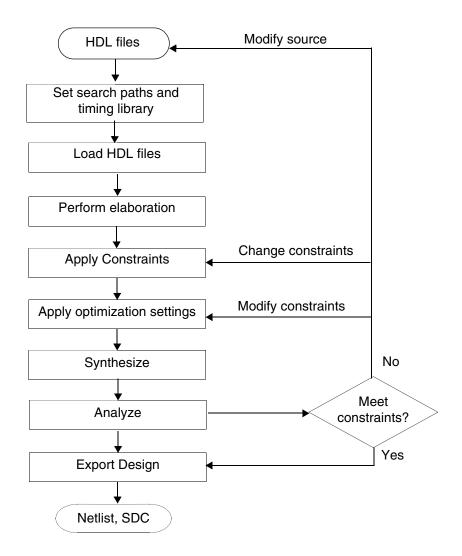
- Overview on page 18
- Tasks on page 19
  - Specifying Explicit Search Paths on page 19
  - Setting the Target Technology Library on page 20
  - □ Setting the Appropriate Synthesis Mode on page 20
  - □ Loading the HDL Files on page 21
  - □ Performing Elaboration on page 22
  - □ Applying Constraints on page 23
  - Applying Optimization Constraints on page 24
  - □ Performing Synthesis on page 25
  - □ Analyzing the Synthesis Results on page 25
  - □ Exporting the Design on page 26
  - Exiting Genus on page 26
- Recommended Flow on page 27

# **Overview**

<u>Figure 1-1</u> on page 18 shows the generic Genus work flow. The term "generic" merely illustrates that whatever flow you use, you will most likely use most or all of the steps in the generic flow. This section briefly and sequentially describes all the tasks within the work flow.

Figure 1-1 Generic Genus Work Flow



Getting Started with the Generic Flow

# **Tasks**

- Specifying Explicit Search Paths on page 19
- Setting the Target Technology Library on page 20
- Setting the Appropriate Synthesis Mode on page 20
- Loading the HDL Files on page 21
- Performing Elaboration on page 22
- Applying Constraints on page 23
- Applying Optimization Constraints on page 24
- Performing Synthesis on page 25
- Analyzing the Synthesis Results on page 25
- Exporting the Design on page 26
- Exiting Genus on page 26
- Recommended Flow on page 27

# **Specifying Explicit Search Paths**

You can specify the search paths for libraries, scripts, and HDL files. The default search path is the directory in which Genus is invoked.

To set the search paths, type the following set\_db commands:

```
genus@root:> set_db init_lib_search_path path
genus@root:> set_db script_search_path path
genus@root:> set_db init_hdl_search_path path
```

where path is the full path of your target library, script, or HDL file locations.

#### Setting the Target Technology Library

After you set the library search path, you need to specify the target technology library for synthesis using the library attribute.

To specify a single library:

```
genus@root:> set db library lib_name.lib
```

Genus will use the library named lib\_name.lib for synthesis. Ensure that you specify the library at the root-level ("/").

**Note:** If the library is not in a previously specified search path, specify the full path, as follows:

```
genus@root:> set db library /usr/local/files/lib_name.lib
```

To specify a single library compressed with gzip:

```
genus@root:> set db library lib_name.lib.gz
```

To append libraries:

```
genus@root:> set db library {lib1.lib lib2.lib}
```

After lib1.lib is loaded, lib2.lib is appended to lib1.lib. This appended library retains the lib1.lib name.

# **Setting the Appropriate Synthesis Mode**

Genus has two modes to synthesize the design. The synthesis mode is determined by the setting of the <u>interconnect mode</u> attribute:

- wireload (default) indicates to use wire-load models to drive synthesis
- ple indicates to use Physical Layout Estimators (PLEs) to drive synthesis

PLE uses physical information, such as LEF libraries, to provide better closure with backend tools.

Note: When you read in LEF files, the interconnect\_mode attribute is automatically set to ple.

#### Loading the HDL Files

Use the read\_hdl command to read HDL files into Genus. When you issue a read\_hdl command, Genus reads the files and performs syntax checks.

- To load one or more Verilog files:
  - You can read the files sequentially:

```
read_hdl file1.v
read_hdl file2.v
read hdl file3.v
```

Or you can load the files simultaneously:

```
read hdl { file1.v file2.v file3.v }
```

You can also read the design from simulation optionfiles:

```
read hdl -f optionfile
```

For more information on loading the design from optionfiles, see <u>Reading Designs in Simulation Environment</u> on page 59.



Your files may have extra, hidden characters (for example, line terminators) if they are transferred from Windows/Dos to the UNIX environment using the dos2unix command. Be sure to eliminate them because Genus will issue an error when it encounters these characters.

Getting Started with the Generic Flow

#### **Performing Elaboration**

Elaboration is only required for the top-level design. The elaborate command automatically elaborates the top-level design and all of its references. During elaboration, Genus performs the following tasks:

- Builds data structures
- Infers registers in the design
- Performs high-level HDL optimization, such as dead code removal
- Checks semantics

**Note:** If there are any gate-level netlists read in with the RTL files, Genus automatically links the cells to their references in the technology library during elaboration. You do not have to issue an additional command for linking.

At the end of elaboration, Genus displays any unresolved references (immediately after the key words Done elaborating):

```
Done elaborating '<top_level_module_name>'.
Cannot resolve reference to <ref01>
Cannot resolve reference to <ref02>
Cannot resolve reference to <ref03>
```

After elaboration, Genus has an internally created data structure for the whole design so you can apply constraints and perform other operations.

Getting Started with the Generic Flow

# **Applying Constraints**

After loading and elaborating your design, you must specify constraints. The constraints include:

- Operating conditions
- Clock waveforms
- I/O timing

You can apply constraints in several ways:

- Type them manually in the Genus shell.
- Include a constraints file.
- Read in SDC constraints.

.

Getting Started with the Generic Flow

# **Applying Optimization Constraints**

In addition to applying design constraints, you may need to use additional optimization strategies to get the desired performance goals from synthesis.

With Genus, you can perform any of the following optimizations:

- Remove designer-created hierarchies (ungrouping)
- Create additional hierarchies (grouping)
- Synthesize a sub-design
- Create custom cost groups for paths in the design to change the synthesis cost function

For example, the timing paths in the design can be classified into the following four distinct cost groups:

- Input-to-Output paths (I2O)
- Input-to-Register paths (I2C)
- Register-to-Register (C2C)
- Register-to-Output paths (C2O)

For each path group, the worst timing path drives the synthesis cost function.

Getting Started with the Generic Flow

# **Performing Synthesis**

After the constraints and optimizations are set for your design, you can proceed with synthesis.

To synthesize your design, type the following commands:

```
genus@root:> syn generic
genus@root:> syn map
```

For details on the synthesis commands, see *Command Reference*.

After these two steps, you will have a technology-mapped gate-level netlist.

#### **Analyzing the Synthesis Results**

After synthesizing the design, you can generate detailed timing and area reports using the various report\_\* commands:

- To generate a detailed area report, use <u>report\_area</u>.
- To generate a detailed gate selection and area report, use <u>report gates</u>.
- To generate a detailed timing report, including the worst critical path of the current design, use <u>report\_timing</u>.

For more information on generating reports for analysis, see <u>"Analysis and Report Commands"</u> in the *Genus Command Reference*.

#### Genus Synthesis Flows Guide Getting Started with the Generic Flow

# **Exporting the Design**

The last step in the flow involves exporting the design post synthesis to write out the gatelevel netlist, design and SDC constraints.

Note: By default, the write\_\* commands write output to stdout. If you want to save your information to a file, use the redirection symbol (>) and a filename.

To write the gate-level netlist, use the write hdl command.

```
genus@root:> write hdl > design.v
```

This command writes out the gate-level netlist to a file called design.v.

To write out the design constraints and optionally test constraints, use the write\_script command, as shown in the following example:

```
genus@root:> write script > constraints.g
```

This command writes out the constraints to the file constraints.g.

To write the design constraints in SDC format, use the write\_sdc command, as shown in the following example:

```
genus@root:> write sdc > constraints.sdc
```

This command writes the SDC constraints to a file called constraints.sdc.

Note: Because some place and route tools require different structures in the netlist, you may need to make some adjustments either before synthesis or before writing out the netlist.

To export all necessary files for the Innovus System, use the following command:

```
genus@root:> write design -innovus design_name
```

# **Exiting Genus**

There are three ways to exit Genus when you finish your session:

- Use the quit command.
- Use the exit command.
- Use the Control-c key combination twice in succession to exit the tool immediately.

# **Recommended Flow**

```
#general setup
\verb|set_db| init_lib_search_path| path|
set db init hdl search path path
#load the library
set db library library_name
#load and elaborate the design
#-----
read hdl design.v
elaborate
#specify timing and design constraints
read sdc sdc_file
#add optimization constraints
#synthesize the design
syn generic
syn map
#analyze design
report area
report timing
report gates
#export design
write hdl > dessign.vm
write sdc > constraints.sdc
write script > constraints.g
# export design for Innovus
write design [-basename string] [-gzip files] [-tcf]
[-innovus] [-hierarchical] [design]
```

# **Genus Synthesis Flows Guide** Getting Started with the Generic Flow