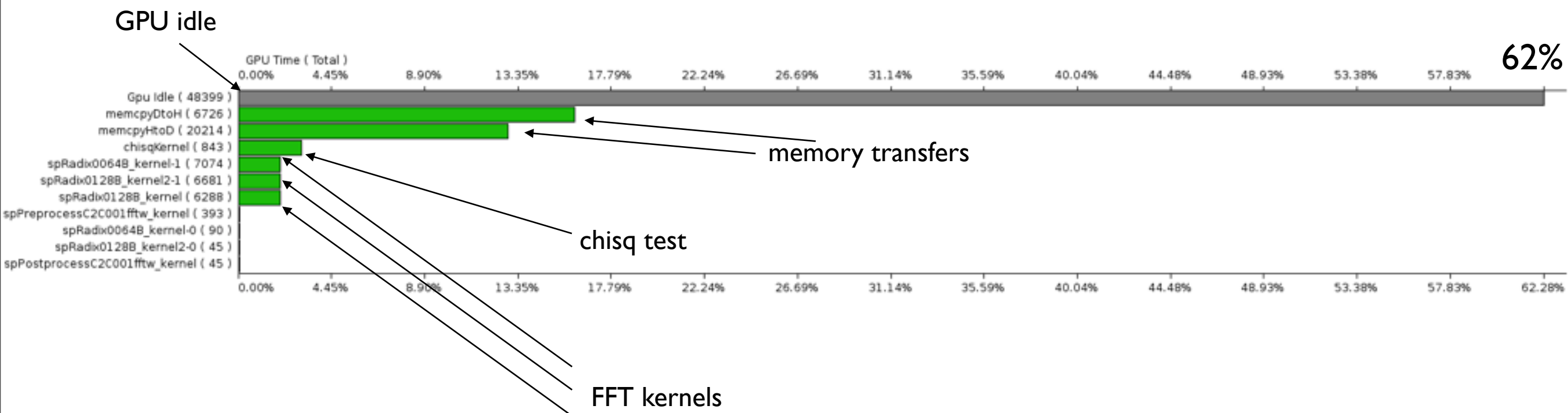


# PyCBC: a device independent approach to CBC analysis

Karsten Wiesner

## Previous work

- Acceleration of lalapps\_inspirar by GPUs obtained a **speedup factor of 15** by performing all FFTs and the chi-squared test on a GPU. (CUDA) <https://dcc.ligo.org/cgi-bin/private/DocDB/ShowDocument?docid=40432>
- Results of profiling: largest portions of time spent...
  - transferring memory to and from the GPU
  - running computations on the CPU (GPU is idle)



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## Previous work

- To optimize this, we need to implement more of the search engine (i.e., the whole hot loop) on the GPU.
- the Budapest group has shown a possible **speedup factor of 92** by porting the search engine completely to the GPU. (OpenCL)  
[http://www.grid.kfki.hu/twiki/bin/view/RmkiVirgo/GPU\\_inspiral](http://www.grid.kfki.hu/twiki/bin/view/RmkiVirgo/GPU_inspiral)
- Studying `lalapps_inspiral`, its procedural code structure and memory management do not meet the requirements of a sustainable framework for GPU accelerated CBC analysis.
  - necessary for targeting offline compute intensive searches (e.g., very large parameter spaces, coherent analyses, etc.)
- **Conclusion:** a redesign focused on transparent GPU acceleration (or future processing architectures) is needed

# ***Requirements of a novel software framework for CBC analysis***

- Primary Requirements:
  - flexible (easily reconfigurable from the top layer)
    - decouple algorithm from implementation
  - transparent processing on different architectures
  - transparent memory management
  - better readability (code shall be self explanatory ==> graph oriented processing framework)
  
- Secondary Requirements:
  - modularity and simple API
    - simple processing python objects (object oriented design)
    - new features are encapsulated in new objects or extensions of existing objects
    - robustness from unit tests
  - bindings to 3<sup>rd</sup> party libraries (e.g., lalsuite, fftw, numpy, etc.)
  - auto documentation (epydoc)

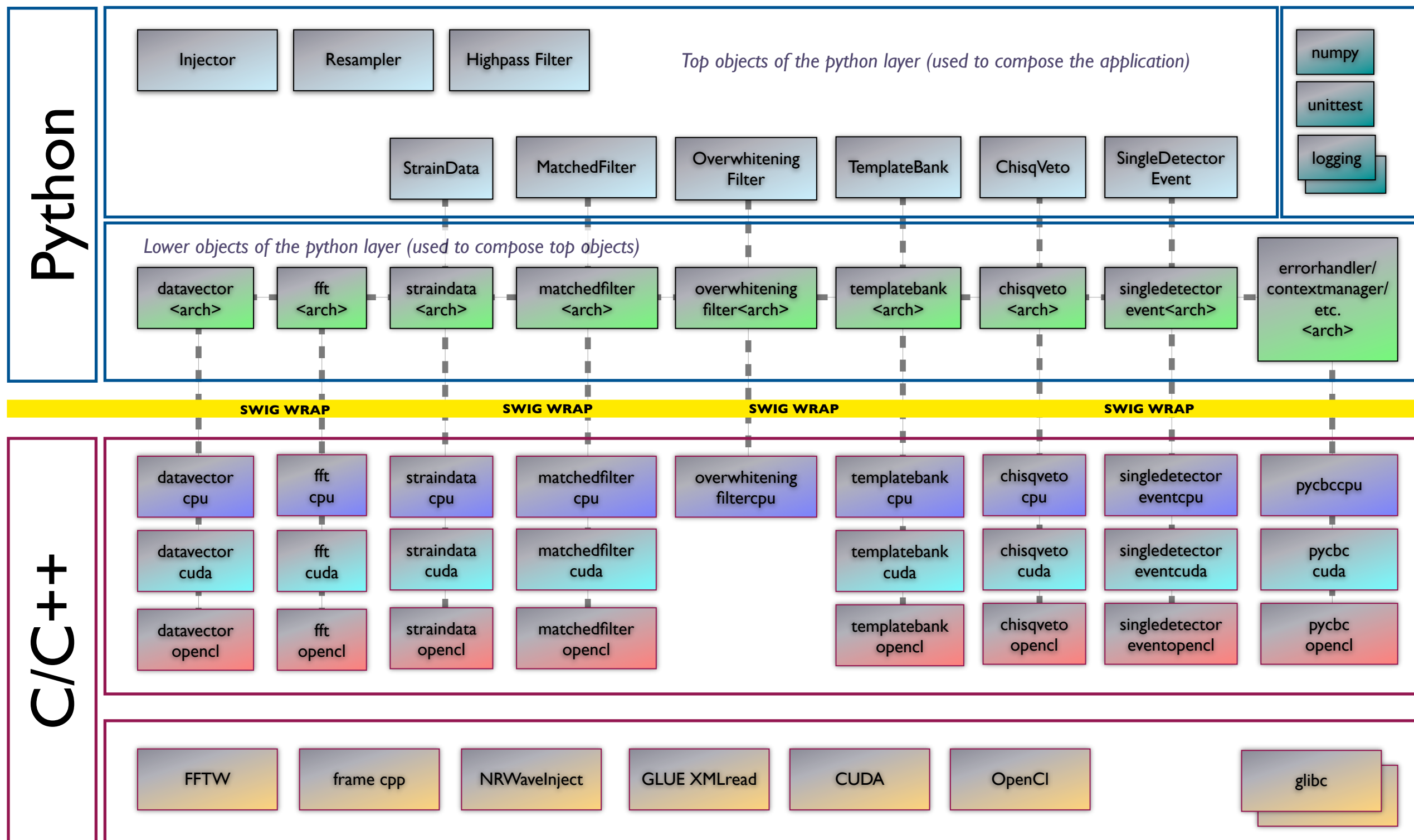
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# ***People and sites involved in Pycbc development***

- **Albert Einstein Institute Hannover**
  - Karsten Wiesner, Drew Keppel, Badri Krishnan
- **Syracuse University**
  - Duncan Brown, Alex Nitz,
- **University of Wisconsin - Milwaukee**
  - Adam Mercer
- **Abilene Christian University**
  - Josh Willis
- **MTA KFKI RMKI Budapest**
  - Bence Somhegyi, Gergely Debreczeni

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# Pycbc Layers and packages



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# Code example: Application layer of the test prototype

```
import sys
import random

# preliminary hard coded path to packages
sys.path.append('/Users/kawies/dev/src/pycbc')

from pycbc.pycbc import CPUDeviceContext as ProcessingTargetContext

from pycbc.straindata.straindata_cpu import StrainDataCpu as StrainData
from pycbc.templatebank.templatebank_cpu import TemplateBankCpu as TemplateBank
from pycbc.matchedfilter.matchedfilter_cpu import MatchedFilterCpu as
MatchedFilter
from pycbc.chisqveto.chisqveto_cpu import ChisqVetoCpu as ChisqVeto
from pycbc.singledetectorevent.singledetectorevent_cpu import
SingleDetectorEventCpu as SingleDetectorEvent
from pycbc.datavector.datavectorcpu import real_vector_single_t as
SnrResultTimeSeries

import logging

logging.basicConfig(level=logging.DEBUG,
                    format='%(name)s %(asctime)s %(levelname)s %(message)s',
                    filename='pycbc_min_pipeline.log',
                    filemode='w')

logger= logging.getLogger('pycbc.main_script')

start_message = 'Starting pycbc single detector minimal pipeline ...'
logger.debug(start_message)
print start_message

# setup straindata
search_time = 128 # typ design spec: 2048
sample_freq = 256 # typ design spec: 4096
length = search_time * sample_freq
segments = 15
gps_start_time= 871147532
gps_end_time= gps_start_time + search_time
interferometer = "H1"

# setup chisq veto
chisq_bins = 16

# setup event finder
snr_threshold = 5.5

with ProcessingTargetContext(1) as context:

    strain_data = StrainData(gps_start_time, gps_end_time,
                             segments, sample_freq,
                             interferometer, context)

    # initialize straindata w/ noise
    for i in range(length):
        tmp = random.uniform(-1,1)
        strain_data.time_series[i] = tmp

    # convert straindata to single precision
    strain_data.convert_to_single_preci()

    # segmenting straindata and transform into frequency domain
    strain_data.perform_fft_segments()
```

```
# transfer straindata to appropriate memory space on target device
strain_data.render()

# create 5 templates (testing the iterator of TemplateBank)
bank = TemplateBank(5, strain_data.segments_length,
                    strain_data.segments_delta_x, context)
logger.debug("instantiated TemplateBank w/ waveform length: {0}"
              .format(bank.waveform_length))

# create matched filter (only generate_snr() has to be implemented
# for the minimal pipeline)
matched_filter = MatchedFilter(strain_data.segments_length, context)
logger.debug("instantiated MatchedFilter w/ length: {0}".format
              (matched_filter.length))

# instantiate result vectors
snr = SnrResultTimeSeries(strain_data.segments_length,
                           strain_data.segments_delta_x, context)
logger.debug("instantiated SnrResultTimeSeries as {0}".format(repr(snr)))

# instantiate chisq_veto
chisq_veto = ChisqVeto(strain_data.segments_length, chisq_bins, context)
logger.debug("instantiated ChisqVeto as {0}".format(repr(chisq_veto)))

# instantiate event finder
events = SingleDetectorEvent(snr_threshold, context)
logger.debug("instantiated SingleDetectorEvent as {0}".format(repr(events)))

# filter the data against the template bank
for template in bank:
    htilde = bank.perform_generate_waveform(template)
    for stilde in strain_data:
        matched_filter.perform_generate_snr(stilde, htilde, snr)
        if matched_filter.max() > snr_threshold:
            chisq = chisq_veto.generate_chisq(snr, qtilde)
            events.find_events(snr, chisq)

# cluster the events across the template bank
events.cluster_events(0.1)
events.write("/path/to/output.xml")

# leaving the ProcessingTargetContext NOW (destroy the device context)
#####

end_message = '... end of pycbc single detector minimal pipeline.'
logger.debug(end_message)
print end_message
```

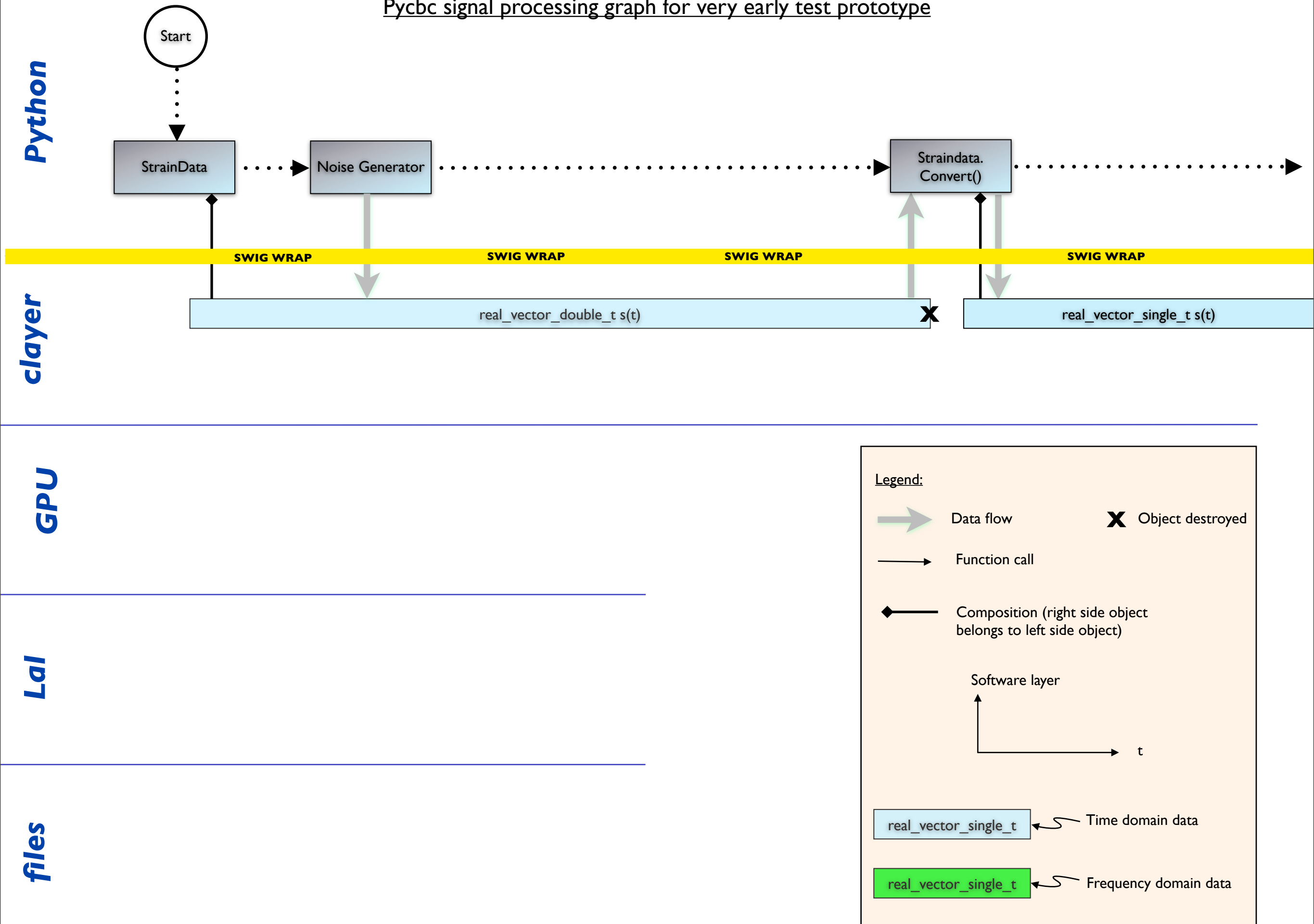


# Pycbc signal processing graphs

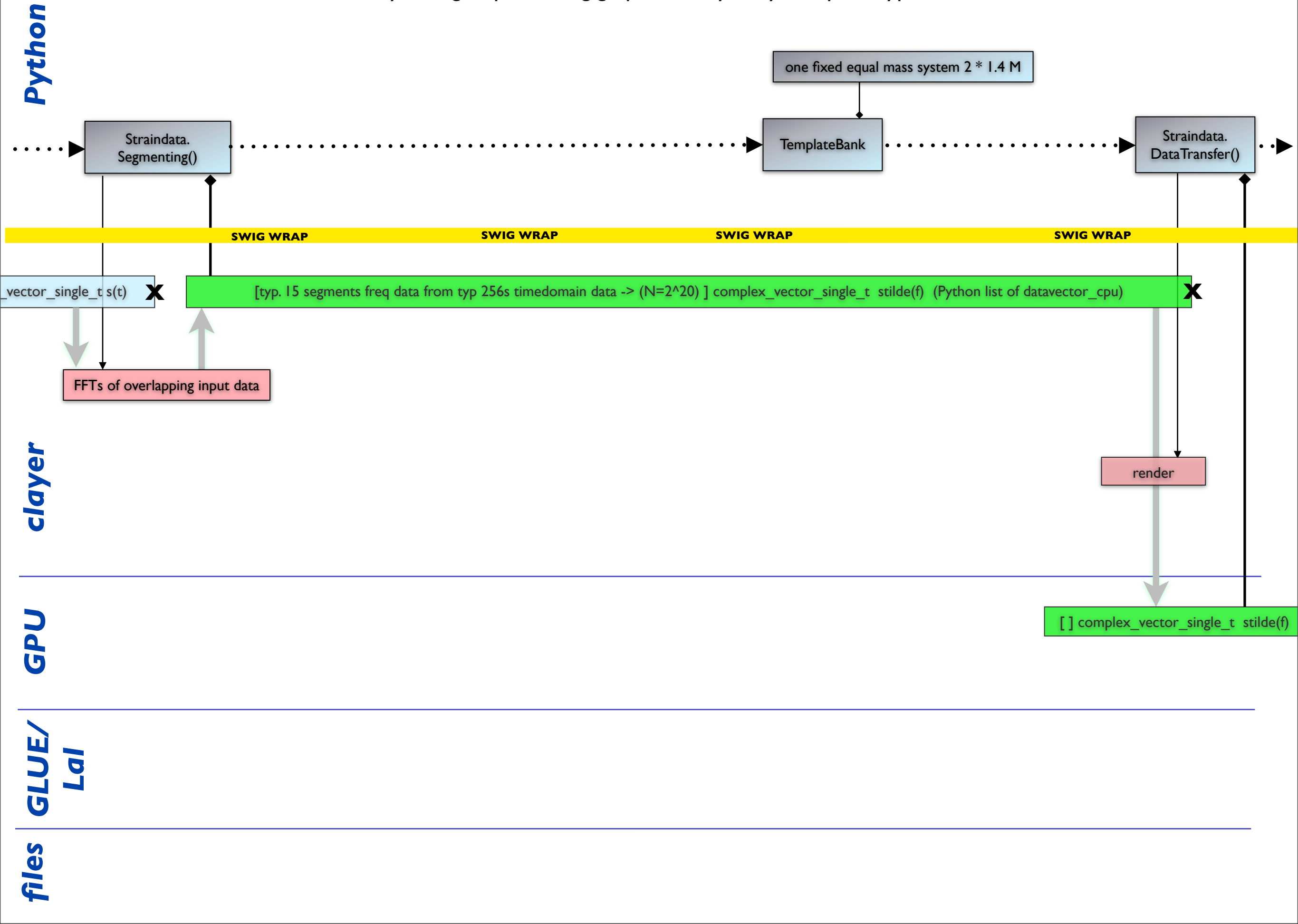
- Shows processing graph from the application programmers viewpoint
- Shows how functions and kernels are called and where they live (layers)
- Shows how data flows
- Shows memory objects
  - Where they live
  - Who is the owner
  - Which kind of data do they hold
  - How long they live



# Pycbc signal processing graph for very early test prototype



Pycbc signal processing graph for very early test prototype



# Pycbc signal processing graph for very early test prototype

Python

clayer

GPU

```
for 5 templates in bank:
```

one waveform

TemplateBank

```
for 15 Segments in data:
```

MatchedFilter

If(max>thresh)

SWIG WRAP

SWIG WRAP

SWIG WRAP

SWIG WRAP

`[] complex_vector_single_t stilde(f) (Python list of datavector_cuda)`

X

`complex_vector_single_t htilde`

X

Generate\_snr

Find\_maximum

`complex_vector_single_t qtilde (snr tilde)`

X

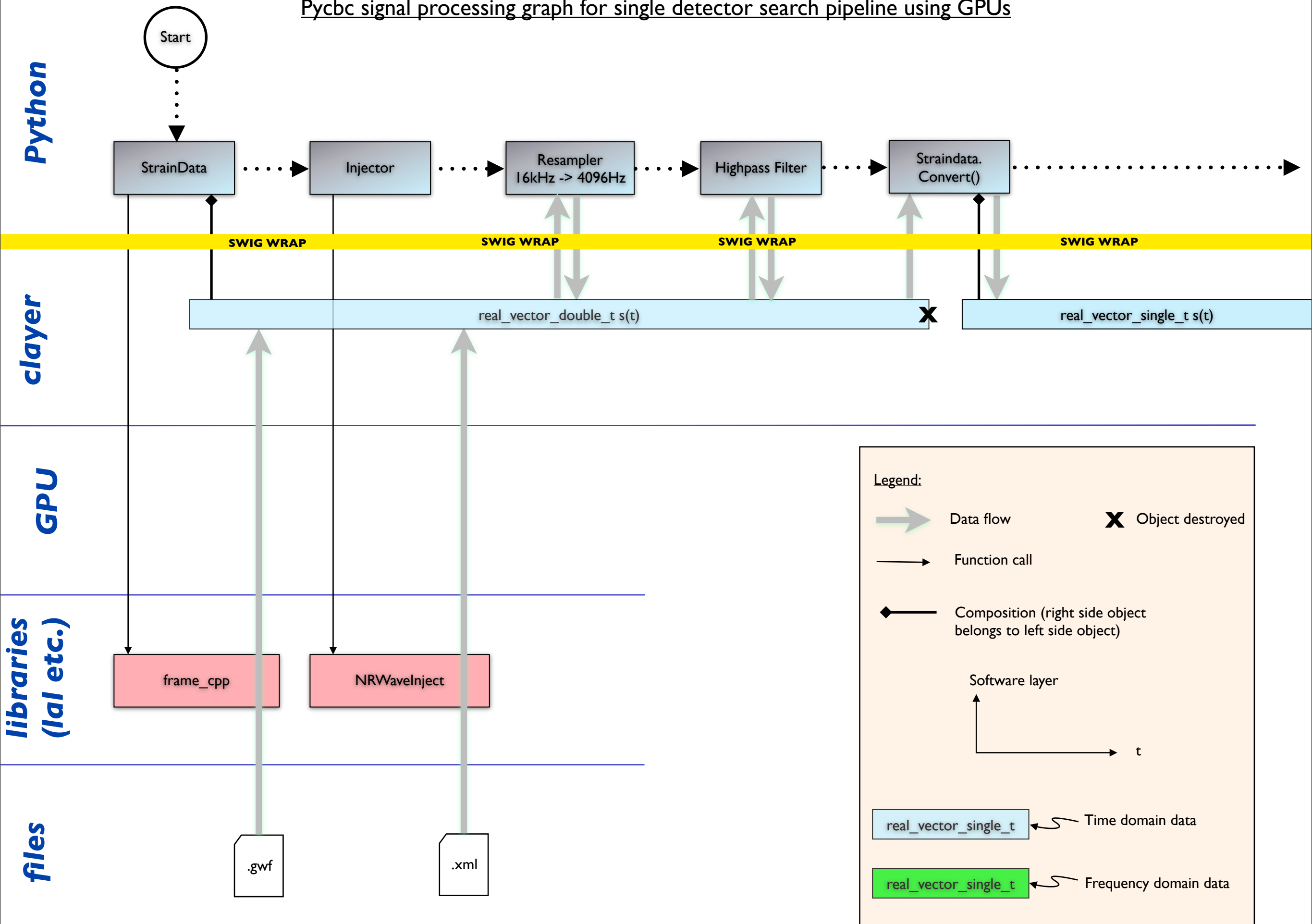
FFT

`real_vector_single_t q (snr)`

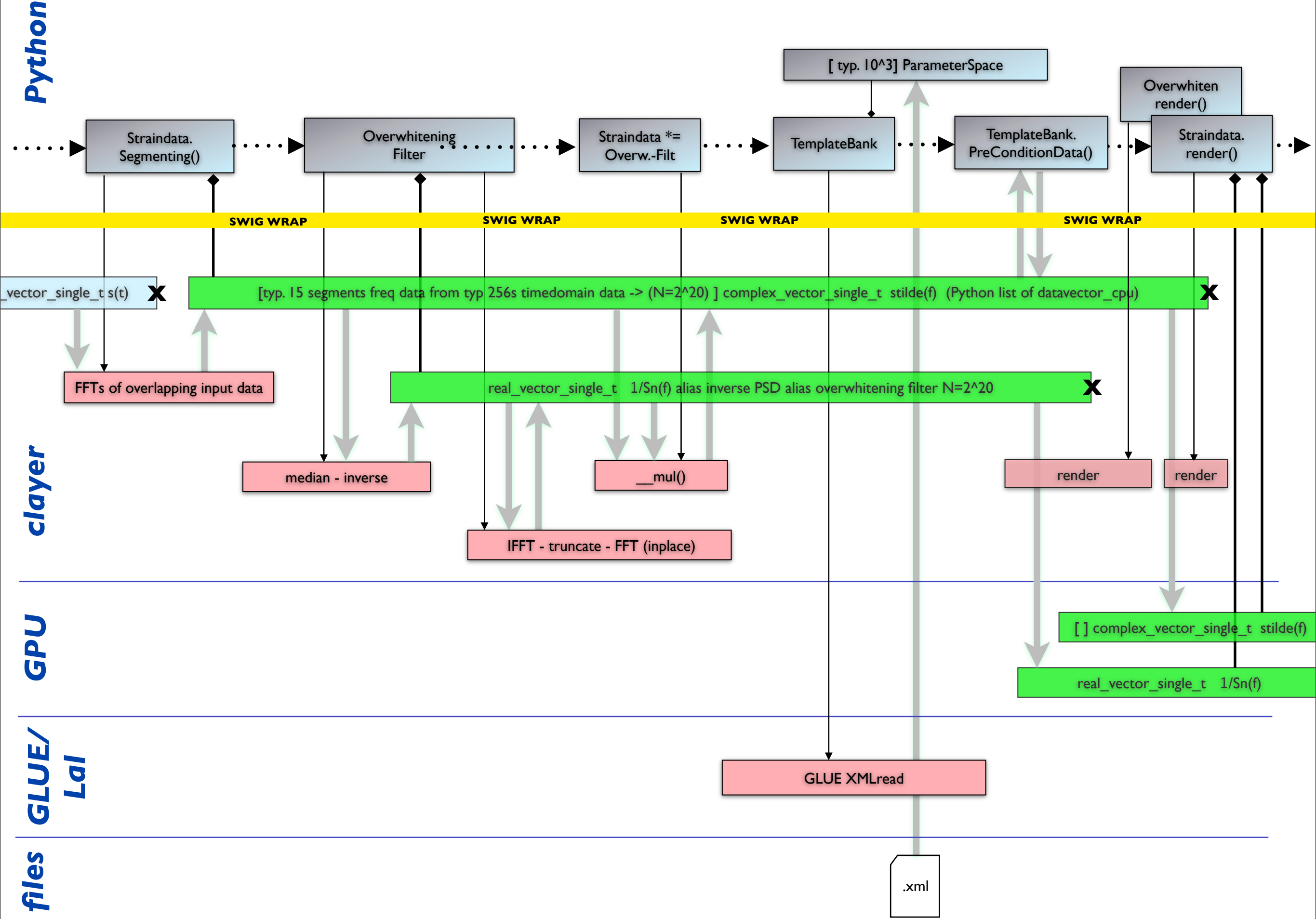
X

```
# filter the data against the template bank
for template in bank:
    htilde = bank.perform_generate_waveform(template)
    for stilde in strain_data:
        matched_filter.perform_generate_snr(snr, stilde, htilde)
        matched_filter.perform_find_max(max, snr)
```

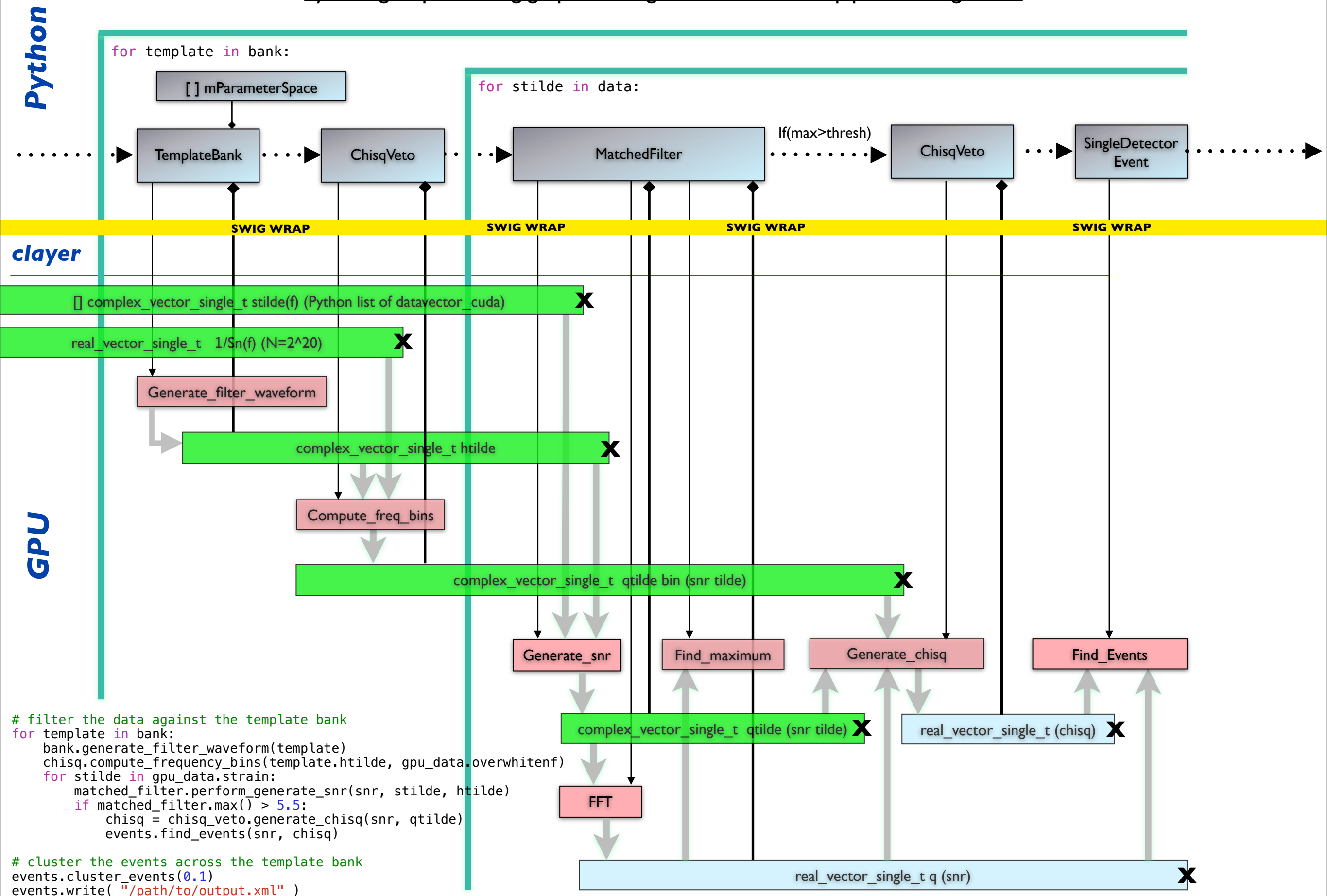
# Pycbc signal processing graph for single detector search pipeline using GPUs



Pycbc signal processing graph for single detector search pipeline using GPUs



# Pycbc signal processing graph for single detector search pipeline using GPUs



Pycbc signal processing graph for single detector search pipeline using GPUs

