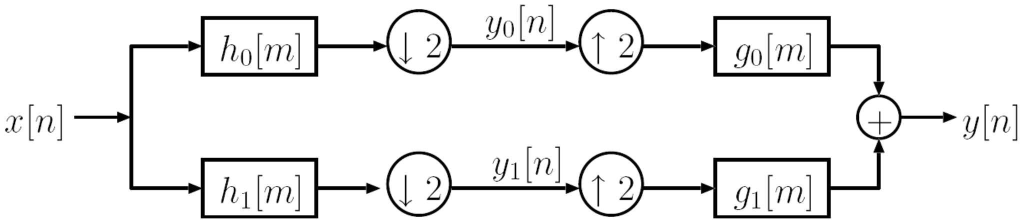
- Filter $g_0[n] = \varphi_0[n], g_1[n] = \varphi_1[n]$
- Periodic $\varphi_{2k}[n] = g_0[n-2k], \varphi_{2k+1}[n] = g_1[n-2k]$

$$\begin{aligned} x[n] &= \sum_{k\in\mathcal{Z}} X[k]\varphi_k[n] \\ &= \sum_{k\in\mathcal{Z}} X[2k]\varphi_{2k}[n] + \sum_{k\in\mathcal{Z}} X[2k+1]\varphi_{2k+1}[n] \\ &= \sum_{k\in\mathcal{Z}} y_0[k]g_0[n-2k] + \sum_{k\in\mathcal{Z}} y_1[k]g_1[n-2k] \end{aligned}$$

Upsampling by 2 followed by convolution with g_i

Each sample of $y_i[k]$ adds one sample of $g_i[k]$ shifted by 2k. That can be implemented by an upsampling by 2 (inserting a zero between evry second sample of $y_i[k]$).

Filterbank

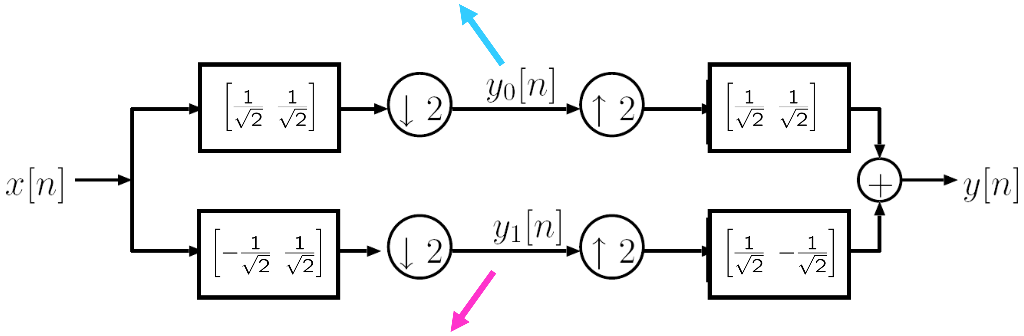


- Synthesis Filter $g_i[n] = \varphi_i[n]$
- Analysis Filter $h_i[n] = \varphi_i[-n]$

The final result- a two channel filter bank.

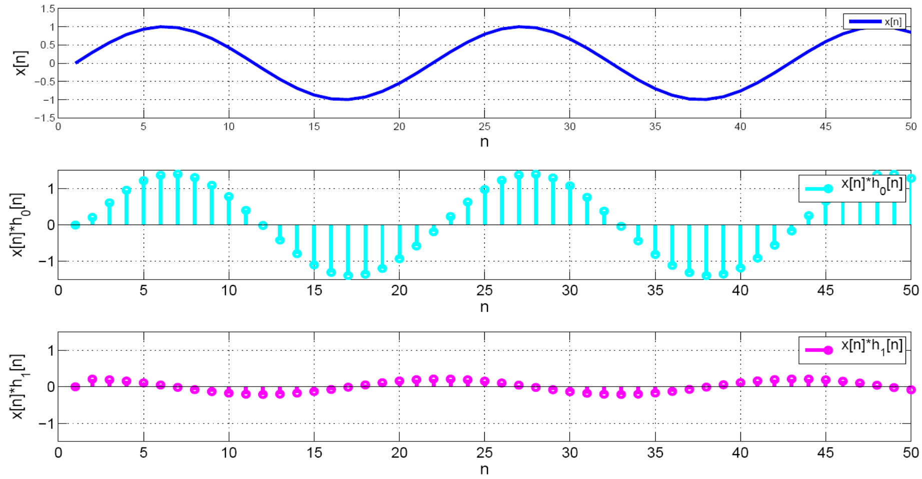
Filterbank

$$y_0[k] = X[2k] = \frac{1}{\sqrt{2}}x[2k] + \frac{1}{\sqrt{2}}x[2k+1]$$



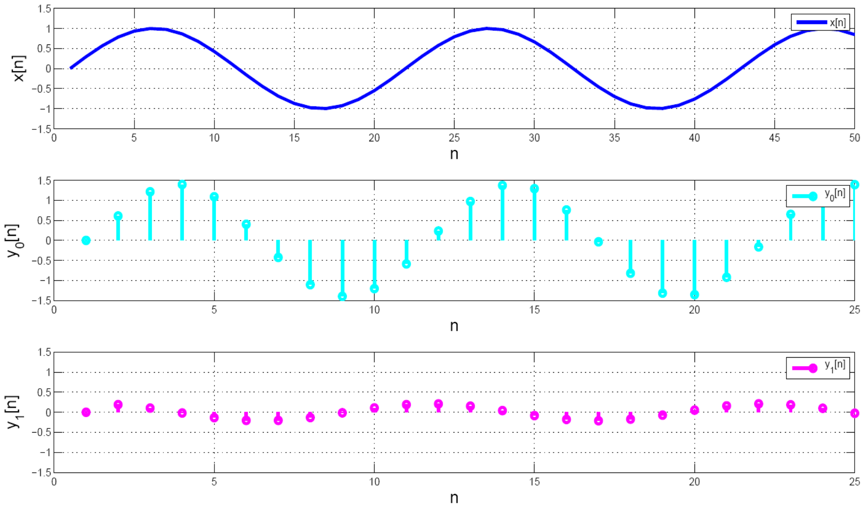
$$y_1[k] = X[2k+1] = \frac{1}{\sqrt{2}}x[2k] - \frac{1}{\sqrt{2}}x[2k+1]$$

Expansion Example – Analysis Filter



We can see the average (middle) and the coarse (bottom) information of the input signal (top).

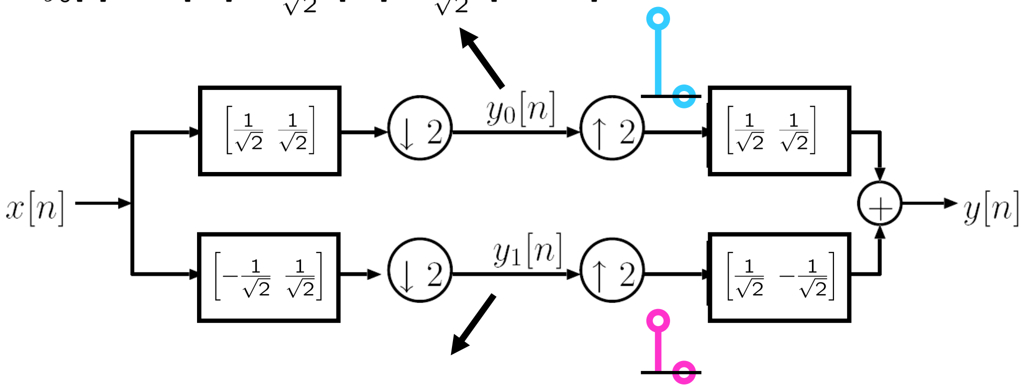
Haar Example - Downsampling



Downsampling by 2: Every second sample is taken – only 25 instead of 50 samples.

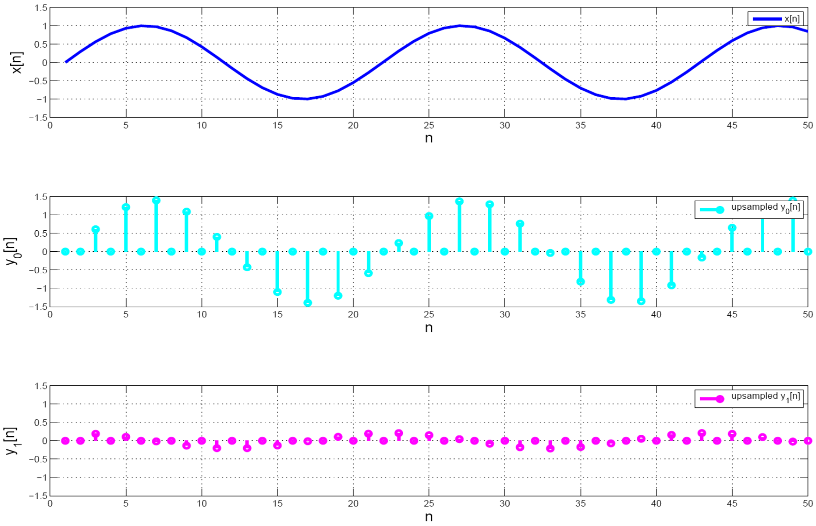
Filterbank

$$y_0[k] = X[2k] = \frac{1}{\sqrt{2}}x[2k] + \frac{1}{\sqrt{2}}x[2k+1]$$



$$y_1[k] = X[2k+1] = \frac{1}{\sqrt{2}}x[2k] - \frac{1}{\sqrt{2}}x[2k+1]$$

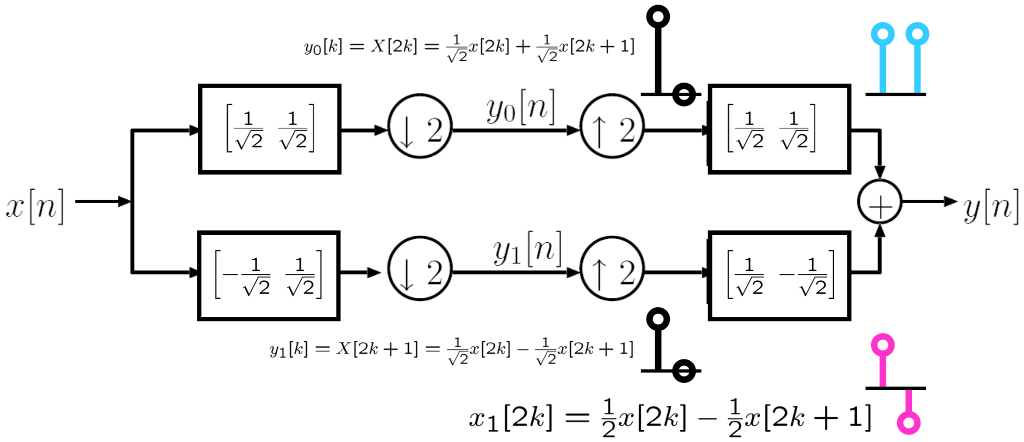
Haar Example - Upsampling



Upsampling by 2: Inserting yeros, i.e., every second sample is zero.

Filterbank

$$x_1[2k] = x_1[2k+1] = \tfrac{1}{2}x[2k] + \tfrac{1}{2}x[2k+1]$$



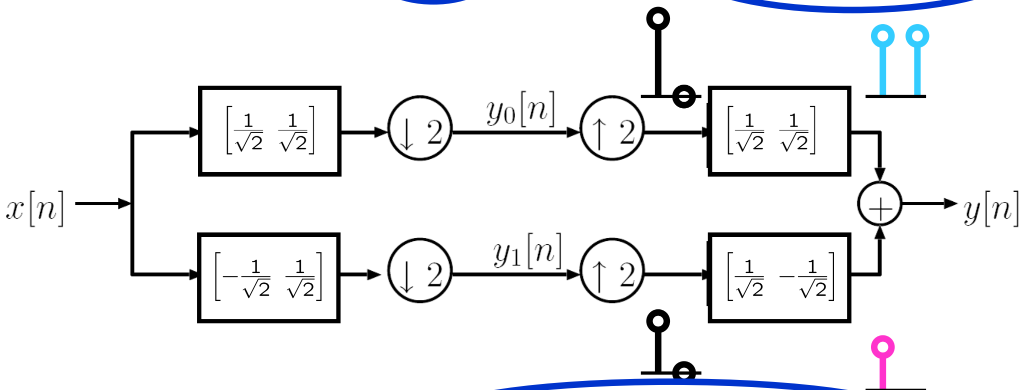
$$x_1[2k] = \tfrac{1}{2}x[2k] - \tfrac{1}{2}x[2k+1]$$

$$x_1[2k+1] = -\tfrac{1}{2}x[2k] + \tfrac{1}{2}x[2k+1]$$

The impulse response of g_0 reproduces a scaled (by 1/sqrt(2)) version of the input sample (since the second sample is zero), whereas g_1 produces the same output, but once time -1.

Filterbank

$$x_1[2k] = x_1[2k+1] = \tfrac{1}{2}x[2k] + \tfrac{1}{2}x[2k+1]$$



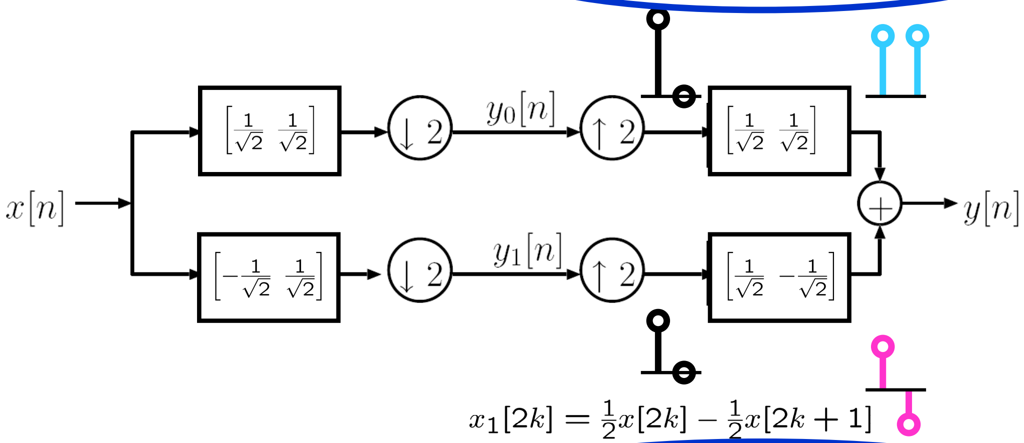
$$x_1[2k] = \tfrac{1}{2}x[2k] - \tfrac{1}{2}x[2k+1]$$

$$x_1[2k+1] = -\tfrac{1}{2}x[2k] + \tfrac{1}{2}x[2k+1]$$

Even samples y[2k] = x_0[2k] + x_1[2k] = (½ x[2k] + ½ x[2k+1]) + (½ x[2k] - ½ x[2k+1]) = x[2k].

Filterbank

$$x_1[2k] = x_1[2k+1] = \tfrac{1}{2}x[2k] + \tfrac{1}{2}x[2k+1]$$

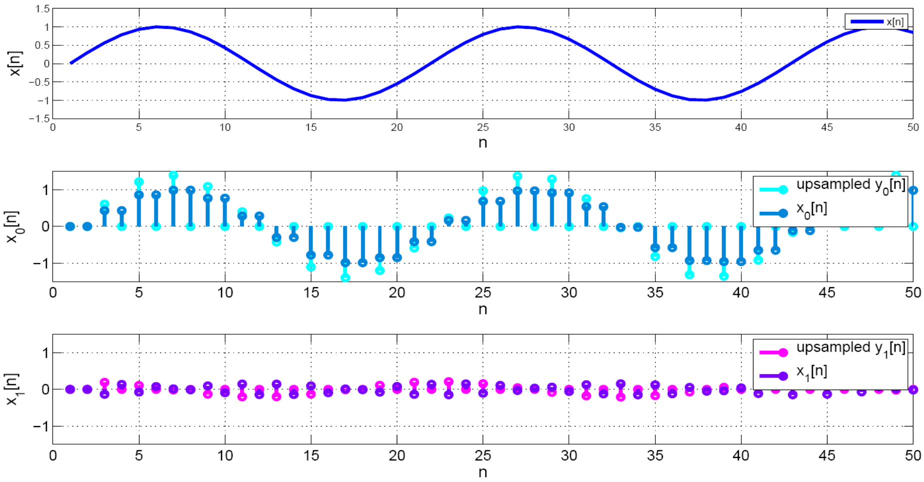


$$x_1[2k] = \tfrac{1}{2}x[2k] - \tfrac{1}{2}x[2k+1]$$

$$x_1[2k+1] = -\tfrac{1}{2}x[2k] + \tfrac{1}{2}x[2k+1]$$

Odd samples $y[2k+1] = x_0[2k+1] + x_1[2k+1] = (½\, x[2k] + ½\, x[2k+1]) + (-½\, x[2k] + ½\, x[2k+1]) = x[2k+1]$.

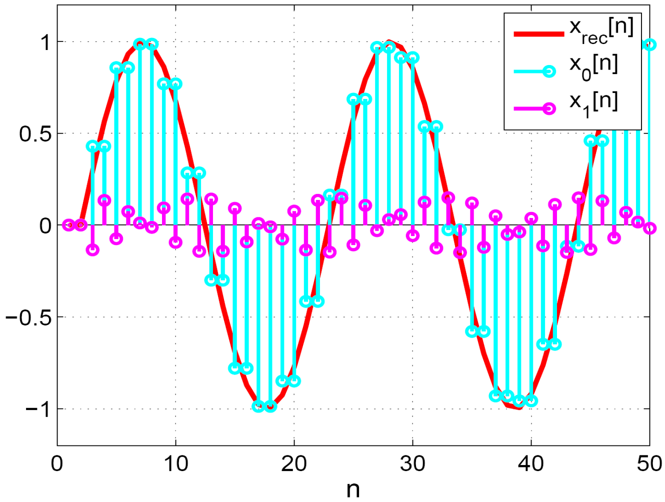
Haar Example – Synthesis Filter



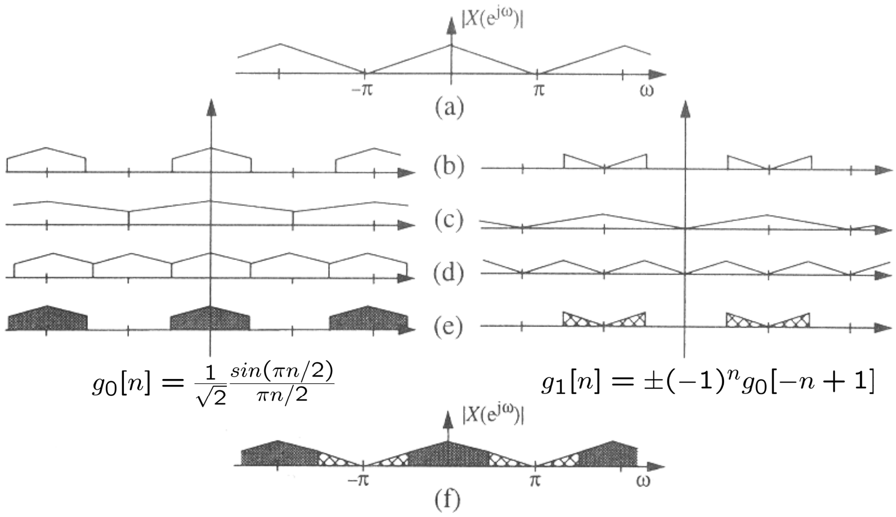
Synthesis filter: $g_0[n] = \varphi_0[n]$ = (1/sqrt(2) 1/sqrt(2)). That means that for a delta impulse we have the response $\varphi_0[n]$, which is a scaled reproduction of the sample.

For $g_1[n] = \varphi_1[n]$ = (1/sqrt(2) -1/sqrt(2)).

Haar Example - Reconstruction



Sinc Expansion



$$g_0[n] = \frac{1}{\sqrt{2}} \frac{sin(\pi n/2)}{\pi n/2}$$

$$g_1[n] = \pm(-1)^n g_0[-n+1]$$

On the left side we see the projection of the input signal x[n] onto the subspace of sequences bandlimited to [-π/2 +π/2] (i.e. lowpass) shown in black.

On the right side we see the orthogonal counterpart (highpass).

Orthogonal Expansions - Summary

- Synthesis filter $g_i[n] = \varphi_i[n]$
- Analysis filter $h_i[n] = g_i[-n] = \varphi_i[-n]$
- Expansions are periodically time- varying
- Haar expansion
  - Good time resolution
- Sinc expansion
  - Good frequency resolution

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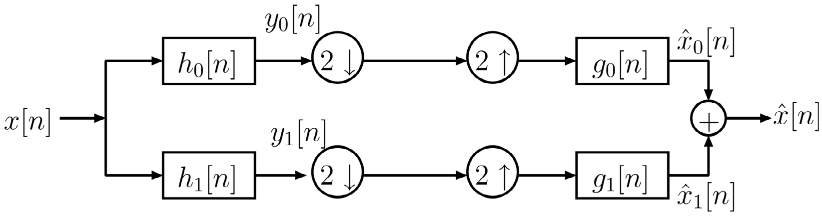
Analysis of Filter Banks: Time Domain



- **Analysis:** $y_k[n] = x[n] \star h_k[n] \;=\; < x[n], h_k[-n] >$

  $\Rightarrow h_k[-n] = \tilde{\varphi}_k[n]$, i.e. non-causal filter

- **Synthesis:** (from decimated y_k) $$\hat{x}[bN+n] = \sum_{k=0}^{N} \sum_{m=b-n/N}^{\frac{L-1-n}{N}-b} y_k[lN]\cdot g_k[mN-bN+n]$$

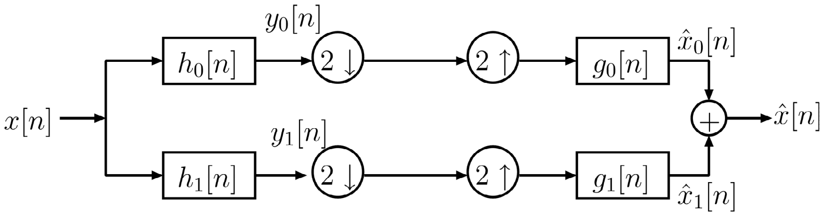
  $\Rightarrow g_k[n] = \varphi_k[n]$

Like in the previous section, but now for the general case, we want to provide an example of a time domain filter bank implementation. In the implementation, our signal decomposition is performed with digital filters $h_k[n]$ and $g_k[n]$. The figure shows a 2 channel example of such a time domain filter bank.

We can now link the mathematical expression of a convolution to the expression for the scalar product, and observe that the base vector of the analysis must time reversed within a convolutive formulation. On the other hand, for the synthesis task, we recognize that within the decimation time step N, the base vectors for the resynthesis are involved without time reversal.

Systems involving decimation (only) represent time varying systems, hence the analysis step is time varying too. We can call it „periodically time-varying“, as only for time instants of the original sampling rate that are multiples nN, the decimated signal is time-invariant. I.e. y[nN+m]=x[nN+m] only for m equals N.

Analysis of Filter Banks: Time Domain



- Synthesis/analysis: decimated, interlaced channels:

Analysis: $\tilde{\mathbf{X}} = \mathbf{T_a} \cdot \mathbf{x}$

$$\begin{pmatrix} \vdots \\ y_0[0] \\ y_1[0] \\ y_0[2] \\ y_1[2] \\ \vdots \end{pmatrix} = \mathbf{T}_\mathrm{a} \cdot \begin{pmatrix} \vdots \\ x[0] \\ x[1] \\ x[2] \\ x[3] \\ \vdots \end{pmatrix}$$

Synthesis: $\mathbf{y} = \mathbf{T_s} \cdot \tilde{\mathbf{X}}$

$$\begin{pmatrix} \vdots \\ \hat{x}[0] \\ \hat{x}[1] \\ \hat{x}[2] \\ \hat{x}[3] \\ \vdots \end{pmatrix} = \mathbf{T}_\mathrm{s} \cdot \begin{pmatrix} \vdots \\ y_0[0] \\ y_1[0] \\ y_0[2] \\ y_1[2] \\ \vdots \end{pmatrix}$$

We obtain a compact matrix notation when interlacing the filter bank channels corresponding to one time instant. The analysis matrix operates on the continuous intput signal x[n] at full sampling rate, and yields the decimated filter bank channels (att.: chose the notation for $y_k[m]$ without decimation, i.e. m=Nn, in contrast to notation in the previous section). Of course, this system again is periodically time-variant.

Analysis of Filter Banks: Time Domain

- Decimated, interlaced: Analysis

$$\underbrace{\begin{pmatrix} \vdots \\ y_0[0] \\ y_1[0] \\ y_0[2] \\ y_1[2] \\ \vdots \end{pmatrix}}_{\mathbf{y}} = \underbrace{\begin{pmatrix} \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\ \dots & 0 & h_0[0] & h_0[-1] & h_0[-2] & \dots & h_0[1-L] & 0 & 0 & 0 & \dots \\ \dots & 0 & h_1[0] & h_1[-1] & h_1[-2] & \dots & h_1[1-L] & 0 & 0 & 0 & \dots \\ \dots & 0 & 0 & 0 & h_0[0] & \dots & h_0[3-L] & h_0[2-L] & h_0[1-L] & 0 & \dots \\ \dots & 0 & 0 & 0 & h_1[0] & \dots & h_1[3-L] & h_1[2-L] & h_1[1-L] & 0 & \dots \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \end{pmatrix}}_{\mathbf{T_a}} \underbrace{\begin{pmatrix} \vdots \\ x[0] \\ x[1] \\ x[2] \\ x[3] \\ \vdots \end{pmatrix}}_{\mathbf{x}}$$

- Synthesis:

$$\overbrace{\begin{pmatrix} \vdots \\ \hat{x}[0] \\ \hat{x}[1] \\ \hat{x}[2] \\ \hat{x}[3] \\ \vdots \end{pmatrix}}^{\hat{\mathbf{x}}} = \overbrace{\begin{pmatrix} \dots & \vdots & \vdots & \vdots & \vdots & \dots \\ \dots & 0 & 0 & 0 & 0 & \dots \\ \dots & g_0[0] & g_1[0] & 0 & 0 & \dots \\ \dots & g_0[1] & g_1[1] & 0 & 0 & \dots \\ \dots & g_0[2] & g_1[2] & g_0[0] & g_1[0] & \dots \\ \dots & \vdots & \vdots & \vdots & \vdots & \dots \\ \dots & g_0[L-1] & g_1[L-1] & g_0[L-3] & g_1[L-3] & \dots \\ \dots & 0 & 0 & g_0[L-2] & g_1[L-2] & \dots \\ \dots & 0 & 0 & g_0[L-1] & g_1[L-1] & \dots \\ \dots & 0 & 0 & 0 & 0 & \dots \\ \dots & \vdots & \vdots & \vdots & \vdots & \dots \end{pmatrix}}^{\mathbf{T_s}} \overbrace{\begin{pmatrix} \vdots \\ y_0[0] \\ y_1[0] \\ y_0[2] \\ y_1[2] \\ \vdots \end{pmatrix}}^{\mathbf{y}}$$

Analysis of Filter Banks: Time Domain

- Decimated, interlaced: Analysis $\tilde{\varphi}_0[n]$ $\tilde{\varphi}_1[n]$

$$\underbrace{\begin{pmatrix} \vdots \\ y_0[0] \\ y_1[0] \\ y_0[2] \\ y_1[2] \\ \vdots \end{pmatrix}}_{\mathbf{y}} = \underbrace{\begin{pmatrix} \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\ \dots & 0 & h_0[0] & h_0[-1] & h_0[-2] & \dots & h_0[1-L] & 0 & 0 & 0 & \dots \\ \dots & 0 & h_1[0] & h_1[-1] & h_1[-2] & \dots & h_1[1-L] & 0 & 0 & 0 & \dots \\ \dots & 0 & 0 & 0 & h_0[0] & \dots & h_0[3-L] & h_0[2-L] & h_0[1-L] & 0 & \dots \\ \dots & 0 & 0 & 0 & h_1[0] & \dots & h_1[3-L] & h_1[2-L] & h_1[1-L] & 0 & \dots \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \end{pmatrix}}_{\mathbf{T_a}} \underbrace{\begin{pmatrix} \vdots \\ x[0] \\ x[1] \\ x[2] \\ x[3] \\ \vdots \end{pmatrix}}_{\mathbf{x}}$$

- Synthesis: $\varphi_0[n]$ $\varphi_1[n]$

$$\overbrace{\begin{pmatrix} \vdots \\ \hat{x}[0] \\ \hat{x}[1] \\ \hat{x}[2] \\ \hat{x}[3] \\ \vdots \end{pmatrix}}^{\hat{\mathbf{x}}} = \overbrace{\begin{pmatrix} \dots & \vdots & \vdots & \vdots & \vdots & \dots \\ \dots & 0 & 0 & 0 & 0 & \dots \\ \dots & g_0[0] & g_1[0] & 0 & 0 & \dots \\ \dots & g_0[1] & g_1[1] & 0 & 0 & \dots \\ \dots & g_0[2] & g_1[2] & g_0[0] & g_1[0] & \dots \\ \dots & \vdots & \vdots & \vdots & \vdots & \dots \\ \dots & g_0[L-1] & g_1[L-1] & g_0[L-3] & g_1[L-3] & \dots \\ \dots & 0 & 0 & g_0[L-2] & g_1[L-2] & \dots \\ \dots & 0 & 0 & g_0[L-1] & g_1[L-1] & \dots \\ \dots & 0 & 0 & 0 & 0 & \dots \\ \dots & \vdots & \vdots & \vdots & \vdots & \dots \end{pmatrix}}^{\mathbf{T_s}} \overbrace{\begin{pmatrix} \vdots \\ y_0[0] \\ y_1[0] \\ y_0[2] \\ y_1[2] \\ \vdots \end{pmatrix}}^{\mathbf{y}}$$

Expanding the analysis and synthesis matrices, Ta and Ts, respectively, we obtain the above expressions.

For illustration, we can now highlight the corresponding base vectors connected to the filter responses. The non-causal analysis filters involve the time-reverse base vectors.

Analysis of Filter Banks: Time Domain

- Perfect reconstruction: $\mathbf{T_s T_a} = \mathbf{I}$

  (Biorthogonality)

$$\begin{pmatrix} & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \\ \dots & 0 & h_0[0] & h_0[-1] & h_0[-2] & \dots & h_0[1-L] & 0 & 0 & 0 & \dots \\ \dots & 0 & h_1[0] & h_1[-1] & h_1[-2] & \dots & h_1[1-L] & 0 & 0 & 0 & \dots \\ \dots & 0 & 0 & 0 & h_0[0] & \dots & h_0[3-L] & h_0[2-L] & h_0[1-L] & 0 & \dots \\ \dots & 0 & 0 & 0 & h_1[0] & \dots & h_1[3-L] & h_1[2-L] & h_1[1-L] & 0 & \dots \\ & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \end{pmatrix} \times \begin{pmatrix} \dots & \vdots & \vdots & \vdots & \vdots & \dots \\ \dots & 0 & 0 & 0 & 0 & \dots \\ \dots & g_0[0] & g_1[0] & 0 & 0 & \dots \\ \dots & g_0[1] & g_1[1] & 0 & 0 & \dots \\ \dots & g_0[2] & g_1[2] & g_0[0] & g_1[0] & \dots \\ \dots & \vdots & \vdots & \vdots & \vdots & \dots \\ \dots & g_0[L-1] & g_1[L-1] & g_0[L-3] & g_1[L-3] & \dots \\ \dots & 0 & 0 & g_0[L-2] & g_1[L-2] & \dots \\ \dots & 0 & 0 & g_0[L-1] & g_1[L-1] & \dots \\ \dots & 0 & 0 & 0 & 0 & \dots \\ \dots & \vdots & \vdots & \vdots & \vdots & \dots \end{pmatrix} = \mathbf{I}$$

- Orthonormality:
  - Analysis filters are time reversed synthesis filters

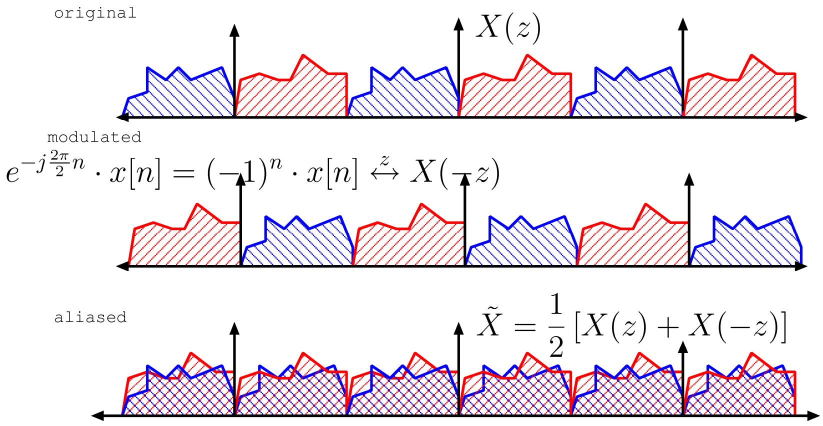
    $\mathbf{T_a} = \mathbf{T_s^T}$, i.e. $h_k[n] = g_k[-n]$, and $\mathbf{T_s^T T_s} = \mathbf{I}$

Connecting the synthesis and analysis matrix, we can now desire perfect reconstruction, i.e. a unity transfer function from x[n] to ^x[n]. In particular, this means that each scalar product involving vectors $h_l[n]$ and $g_k[n]$ having different indices $l \neq k$ and involving shifted versions has to yield 0 (=orthogonality). Furthermore, filter banks with perfect reconstruction are then time-invariant systems again, as time shifts at the input x[n+m] always yield a time-shifted output ^x[n+m]. We most often call this property „alias free reconstruction“.

Like in the first two sections of this talk, orthonormal systems involve the same base vectors for analysis, as well as synthesis. Therefore, in our filter implementation, the analysis vector must be equal to the time-reversed synthesis filters. We may then express the orthonormality as a special case of perfect reconstruction.

Analysis of Filter Banks: Modulation Domain

- Aliased spectra by modulation: A decimation by 2 example

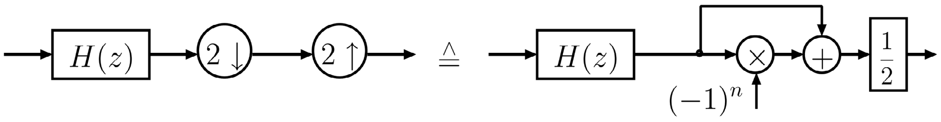


For frequency domain representations of decimated filter banks, we have to do some tricky manipulation, in order to provide sufficient description of „aliasing“, i.e. time-variance. A straight-forward way is to build the aliased spectrum obtained from downsampling and expansion by modulation and sum of the original signal spectrum. Mind the re-normalization term deviding by the number of modulated spectra. This normalization is necessary, as downsampling and upsampling scales the signal energy.

The above Figure shows an example for down- and upsampling by a factor 2.

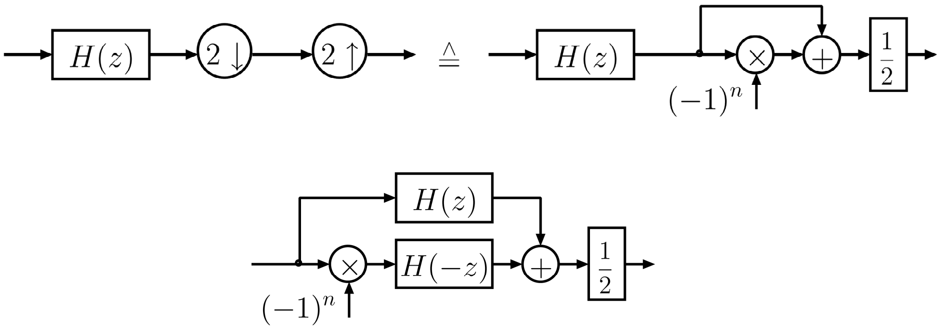
Analysis of Filter Banks: Modulation Domain

- Aliased spectra by modulation: A decimation by 2 example
  - Replacing decimation and upsampling by modulation



Analysis of Filter Banks: Modulation Domain

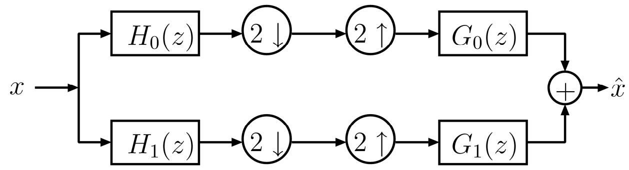
- Aliased spectra by modulation: A decimation by 2 example
  - Replacing decimation and upsampling by modulation
  - Employing modulated versions of the filter

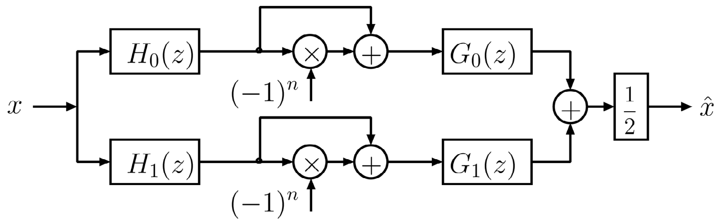


We can now employ this approach into our block diagrams. It is furhtermore possible now, to use modulated versions of the filter, because Y(W^n z)=X(W^n z) H(W^n z).

Analysis of Filter Banks: Modulation Domain

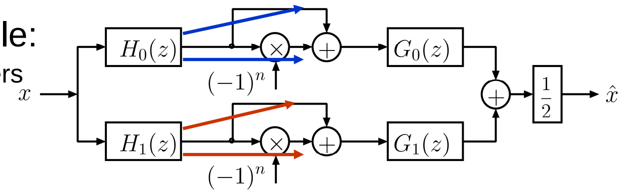
- A 2-channel example:
  - Replacing decimation+upsamling by modulation

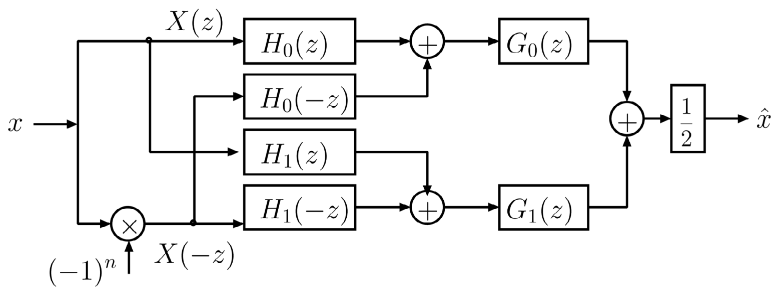




Analysis of Filter Banks: Modulation Domain

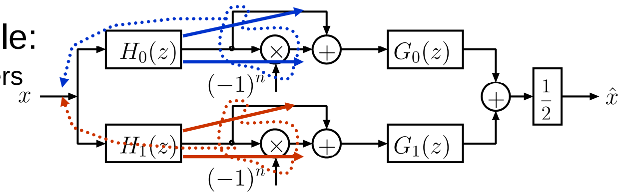
- A 2-channel example:
  - Pulling modulated filters into modulation path

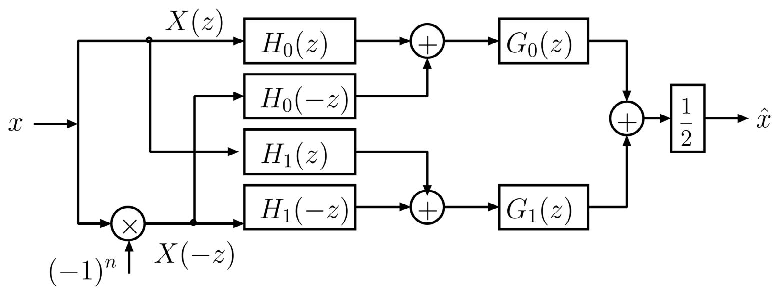




Analysis of Filter Banks: Modulation Domain

- A 2-channel example:
  - Pulling modulated filters into modulation path





Analysis of Filter Banks: Modulation Domain

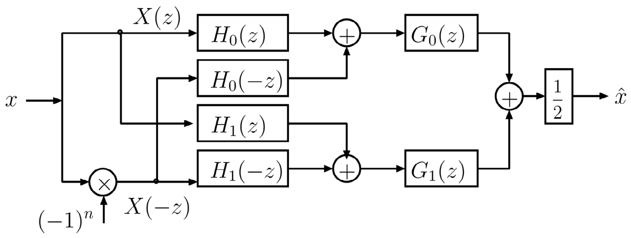
- A 2-channel example:
  - We finally get the system as matrix of modulated filters

Analysis:

$$\mathbf{Y}(z) = \frac{1}{2} \underbrace{\begin{pmatrix} H_0(z) & H_0(-z) \\ H_1(z) & H_1(-z) \end{pmatrix}}_{\mathbf{H_m}} \begin{pmatrix} X(z) \\ X(-z) \end{pmatrix}$$

Synthesis:

$$\hat{X}(z) = \begin{pmatrix} G_0(z) & G_1(z) \end{pmatrix} \mathbf{Y}(z)$$



Using this approach to replace up- and downsampling in our filter bank structure (2 channel example), we find the modulation domain representation with ist multiple input multiple output (MIMO) transfer matrix, containing modulated versions of the analysis filters. Note that the output of the analysis section is calculated at the high sampling rate. The synthesis filters remain unchanged. The advantage of this structure is that the insertion of decimators and expanders before re-synthesis, according to the number of modulated signals, doesn‘t effect the output.

Analysis of Filter Banks: Modulation Domain

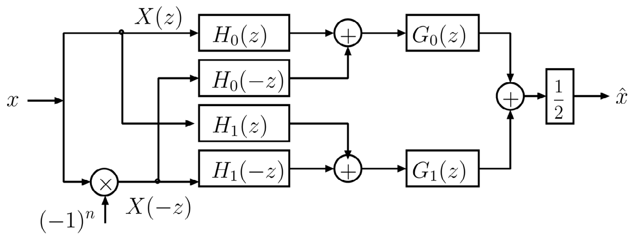
- A 2-channel example:
  - We finally get the system as matrix of modulated filters

Analysis:

$$\mathbf{Y}(z) = \frac{1}{2}\underbrace{\begin{pmatrix} H_0(z) & H_0(-z) \\ H_1(z) & H_1(-z) \end{pmatrix}}_{\mathbf{H_m}} \begin{pmatrix} X(z) \\ X(-z) \end{pmatrix}$$

Synthesis:

$$\hat{X}(z) = \begin{pmatrix} G_0(z) & G_1(z) \end{pmatrix} \mathbf{Y}(z)$$



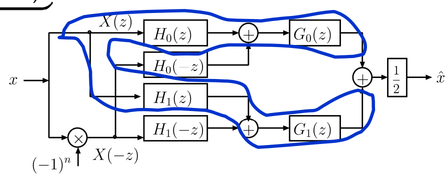
Analysis of Filter Banks: Modulation Domain

- Perfect reconstruction:
  (Biorthogonality)

$$\frac{1}{2}\begin{pmatrix} G_0(z) & G_1(z) \end{pmatrix} \underbrace{\begin{pmatrix} H_0(z) & H_0(-z) \\ H_1(z) & H_1(-z) \end{pmatrix}}_{\mathbf{H_m}} \begin{pmatrix} X(z) \\ X(-z) \end{pmatrix} \stackrel{!}{=} X(z)$$

1:1 transfer function

$$\Rightarrow \frac{1}{2}\begin{pmatrix} G_0(z) & G_1(z) \end{pmatrix} \underbrace{\begin{pmatrix} H_0(z) & H_0(-z) \\ H_1(z) & H_1(-z) \end{pmatrix}}_{\mathbf{H_m}} = \begin{pmatrix} 1 & 0 \end{pmatrix}$$



- Orthonormality:

Merging the analysis and synthesis equations, we get a description of the over-all transfer function. Desiring perfect reconstruction, the transfer function for the unmodulated X(z) has to be unity, and the modulated versions of the output must cancel.

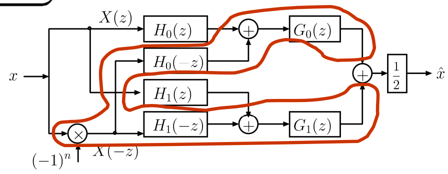
Analysis of Filter Banks: Modulation Domain

- Perfect reconstruction:
  (Biorthogonality)

$$\frac{1}{2}\begin{pmatrix} G_0(z) & G_1(z) \end{pmatrix} \underbrace{\begin{pmatrix} H_0(z) & H_0(-z) \\ H_1(z) & H_1(-z) \end{pmatrix}}_{\mathbf{H_m}} \begin{pmatrix} X(z) \\ X(-z) \end{pmatrix} \stackrel{!}{=} X(z)$$

$$\Rightarrow \frac{1}{2}\begin{pmatrix} G_0(z) & G_1(z) \end{pmatrix} \underbrace{\begin{pmatrix} H_0(z) & H_0(-z) \\ H_1(z) & H_1(-z) \end{pmatrix}}_{\mathbf{H_m}} = \begin{pmatrix} 1 & 0 \end{pmatrix}$$

no aliasing



- Orthonormality:

Analysis of Filter Banks: Modulation Domain

- Perfect reconstruction:
  (Biorthogonality)

$$\underbrace{\frac{1}{2}\begin{pmatrix} G_0(z) & G_1(z) \\ G_0(-z) & G_1(-z) \end{pmatrix}}_{\mathbf{G_m}} \underbrace{\begin{pmatrix} H_0(z) & H_0(-z) \\ H_1(z) & H_1(-z) \end{pmatrix}}_{\mathbf{H_m}} \begin{pmatrix} X(z) \\ X(-z) \end{pmatrix} \stackrel{!}{=} \begin{pmatrix} X(z) \\ X(-z) \end{pmatrix}$$

$$\Rightarrow \frac{1}{2}\underbrace{\begin{pmatrix} G_0(z) & G_1(z) \\ G_0(-z) & G_1(-z) \end{pmatrix}}_{\mathbf{G_m}} \underbrace{\begin{pmatrix} H_0(z) & H_0(-z) \\ H_1(z) & H_1(-z) \end{pmatrix}}_{\mathbf{H_m}} = \mathbf{I}$$

with modulated synthesis filters:
- elegant notation!

$$\frac{1}{2}\mathbf{G_m}(z)\mathbf{H_m}(z) = \mathbf{I}$$

- Orthonormality:

We may also expand the synthesis filters with the modulated versions of the filters. This provides a compact notation that essentially says: All transfer functions of the modulated versions of $X(W^n z)$ have to yield $\hat{X}(W^n z)=X(W^m z)$ for n=m only, while all the cross-modulation terms have to cancel (time-invariance).

Analysis of Filter Banks: Modulation Domain

- Perfect reconstruction:
  (Biorthogonality)

$$\frac{1}{2}\underbrace{\begin{pmatrix} G_0(z) & G_1(z) \\ G_0(-z) & G_1(-z) \end{pmatrix}}_{\mathbf{G_m}}\underbrace{\begin{pmatrix} H_0(z) & H_0(-z) \\ H_1(z) & H_1(-z) \end{pmatrix}}_{\mathbf{H_m}}\begin{pmatrix} X(z) \\ X(-z) \end{pmatrix} \overset{!}{=} \begin{pmatrix} X(z) \\ X(-z) \end{pmatrix}$$

$$\Rightarrow \frac{1}{2}\underbrace{\begin{pmatrix} G_0(z) & G_1(z) \\ G_0(-z) & G_1(-z) \end{pmatrix}}_{\mathbf{G_m}}\underbrace{\begin{pmatrix} H_0(z) & H_0(-z) \\ H_1(z) & H_1(-z) \end{pmatrix}}_{\mathbf{H_m}} = \mathbf{I}$$

with modulated synthesis filters:
- elegant notation!

$$\frac{1}{2}\mathbf{G_m}(z)\mathbf{H_m}(z) = \mathbf{I}$$

- Orthonormality:
  - Analysis filters are time reversed synthesis filters

$$\mathbf{H_m}(z) = \mathbf{G_m^T}(z^{-1}) \qquad \frac{1}{2}\mathbf{G_m}(z)\mathbf{G_m^T}(z^{-1}) = \mathbf{I}$$

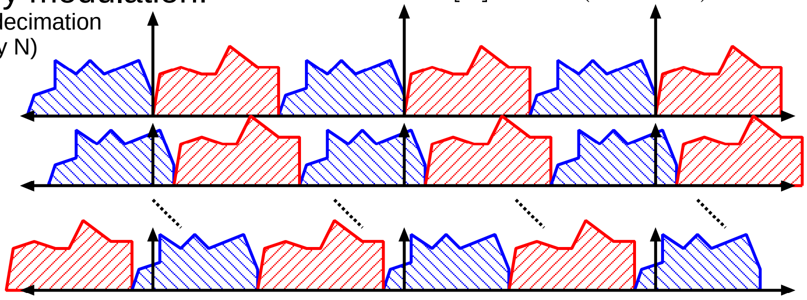
$\{\}^{\mathbf{T}}$ is the hermitian transpose

In order to provide orhtonormality, again, the analysis filters have to be time-reversed versions of the synthesis filters. In the z-Domain, this corresponds to taking the hermitian transpose (transpose and complex conjugate), as well as z^{-1}.

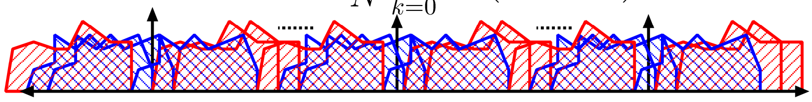
Analysis of Filter Banks: Modulation Domain

- Aliased spectra by modulation:
  (decimation by N)

$$e^{-j\frac{2\pi}{L}k} \cdot x[n] \overset{z}{\leftrightarrow} X(ze^{-j\frac{2\pi}{L}k})$$



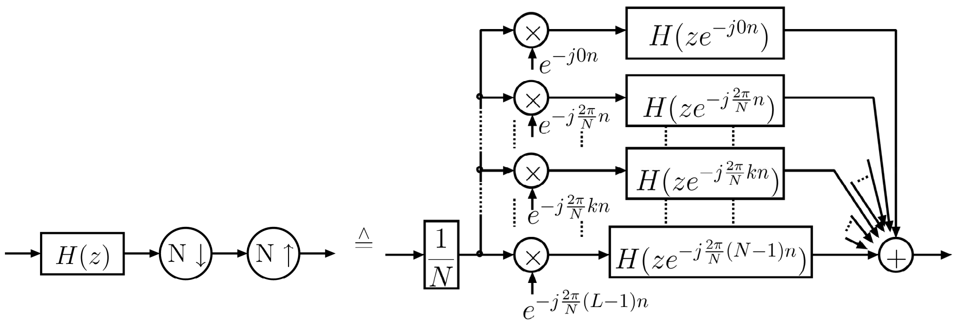
$$\tilde{X}(z) = \frac{1}{N} \sum_{k=0}^{L-1} X\left(ze^{-j\frac{2\pi}{L}kn}\right)$$



The following slides shall illustrate, how the more general case of decimation by N, as well as the N-channel filter bank can be constructed in the modulation domain.

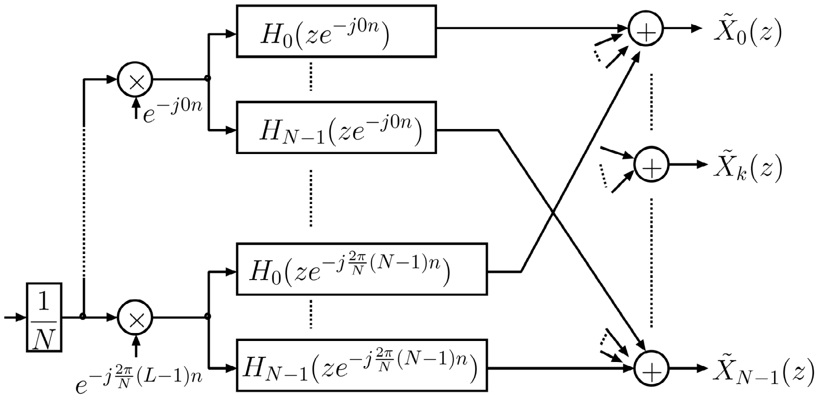
Analysis of Filter Banks: Modulation Domain

- Aliased spectra
  by modulation: single filter, decimation by N
  - Replacing decimation and upsampling by modulation
  - Pulling filters into modulation paths



Analysis of Filter Banks: Modulation Domain

- Aliased spectra
  by modulation: N channel filter bank
  - Modulation domain for N-channel filter banks



Analysis of Filter Banks: Modulation Domain

- Perfect reconstruction: arbitrary N-channel case
  (Biorthogonality)

with modulated synthesis filters

$$\mathbf{G_m} = \begin{pmatrix} G_0\left(e^{-j\frac{2\pi}{N}0}z\right) & \dots & G_{N-1}\left(e^{-j\frac{2\pi}{N}0}z\right) \\ \vdots & \dots & \vdots \\ G_0\left(e^{-j\frac{2\pi}{N}(N-1)}z\right) & \dots & G_{N-1}\left(e^{-j\frac{2\pi}{N}(N-1)}z\right) \end{pmatrix}$$

$$\frac{1}{N}\mathbf{G_m}(z)\mathbf{H_m}(z) \cdot \begin{pmatrix} X(e^{-j\frac{2\pi}{N}0}z) \\ \vdots \\ X(e^{-j\frac{2\pi}{N}(N-1)}z) \end{pmatrix} \stackrel{!}{=} \begin{pmatrix} X(e^{-j\frac{2\pi}{N}0}z) \\ \vdots \\ X(e^{-j\frac{2\pi}{N}(N-1)}z) \end{pmatrix}$$

$$\frac{1}{N}\mathbf{G_m} \cdot \mathbf{H_m} = \mathbf{I}$$

- Orthonormality:

Basically, the extended notation for the N-channel case is similar to the 2-channel case given before. Using the above notation, the conditions for perfect reconstruction (biorthogonality) and orthonormality are the same, except for the normalization term 1/N.

Analysis of Filter Banks: Modulation Domain

- Perfect reconstruction: arbitrary N-channel case
  (Biorthogonality)

with modulated synthesis filters

$$\mathbf{G_m} = \begin{pmatrix} G_0\left(e^{-j\frac{2\pi}{N}0}z\right) & \dots & G_{N-1}\left(e^{-j\frac{2\pi}{N}0}z\right) \\ \vdots & \dots & \vdots \\ G_0\left(e^{-j\frac{2\pi}{N}(N-1)}z\right) & \dots & G_{N-1}\left(e^{-j\frac{2\pi}{N}(N-1)}z\right) \end{pmatrix}$$

$$\frac{1}{N}\mathbf{G_m}(z)\mathbf{H_m}(z) \cdot \begin{pmatrix} X(e^{-j\frac{2\pi}{N}0}z) \\ \vdots \\ X(e^{-j\frac{2\pi}{N}(N-1)}z) \end{pmatrix} \stackrel{!}{=} \begin{pmatrix} X(e^{-j\frac{2\pi}{N}0}z) \\ \vdots \\ X(e^{-j\frac{2\pi}{N}(N-1)}z) \end{pmatrix}$$

$$\frac{1}{N}\mathbf{G_m} \cdot \mathbf{H_m} = \mathbf{I}$$

- Orthonormality:
  - Analysis filters are time reversed synthesis filters

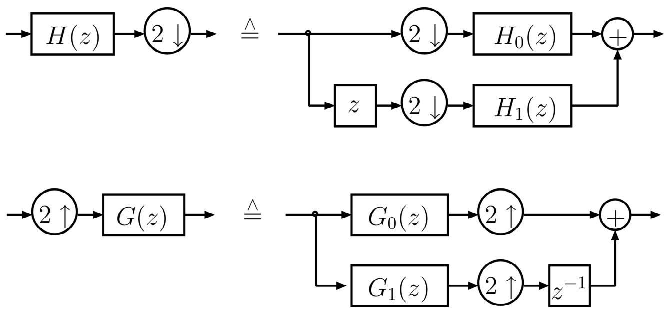
$$\mathbf{H_m}(z) = \mathbf{G_m^T}(z^{-1}) \qquad \frac{1}{N}\mathbf{G_m}(z)\mathbf{G_m^T}(z^{-1}) = \mathbf{I}$$

$\{\}^{\mathbf{T}}$ is the hermitian transpose

Analysis of Filter Banks: Polyphase Domain

- Polyphase implementation of anti-aliasing and interpolation filters: A decimation by 2 example

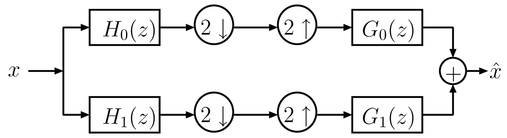
(recall Mr. Saleem's talk in 1st session)

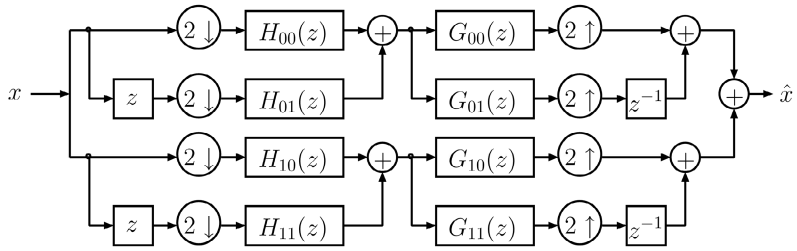


The third way to implement our filter bank is the polyphase domain. While the modulation domain employed filters at the original sampling rate, the polyphase domain more efficiently utilizes the polyphase realizations of decimation and reconstruction filters, we already heard about.

Analysis of Filter Banks: Polyphase Domain

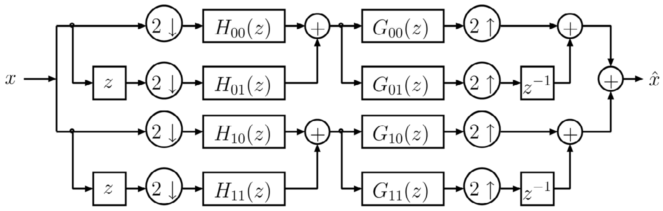
- Decimation and upsampling: 2-channel example

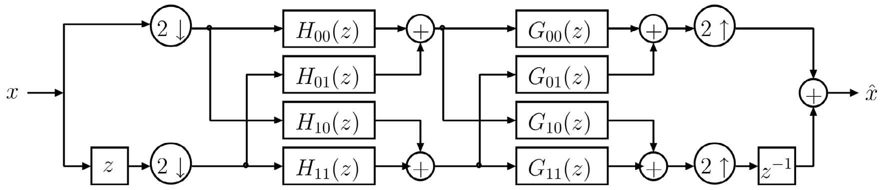




Analysis of Filter Banks: Polyphase Domain

- Decimation and upsampling: 2-channel example
  - Gathering common branches:





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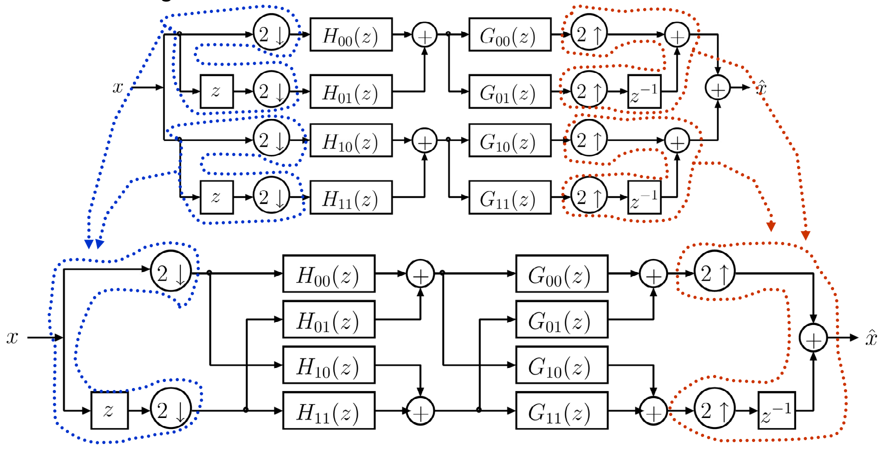
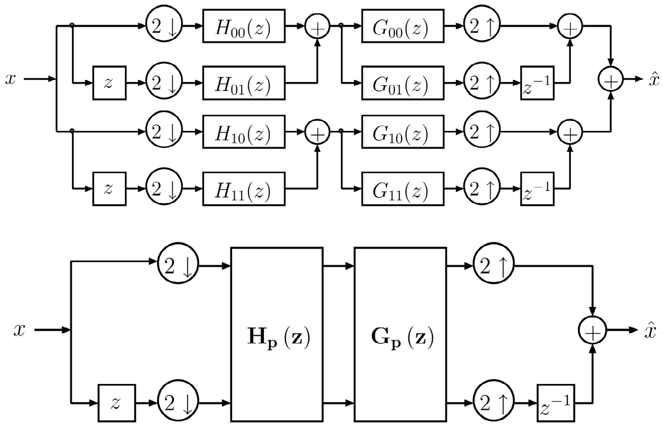


Analysis of Filter Banks: Polyphase Domain

- Decimation and upsampling: 2-channel example
  - Gathering common branches:



Again, we yield a MIMO system for the analysis section, but in contrast to the modulation domain for the synthesis here too.

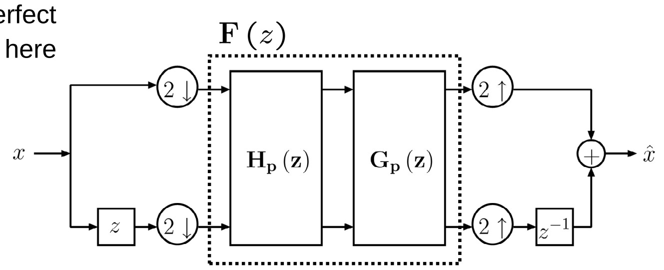
Analysis of Filter Banks: Polyphase Domain

- What's special about the *"Polyphase-Domain"*?
  - We know what ***aliasing free*** polyphase transfer functions must look like:

pseudo-circulant transfer function

$$\mathbf{F}(z) = \begin{pmatrix} F_0(z) & F_1(z) & \cdots & F_{N-1}(z) \\ zF_1(z) & \ddots & \cdots & F_{N-2}(z) \\ \ddots & \ddots & \ddots & \vdots \\ zF_{N-1}(z) & \cdots & zF_1(z) & F_0(z) \end{pmatrix}$$

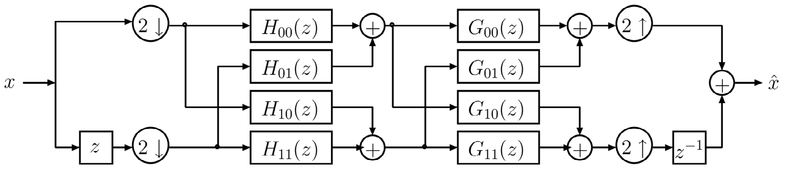
No need for perfect reconstruction here



A main advantage in the polyphase domain, besides its ressource efficient implementation, is the concept of pseudo-circulant matrices. Given a general MIMO transfer function in polyphase domain, pseudo-circulant transfer matrices provide aliasing free (time-invariant) output signals, as known from literature (e.g. Vaidyanathan). For alias free filter banks, only one joint transfer function in the polyphase domain containing both, the analysis and synthesis matrix, is needed to build this condition.

Analysis of Filter Banks: Polyphase Domain

- Decimation and upsampling: 2-channel example
  - Analysis and Synthesis: (z^2 is used in the full sampling rate domain)



$$\mathbf{Y}(z^2) = \underbrace{\begin{pmatrix} H_{00}(z^2) & H_{01}(z^2) \\ H_{10}(z^2) & H_{11}(z^2) \end{pmatrix}}_{\mathbf{H_p}(z)} \begin{pmatrix} 1 \\ z \end{pmatrix} X(z)$$

$$\hat{X}(z) = \begin{pmatrix} 1 & z^{-1} \end{pmatrix} \underbrace{\begin{pmatrix} G_{00}(z^2) & G_{10}(z^2) \\ G_{01}(z^2) & G_{11}(z^2) \end{pmatrix}}_{\mathbf{G_p}(z)} \mathbf{Y}(z^2)$$

Transcribing the polyphase transfer functions from the block diagram (att.: in the formulae these are expressed with respect to the full sampling rate, thus z^2), we can now set up our analysis and syhthesis equations in matrix notation.

Analysis of Filter Banks: Polyphase Domain

- Perfect reconstruction: 2-channel example

$$\begin{pmatrix}1 & z^{-1}\end{pmatrix} \underbrace{\begin{pmatrix}G_{00}(z^2) & G_{10}(z^2) \\ G_{01}(z^2) & G_{11}(z^2)\end{pmatrix}}_{\mathbf{G_p}(z)} \underbrace{\begin{pmatrix}H_{00}(z^2) & H_{01}(z^2) \\ H_{10}(z^2) & H_{11}(z^2)\end{pmatrix}}_{\mathbf{H_p}(z)} \begin{pmatrix}1 \\ z\end{pmatrix} = \mathbf{I}$$

$$\mathbf{G_p}(z)\mathbf{H_p}(z) = \mathbf{I}$$

- Orthonormality:

Analysis of Filter Banks: Polyphase Domain

- Perfect reconstruction: 2-channel example

$$\begin{pmatrix}1 & z^{-1}\end{pmatrix} \underbrace{\begin{pmatrix}G_{00}(z^2) & G_{10}(z^2) \\ G_{01}(z^2) & G_{11}(z^2)\end{pmatrix}}_{\mathbf{G_p}(z)} \underbrace{\begin{pmatrix}H_{00}(z^2) & H_{01}(z^2) \\ H_{10}(z^2) & H_{11}(z^2)\end{pmatrix}}_{\mathbf{H_p}(z)} \begin{pmatrix}1 & 0 \\ 0 & z\end{pmatrix} = \mathbf{I}$$

$$\mathbf{G_p}(z)\mathbf{H_p}(z) = \mathbf{I}$$

- Orthonormality:
  - Analysis filters are time reversed synthesis filters

$$\mathbf{H_p}(z) = \mathbf{G_p^T}(z^{-1}) \qquad \mathbf{G_p}(z)\mathbf{G_p^T}(z^{-1}) = \mathbf{I}$$

$\{\}^{\mathbf{T}}$ is the hermitian transpose

Analysis of Filter Banks: Polyphase Domain

- Perfect reconstruction: 2-channel example

$$\begin{pmatrix}1 & z^{-1}\end{pmatrix} \underbrace{\begin{pmatrix}G_{00}(z^2) & G_{10}(z^2) \\ G_{01}(z^2) & G_{11}(z^2)\end{pmatrix}}_{\mathbf{G_p}(z)} \underbrace{\begin{pmatrix}H_{00}(z^2) & H_{01}(z^2) \\ H_{10}(z^2) & H_{11}(z^2)\end{pmatrix}}_{\mathbf{H_p}(z)} \begin{pmatrix}1 & 0 \\ 0 & z\end{pmatrix} = \mathbf{I}$$

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- Orthonormality:
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$$\mathbf{H_p}(z) = \mathbf{G_p^T}(z^{-1}) \qquad \mathbf{G_p}(z)\mathbf{G_p^T}(z^{-1}) = \mathbf{I}$$

- Alias free:

$\mathbf{G_p}(z)\mathbf{H_p}(z)$ pseudo-circulant

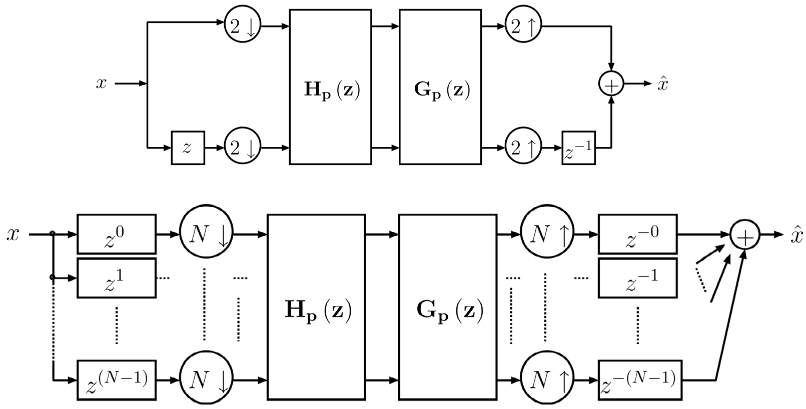
or $det(\mathbf{H_p}(z)) \neq 0$, i.e. $\mathbf{H_p}(z)$ full rank

$\{\}^{\mathbf{T}}$ is the hermitian transpose

Additionally to our criteria for perfect reconstruction (biorthogonality) and its special case, i.e. orthonormality, we gain a more relaxed criterion for alias free reconstruction. Further, if the determinant of the analysis matrix doesn‘t equal zero, the prerequisites for alias free reconstruction are fulfilled.

Analysis of Filter Banks: Polyphase Domain

- The results from the 2-channel case can be generalized to N-channel filter banks



Of course, like in the modulation domain before, we can extend the notations for N-channel filter banks. Here, the criteria remain exactly the same, as no re-normalization is involved.

Relations between Modulation & Polyphase Domain

- Analysis

$$\underbrace{\begin{pmatrix} H_{00}(z^2) & H_{01}(z^2) \\ H_{10}(z^2) & H_{11}(z^2) \end{pmatrix}}_{H_p(z^2)} = \frac{1}{2} \underbrace{\begin{pmatrix} H_0(z) & H_0(-z) \\ H_1(z) & H_1(-z) \end{pmatrix}}_{H_m(z)} \begin{pmatrix} 1 & 1 \\ 1 & -1 \end{pmatrix} \begin{pmatrix} 1 & 0 \\ 0 & z^{-1} \end{pmatrix}$$

- Synthesis

$$\underbrace{\begin{pmatrix} G_{00}(z^2) & G_{01}(z^2) \\ G_{10}(z^2) & G_{11}(z^2) \end{pmatrix}}_{G_p(z^2)} = \frac{1}{2} \begin{pmatrix} 1 & 0 \\ 0 & z \end{pmatrix} \begin{pmatrix} 1 & 1 \\ 1 & -1 \end{pmatrix} \underbrace{\begin{pmatrix} G_0(z) & G_0(-z) \\ G_1(z) & G_1(-z) \end{pmatrix}}_{G_m(z)}$$

Now, given three variants of filter bank implementation and description (time domain, modulation domain, and polyphase domain), it is very interesting to see that the corresponding representaion can be connected analytically. First of all, the connection between modulation domain matrices Hm(z) with polyphase domain analysis Hp(z) consists of a delay matrix containing delays z^{-k} and a modulation matrix with the modulation terms. Similar expressions hold for the synthesis equations.

Actually, we can now freely choose between the domains of impementation, and apply criteria of whatever domain on the corresponding filter set freely, just as we like.

Relations between Time & Polyphase Domain

- Consider the time- domain synthesis matrix in the frequency domain

$$\mathbf{T}_s(z) = \sum_{i=0}^{K-1} \mathbf{S}_i z^{-i} \qquad \mathbf{S}_i = \begin{pmatrix} g_0[2i] & g_1[2i] \\ g_0[2i+1] & g_1[2i+1] \end{pmatrix}$$

$$\boxed{\mathbf{T}_s(z) = \mathbf{G}_p(z)}$$

- The same for the analysis matrix

$$\mathbf{T}_a(z) = \sum_{i=0}^{K-1} \mathbf{A}_i z^{-i} \quad \mathbf{A}_i = \begin{pmatrix} h_0[2(K-i)-1] & h_0[2(K-i)-2] \\ h_1[2(K-i)-1] & h_1[2(K-i)-2] \end{pmatrix}$$

$$\boxed{\mathbf{T}_a(z) = z^{-K+1}\mathbf{H}_p(z^{-1}) \begin{pmatrix} 0 & 1 \\ z^{-1} & 0 \end{pmatrix}}$$

For the connection between time and polyphase domain, we can use NxN partitions of the time domain analysis and synthesis matrices, to build z-transforms. In the analysis case, delays are involved in the computation, too.

Outline

- Introduction
  - Orthonormality
  - Biorthogonality
- Orthonormal expansions and filter banks
  - Haar expansion
  - Sinc expansion
- Analysis of filter banks
  - Time domain
  - Modulation domain
  - Polyphase domain
  - Relations between time, modulation, and polyphase domain
- **Results on filter banks**
  - **Biorthogonal Relations**

Reconstruction

- Alias free reconstruction

- Perfect reconstruction
  - Filter bank output is a possibly scaled and delayed version of the input

$$\hat{X}(z) = cz^{-k}X(z)$$

Alias- free Reconstruction

- Polyphase domain
  - Transfer matrix T_P is pseudocirculant

$$F_{ij}(z) = \begin{cases} F_{0,j-i}(z) & j \geq i, \\ zF_{0,N+j-i}(z) & j < i. \end{cases}$$

  - 2 channel case

$$F(z) = \begin{pmatrix} F_0(z) & F_1(z) \\ zF_1(z) & F_0(z) \end{pmatrix}$$

- Polyphase analysis filters
  - Determinant of $H_P(z)$ is not identically zero, so that $H_P(z)$ has full rank

W

Perfect Reconstruction

- FIR filter
  - For a critically sampled FIR analysis filter bank, perfect reconstruction with FIR filter is possible *if and only if* **det(H_p(z)) is a pure delay**.

  - Cosine modulated filter banks
    - All filters are calculated from one L=2N length prototype low-pass filter $h_{pr}[n]$ by modulation $\left[-\frac{\pi}{2N}, \frac{\pi}{2N}\right]$
    - For perfect reconstruction $h_{pr}^2[i] + h_{pr}^2[N-1-i] = 2$ (power complementary)
    - Cosine modulated filters form the orthonormal base:

$$h_k[i] = \frac{1}{\sqrt{N}} h_{pr}[n] \cdot \cos\left(\frac{2k+1}{4N}(2n - N + 1)\pi\right)$$

Summary of Biorthongonality Relations

These statements are equivalent

1) $< h_i[-n], g_j[n - Nm] >= \delta[i-j]\delta[m]$

2) $\mathbf{T}_s \cdot \mathbf{T}_a = \mathbf{T}_a \cdot \mathbf{T}_s = \mathbf{I}$

3) $\frac{1}{N}\mathbf{G}_m(z)\mathbf{H}_m(z) = \frac{1}{N}\mathbf{H}_m(z)\mathbf{G}_m(z) = \mathbf{I}$

4) $\mathbf{G}_p(z)\mathbf{H}_p(z) = \mathbf{H}_p(z)\mathbf{G}_p(z) = \mathbf{I}$

Biorthogonality is equal to perfect reconstruction

Summary of Orthonormality Relations

These statements are equivalent

1) $< g_i[n], g_j[n+Nm] >= \delta[i-j]\delta[m]$

2) $\mathbf{T}_s^T \cdot \mathbf{T}_s = \mathbf{T}_s \cdot \mathbf{T}_s^T = \mathbf{I}$

3) $\frac{1}{N}\mathbf{G}_m^T(z^{-1})\mathbf{G}_m(z) = \frac{1}{N}\mathbf{G}_m^T(z^{-1})\mathbf{G}_m(z) = \mathbf{I}$

4) $\mathbf{G}_p^T(z^{-1})\mathbf{G}_p(z) = \mathbf{G}_p(z)\mathbf{G}_p^T(z^{-1}) = \mathbf{I}$

$\mathbf{T}_a = \mathbf{T}_s^T$

$\mathbf{H}_m(z) = \mathbf{G}_m^T(z^{-1})$

$\mathbf{H}_p(z) = \mathbf{G}_p^T(z^{-1})$

Main Reference

M. Vetterli and J. Kovacevic:
Wavelets and subband coding
Prentice Hall, 1995.

Thank you for your attention!

Please feel free to ask questions.