

IBM XL Fortran Advanced Edition for Blue Gene, V11.1



# Installation Guide



IBM XL Fortran Advanced Edition for Blue Gene, V11.1



# Installation Guide

**Note!**

Before using this information and the product it supports, be sure to read the general information under “Notices” on page 37.

**First Edition**

This edition applies to IBM XL Fortran Advanced Edition for Blue Gene/P, V11.1 (Program 5799-HJF) and IBM XL Fortran Advanced Edition for Blue Gene/L, V11.1 (Program 5799-HJG) and to all subsequent releases and modifications until otherwise indicated in new editions. Make sure you are using the correct edition for the level of the product.

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## About this document

This document contains essential information about installing IBM® XL Fortran Advanced Edition for Blue Gene®, V11.1. Read the documentation carefully before installing this product. Be sure to read the README.FIRST file, which contains the installation image layout on the CD and the README file on the CD, which contains the most current information about the product. After you install the product, you can find the README file in the *installation\_path*/xlf/bg/11.1 directory, where *installation\_path* is the location of the compiler on your system. If you install the compiler in the default location, the *installation\_path* is /opt/ibmcmp/.

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## Who should read this document

This document is intended for anyone responsible for installing IBM XL Fortran Advanced Edition for Blue Gene, V11.1.

This document addresses the needs of the majority of users who will use the basic installation method, which provides guidance during the installation process. *Basic examples* are tailored to reflect, as much as possible, the procedures for a basic installation.

This document also addresses the needs of users who want to perform a customized installation for various purposes, such as maintaining more than one version of IBM XL Fortran Advanced Edition for Blue Gene on a single system. These are users who are familiar with compiler installations and with the file structures of all versions of all compiler products installed on the system. In this document, these users are referred to as advanced users. The additional information that you will need is labeled “for advanced users”.

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## How to use this document

This document provides procedures for three main installation scenarios:

### **“Basic” installation**

This scenario allows you to install a single version of IBM XL Fortran Advanced Edition for Blue Gene to a default location. It is applicable to the majority of users, and is the recommended method of installing the product. For an overview of the steps that you need to follow to perform a basic installation, refer to “Tasks for basic installation” on page 3.

### **“Advanced” installation**

This scenario allows you to maintain multiple versions of IBM XL Fortran Advanced Edition for Blue Gene on a single system, or to install the product to a non-default location. This scenario is applicable only to advanced users, who have specialized needs; it is not recommended for the majority of users. For an overview of the steps that you need to follow to perform an advanced installation, refer to “Tasks for advanced installation” on page 4.

### **“Update” installation**

This scenario applies to users who have obtained an update package for an existing IBM XL Fortran Advanced Edition for Blue Gene, V11.1 basic or

advanced installation. For an overview of the steps that you need to follow to perform an update, refer to “Tasks for basic installation” on page 3 or “Tasks for advanced installation” on page 4, depending on the type of installation you need to update.

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## How this document is organized

This book is organized to reflect the pre-installation, installation, post-installation, and troubleshooting phases of an IBM XL Fortran installation.

*Table 1. Phases of an IBM XL Fortran installation*

Phase	Chapters	User segment
Pre-installation	Chapter 1, “Before installing IBM XL Fortran Advanced Edition for Blue Gene, V11.1,” on page 1	All users
Installation	Chapter 2, “Basic installation,” on page 9	Users who: <ul style="list-style-type: none"><li>• Want to use the simplest, most direct installation process</li><li>• Do not have any special requirements, such as the use of multiple versions of the compilers</li></ul>
	Chapter 3, “Advanced installation,” on page 13	Users who: <ul style="list-style-type: none"><li>• Want to install the compiler in a non-default location</li><li>• Want to have multiple versions of the compiler on the same system</li></ul>
	Chapter 4, “Installing an update,” on page 19	Users who want to update IBM XL Fortran V11.1 to the next fix level
Post-installation	Chapter 5, “Configuring IBM XL Fortran Advanced Edition for Blue Gene, V11.1 (for advanced users),” on page 23	Users who: <ul style="list-style-type: none"><li>• Are using the advanced, non-default method to install or update the compiler</li><li>• Need to update components previously installed to a non-default location</li></ul>
	Chapter 6, “After installing IBM XL Fortran Advanced Edition for Blue Gene, V11.1,” on page 27	All users
Product removal	Chapter 7, “Uninstalling IBM XL Fortran Advanced Edition for Blue Gene, V11.1,” on page 33	Any user who needs to remove an IBM XL Fortran compiler from the system
Troubleshooting	Chapter 8, “Troubleshooting the installation and configuration,” on page 35	Any user who needs to know how to respond to an error message or unexpected results during the installation or configuration of IBM XL Fortran

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## Conventions used in this document

### Typographical conventions

The following table explains the typographical conventions used in this document.



Table 2. *Typographical conventions*

Typeface	Indicates	Example
<b>bold</b>	Lowercase commands, executable names, compiler options and pragma directives	If you specify <b>-O3</b> , the compiler assumes <b>-qhot=level=0</b> . To prevent all HOT optimizations with <b>-O3</b> , you must specify <b>-qnohot</b> .
<i>italics</i>	Parameters or variables whose actual names or values are to be supplied by the user. Italics are also used to introduce new terms	The maximum length of the <i>trigger_constant</i> in fixed source form is 4 for directives that are continued on one or more lines.
monospace	Examples of program code, command strings, or user-defined names	Also, specify the following runtime options before running the program, with a command similar to the following: <code>export XLFRTEOPTS="err_recovery=no:langlvl=90std"</code>

## Syntax diagrams

Throughout this document, diagrams illustrate IBM XL Fortran syntax. This section will help you to interpret and use those diagrams.

- Read the syntax diagrams from left to right, from top to bottom, following the path of the line.

The ►— symbol indicates the beginning of a command, directive, or statement.

The —► symbol indicates that the command, directive, or statement syntax is continued on the next line.

The ►— symbol indicates that a command, directive, or statement is continued from the previous line.

The —►◄ symbol indicates the end of a command, directive, or statement.

Fragments, which are diagrams of syntactical units other than complete commands, directives, or statements, start with the |— symbol and end with the —| symbol.

IBM XL Fortran extensions are marked by a number in the syntax diagram with an explanatory note immediately following the diagram.

Program units, procedures, constructs, interface blocks and derived-type definitions consist of several individual statements. For such items, a box encloses the syntax representation, and individual syntax diagrams show the required order for the equivalent Fortran statements.

- Required items are shown on the horizontal line (the main path):

►—keyword—*required\_argument*—►◄

- Optional items are shown below the main path:

►—keyword—*optional\_argument*—►◄

**Note:** Optional items (not in syntax diagrams) are enclosed by square brackets ([ and ]). For example, [UNIT=]u

- If you can choose from two or more items, they are shown vertically, in a stack.

If you *must* choose one of the items, one item of the stack is shown on the main path.



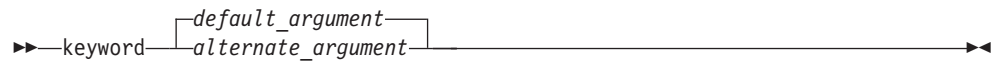
If choosing one of the items is optional, the entire stack is shown below the main path.



- An arrow returning to the left above the main line (a repeat arrow) indicates that you can make more than one choice from the stacked items or repeat an item. The separator character, if it is other than a blank, is also indicated:



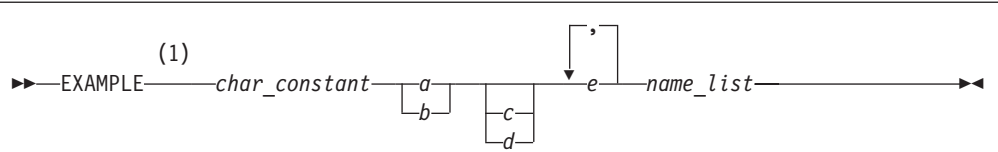
- The item that is the default is shown above the main path.



- Keywords are shown in nonitalic letters and should be entered exactly as shown.
- Variables are shown in italicized lowercase letters. They represent user-supplied names or values. If a variable or user-specified name ends in *\_list*, you can provide a list of these terms separated by commas.
- If punctuation marks, parentheses, arithmetic operators, or other such symbols are shown, you must enter them as part of the syntax.

### Sample syntax diagram

The following is an example of a syntax diagram with an interpretation:



#### Notes:

1 IBM extension

Interpret the diagram as follows:

- Enter the keyword `EXAMPLE`.
- `EXAMPLE` is an IBM extension.
- Enter a value for `char_constant`.
- Enter a value for `a` or `b`, but not for both.
- Optionally, enter a value for `c` or `d`.
- Enter at least one value for `e`. If you enter more than one value, you must put a comma between each.
- Enter the value of at least one `name` for `name_list`. If you enter more than one value, you must put a comma between each. (The `_list` syntax is equivalent to the previous syntax for `e`.)

### Examples and basic examples

The examples in this document are labelled as either “Example” or “Basic example”. *Basic examples* are intended to document a procedure as it would be performed during a basic installation, with little or no modification.

## Related information

### IBM XL Fortran publications

IBM XL Fortran provides product documentation in the following formats:

- README files

README files contain late-breaking information, including changes and corrections to the product documentation. README files are located by default in the *installation\_path*/xlf/bg/11.1 directory and in the root directory of the installation CD.

- Installable man pages

Man pages are provided for the compiler invocations and all command-line utilities provided with the product. Instructions for installing and accessing the man pages are provided in this document.

- Information center

An information center of IBM XL Fortran HTML documentation is viewable on the web at: <http://publib.boulder.ibm.com/infocenter/complbgpl/v9v111/index.jsp>

- PDF documents

PDF documents are located by default in the `/opt/ibmcmp/xlf/bg/11.1/doc/language/pdf/` directory, where *language* is either `en_US` or `en_US.utf8`. The PDFs are also available on the Web at:

<http://www.ibm.com/software/awdtools/fortran/xlfortran/library>

More documentation related to IBM XL Fortran, including redbooks, white papers, tutorials, and other articles, is available on the Web at:

<http://www.ibm.com/software/awdtools/fortran/xlfortran/library>

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## Technical support

Additional technical support is available from the IBM XL Fortran Support page. This page provides a portal with search capabilities to a large selection of Technotes, and other support documents. You can find the IBM XL Fortran Support page on the Web at:

<http://www.ibm.com/software/awdtools/fortran/xlfortran/support>

If you cannot find what you need, you can e-mail:

[compinfo@ca.ibm.com](mailto:compinfo@ca.ibm.com)

For the latest information about IBM XL Fortran, visit the product information site at:

<http://www.ibm.com/software/awdtools/fortran/xlfortran>

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## Future updates and documentation errata

Additional information and documentation errata for all future updates to this product can be found at the following URL:

- Readme updates for IBM XL Fortran Advanced Edition for Blue Gene/L™, V11.1
  - <http://www.ibm.com/support/docview.wss?uid=swg21266094>
- Readme updates for IBM XL Fortran Advanced Edition for Blue Gene/P™, V11.1
  - <http://www.ibm.com/support/docview.wss?uid=swg21266093>

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## How to send your comments

Your feedback is important in helping to provide accurate and high-quality information. If you have any comments about this document or any other IBM XL Fortran documentation, send your comments by e-mail to:

[compinfo@ca.ibm.com](mailto:compinfo@ca.ibm.com)

Be sure to include the name of the document, the part number of the document, the version of IBM XL Fortran, and, if applicable, the specific location of the text you are commenting on (for example, a page number or table number).

**Note:** When you send information to IBM, you grant IBM a nonexclusive right to use or distribute the information in any way it believes appropriate without incurring any obligation to you.

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## Chapter 1. Before installing IBM XL Fortran Advanced Edition for Blue Gene, V11.1

This installation guide covers both IBM XL Fortran Advanced Edition for Blue Gene/L, V9.0 and IBM XL Fortran Advanced Edition for Blue Gene/P, V9.0. The term IBM XL Fortran Advanced Edition for Blue Gene, V9.0 will refer to both /L and /P. /L and /P will be explicitly specified when there is a difference between the two products.

Before you install IBM XL Fortran Advanced Edition for Blue Gene, V11.1:

- Consult the product README file for any last minute updates you may need to be aware of.
- Familiarize yourself with the installation image, which contains the installable compiler packages, and a utility program for installation.
- Determine the tasks you need to perform, depending on your installation requirements.
- Become either the root user or a user with administrator privileges.
- Ensure that system prerequisites are met and that all required software packages are installed.

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### The installation image and packages

The IBM XL Fortran Advanced Edition for Blue Gene, V11.1 installation image is available on an installation CD.

The image includes:

- READMEs, license agreement files, and documentation.
- A set of RPM packages. See “Installation packages.”
- An installation tool, `xlfr_install`, to install and configure the compiler for a basic installation. See “Tasks for basic installation” on page 3.

**Note:** IBM XL Fortran Advanced Edition for Blue Gene/L and IBM XL Fortran Advanced Edition for Blue Gene/P have the same installation path. This is due to the fact that the two compilers are each supported on different platforms:

- **Blue Gene/L** is supported on SUSE Linux® Enterprise Server 9 Service Pack 3 (SLES9 SP3) for IBM POWER™
- **Blue Gene/P** is supported on SUSE Linux Enterprise Server 10 Service Pack 1 10 (SLES10 SP1) for IBM POWER

### Installation packages

Table 3 on page 2 lists the packages that are supplied with the installation image, and the locations to which they are installed by default during a basic installation. (For the rules on installing packages to custom, non-default locations, see Table 11 on page 16.)

You can use the **rpm** utility to review the packages. For example, to view package information and its file list, issue the following **rpm** query command:

`rpm -qip package_name`

*Table 3. IBM XL Fortran for Blue Gene packages and default installation locations*

Package Name	Package Description	Default installation location
xlsmp.bg.msg.rte	IBM SMP messages package	/opt/ibmcmp/msg/bg/
xlsmp.bg.rte	IBM SMP runtime package	/opt/ibmcmp/lib/bg/ /opt/ibmcmp/lib64/bg/
xlsmp.bg.lib	IBM SMP static library package	/opt/ibmcmp/xlsmp/bg/1.7
xlmass.bg.lib	IBM Mathematical Acceleration Subsystem (MASS) package	/opt/ibmcmp/xlmass/bg/4.4
xlf.bg.rte	IBM XL Fortran runtime package	/opt/ibmcmp/lib/bg/ /opt/ibmcmp/lib64/bg/
xlf.bg.rte.lnk	IBM XL Fortran runtime links package	/opt/ibmcmp/xlf/bg/11.1/
xlf.bg.msg.rte	IBM XL Fortran runtime messages package	/opt/ibmcmp/msg/bg/
xlf.bg.lic	IBM XL Fortran license package	/opt/ibmcmp/xlf/bg/11.1/
xlf.bg.lib	IBM XL Fortran compiler libraries package	/opt/ibmcmp/xlf/bg/11.1/
xlf.bg.cmp	IBM XL Fortran compiler package	/opt/ibmcmp/xlf/bg/11.1/
xlf.bg.samples	IBM XL Fortran samples package	/opt/ibmcmp/xlf/bg/11.1/samples/
xlf.bg.help.pdf	IBM XL Fortran Help pdf documentation package	/opt/ibmcmp/xlf/bg/11.1/doc/
xlf.bg.man	IBM XL Fortran compiler man pages	/opt/ibmcmp/xlf/bg/11.1/man/

## National language support

IBM XL Fortran Advanced Edition for Blue Gene, V11.1 messages support the following language locales:

- en\_US
- en\_US.utf8

English is the default national language and en\_US is the default locale. To enable the error messages for en\_US.utf8, see “Enabling the IBM XL Fortran Advanced Edition for Blue Gene error messages” on page 29.

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## Determining the tasks you need to perform

You can use the tables provided in the following sections to help you find the information you need as you install and configure the product.

### Tasks for basic installation

It is highly recommended that you use the "basic", or default method of installation as long as all of the following are true:

- You are maintaining a single version of the product on your system, with or without IBM XL C/C++ Advanced Edition for Blue Gene, V9.0.

**Note:** IBM XL Fortran Advanced Edition for Linux is not considered to be the same product as IBM XL Fortran Advanced Edition for Blue Gene. Therefore, IBM XL Fortran Advanced Edition for Blue Gene, V11.1 can co-reside with compiler products for Linux with no additional installation requirements. However, IBM XL Fortran Advanced Edition for Linux runtime libraries and IBM XL Fortran Advanced Edition for Blue Gene runtime libraries share a common name. Setting the ***LD\_LIBRARY\_PATH*** environment variable may lead to the incorrect runtime library being called. Setting the ***LD\_LIBRARY\_PATH*** in this scenario is unsupported.

- You are installing the product to the default location, /opt/ibmcmp/.
- The Blue Gene tool chain is installed in the default location:
  - The Blue Gene/L tool chain default path is /bgl/BlueLight/ppcfloor.
  - The Blue Gene/P tool chain default path is /bgsys/drivers/ppcfloor.

If these conditions match your needs, the basic installation is the easiest and fastest method, as it allows you to automatically uninstall any previously installed IBM XL Fortran for Blue Gene compiler, install the latest version, and configure the compiler, all through the use of a single installation tool.

If you are installing IBM XL Fortran Advanced Edition for Blue Gene, V11.1 for the first time, perform the steps listed in Table 4.

If you are installing an update to IBM XL Fortran Advanced Edition for Blue Gene, V11.1, perform the steps listed in Table 5 on page 4.

*Table 4. Steps for basic installation*

Task	For more information, see . . .
Become either the root user or a user with administrator privileges.	Documentation supplied with the operating system.
Ensure that all system prerequisites are satisfied.	"System prerequisites" on page 5
Uninstall previously installed packages of the same product type.	Chapter 2, "Basic installation," on page 9
Use the xlf_install tool to accept or decline the license.	Chapter 2, "Basic installation," on page 9
Use the xlf_install tool to install and configure the compiler, using the default paths.	Chapter 2, "Basic installation," on page 9
Confirm that the compiler packages were successfully installed, and test the installation.	<ul style="list-style-type: none"><li>• "Querying for installed packages" on page 27</li><li>• "Testing the installation" on page 27</li></ul>
Enable the compiler man pages.	"Enabling the man pages" on page 28

Table 4. Steps for basic installation (continued)

Task	For more information, see . . .
If your system locale and/or encoding is <i>not</i> English (en_US), enable the compiler error messages. Otherwise, you can skip this step.	"Enabling the IBM XL Fortran Advanced Edition for Blue Gene error messages" on page 29
(Optional) If you did not choose to create symbolic links to the compiler invocation commands during the installation process, set up the environment to locate the invocation commands without the full path. Otherwise, you can skip this step.	"Setting up the environment for the invocation commands" on page 30

Table 5. Steps for basic installation: update installation

Task	For more information, see . . .
Become either the root user or a user with administrator privileges.	Documentation supplied with the operating system.
Use the xlf_install tool to install the update packages.	"Running the xlf_install utility to update a basic installation" on page 19
Confirm that the compiler packages were successfully installed, and test the installation.	<ul style="list-style-type: none"> <li>• "Querying for installed packages" on page 27</li> <li>• "Testing the installation" on page 27</li> </ul>
(Optional) If you did not choose to create symbolic links to the compiler invocation commands during the update process, set up the environment to locate the invocation commands without the full path. Otherwise, you can skip this step.	"Setting up the environment for the invocation commands" on page 30

## Tasks for advanced installation

You will need to use the "advanced" method of installation in the following cases:

- You are maintaining multiple versions of the same product on a single system.
- You are installing the product to a non-default location.
- The Blue Gene tool chain is installed in a non-default location.

If any of these conditions is true, you need to follow an "advanced" installation method which requires that you separately install and configure the compiler. You may also need to manually uninstall previous versions of the compiler from your system.

When installing IBM XL Fortran Advanced Edition for Blue Gene, V11.1 for the first time, perform the steps listed in Table 6. If you are installing an update to IBM XL Fortran Advanced Edition for Blue Gene, V11.1, perform the steps listed in Table 7 on page 5.

Table 6. Steps for advanced installation

Task	For more information, see . . .
Become either the root user or a user with administrator privileges.	Documentation supplied with the operating system.
If you do not need to maintain multiple versions of the product on your system, remove any existing versions of IBM XL Fortran for Blue Gene.	Chapter 7, "Uninstalling IBM XL Fortran Advanced Edition for Blue Gene, V11.1," on page 33



Table 6. Steps for advanced installation (continued)

Task	For more information, see . . .
Ensure that all system prerequisites are satisfied.	"System prerequisites"
Use one of the advanced installation methods to install the compiler.	Chapter 3, "Advanced installation," on page 13
Use the <b>new_install</b> or <b>xlfc_configure</b> tool to configure the compiler.	Chapter 5, "Configuring IBM XL Fortran Advanced Edition for Blue Gene, V11.1 (for advanced users)," on page 23
Confirm that the compiler packages were successfully installed, and test the installation.	<ul style="list-style-type: none"> <li>• "Querying for installed packages" on page 27</li> <li>• "Testing the installation" on page 27</li> </ul>
Enable the compiler man pages.	"Enabling the man pages" on page 28
If your system locale is <i>not</i> en_US, enable the compiler error messages for en_US.utf8. Otherwise, you can skip this step.	"Enabling the IBM XL Fortran Advanced Edition for Blue Gene error messages" on page 29
(Optional) Set up the environment to locate the invocation commands without the full path.	"Setting up the environment for the invocation commands" on page 30

Table 7. Steps for advanced installation: update installation

Task	For more information, see . . .
Become either the root user or a user with administrator privileges.	Documentation supplied with the operating system.
Install the update packages to the non-default location.	"Installing IBM XL Fortran Advanced Edition for Blue Gene, V11.1 to co-reside with earlier versions in separate locations on the same system" on page 15
Configure the compiler.	Chapter 5, "Configuring IBM XL Fortran Advanced Edition for Blue Gene, V11.1 (for advanced users)," on page 23
Confirm that the compiler packages were successfully installed, and test the installation.	<ul style="list-style-type: none"> <li>• "Querying for installed packages" on page 27</li> <li>• "Testing the installation" on page 27</li> </ul>
(Optional) Set up the environment to locate the invocation commands without the full path.	"Setting up the environment for the invocation commands" on page 30

## System prerequisites

The following are the requirements for installing IBM XL Fortran Advanced Edition for Blue Gene, V11.1:

### Blue Gene/L

- **Operating system:**
  - SUSE Linux Enterprise Server 9 Service Pack 3 (SLES9 SP3) for IBM POWER
- **Storage:**
  - Approximately 500 MB for product packages
  - Minimum of 2GB Hard Drive for paging
  - Minimum of 512 MB for temporary files

**Note:** High levels of optimization can require more space for paging and temporary files.

To verify that you have enough hard disk space available, see the procedure in “Verifying the amount of hard disk space available” on page 7.

### Blue Gene/P

- **Operating system:**

- SUSE Linux Enterprise Server 10 Service Pack 1 (SLES10 SP1) for IBM POWER

- **Storage:**

- Approximately 500 MB for product packages
- Minimum of 2GB Hard Drive for paging
- Minimum of 512 MB for temporary files

**Note:** High levels of optimization can require more space for paging and temporary files.

To verify that you have enough hard disk space available, see the procedure in “Verifying the amount of hard disk space available” on page 7.

- **Required software:**

- Blue Gene tool chain and runtime environment packages. For information on these packages, see the redbooks referenced in the preface of this document, or contact your system administrator.
- GNU and Perl packages, as listed in the following tables. To verify that the required packages are installed, see the procedure in “Verifying that the required GNU and Perl packages are installed” on page 8.

*Table 8. Required GNU and Perl packages for the SLES9 SP2 operating system*

Package name	Version requirements
gcc	3.3.3
gcc-c++	3.3.3
gcc-64bit	9
glibc	2.3.3
glibc-64bit	9
glibc-devel-64bit	9
libgcc	3.3.3
libgcc-64bit	9
libstdc++	3.3.3
libstdc++-64bit	9
libstdc++-devel-64bit	9
Perl	5.0 or greater <b>Note:</b> Perl V5.0 is shipped and automatically installed with the SLES9 SP2 operating system.

*Table 9. Required GNU and Perl packages for the SLES10 SP1 operating system*

Package name	Version requirements
gcc	4.1.2
gcc-c++	4.1.2
glibc	2.4

Table 9. Required GNU and Perl packages for the SLES10 SP1 operating system (continued)

glibc-64bit	2.4
glibc-devel	2.4
glibc-devel-64bit	2.4
libgcc	4.1.2
libgcc-64bit	4.1.2
libstdc++	4.1.2
libstdc++-devel	4.1.2
libstdc++-64bit	4.1.2
libstdc++-devel-64bit	4.1.2
Perl	5.0 or greater <b>Note:</b> Perl V5.8 is shipped and automatically installed with the SLES10 SP1 operating system.

- **Other software:**

- If you are installing the documentation that is packaged with IBM XL Fortran Advanced Edition for Blue Gene, V11.1 you will need a graphical desktop environment (such as K Desktop Environment or GNOME) that supports web browsers and PDF viewers
- A frames-capable HTML browser (to access help and other web pages)
- PDF viewer (to access PDF documentation)

## Blue Gene tool chain

IBM XL Fortran Advanced Edition for Blue Gene, V11.1 requires the Blue Gene tool chain for cross-compilations.

- The Blue Gene/L tool chain default path is /bgl/BlueLight/ppcfloor.
- The Blue Gene/P tool chain default path is /bgsys/drivers/ppcfloor.

It is recommended that you install the tool chain to the default directory.

If the tool chain is not installed on your system, you will be able to complete the installation of IBM XL Fortran Advanced Edition for Blue Gene, V11.1, however, configuration will fail.

## Verifying the amount of hard disk space available

IBM XL Fortran Advanced Edition for Blue Gene, V11.1 requires about 500 MB of hard disk storage space. This amount accommodates the optional samples and documentation that are shipped with the product.

You can use the following command to determine the amount of space available in the default installation location (/opt/ibmcmp/):

```
df -h /opt
```

If you plan to install the compiler to a non-default location, you can use the following command:

```
df -h installation_path
```

where *installation\_path* represents the non-default location.

## Verifying that the required GNU and Perl packages are installed

Before you can install IBM XL Fortran for Blue Gene, V11.1 you should verify that the required versions of GNU and Perl packages were installed with the operating system. For a list of the required packages, see Table 8 on page 6.

For a list of the required packages for each supported Linux distribution, see one of the following:

### Blue Gene/L

- Table 8 on page 6 Required GNU and Perl packages for the SLES9 SP3 operating system

### Blue Gene/P

- Table 9 on page 6: Required GNU and Perl packages for the SLES10 SP1 operating system

You can use the following command to verify that the correct versions of the required packages are installed.

```
rpm -q $package --qf="%{version}\n"
```

### Example: Determining the installed version of gcc-c++

To see whether gcc-c++ is installed, query for the gcc-c++ package as follows:

```
rpm -qa | grep gcc-c++
```

If gcc-c++ version 4.1.2 is installed, you will get a result similar to the following output:

```
gcc-c++-4.1.2-43.24
```

---

## Chapter 2. Basic installation

IBM XL Fortran provides an interactive utility, `xlf_install`, that walks you through a basic installation. You can use `xlf_install` to:

- Accept or decline the license agreement. If you accept the agreement, the license files will be output to .txt files for your future reference. If you decline the agreement, the installation process will exit without installing the compiler and no files will have been written to your machine.

You can use `xlf_install` to do any of the following:

- Install IBM XL Fortran Advanced Edition for Blue Gene, V11.1 on a system with no IBM XL compiler currently installed.
- Install IBM XL Fortran Advanced Edition for Blue Gene, V11.1 to co-reside with an existing version of IBM XL Fortran for Blue Gene.
- Install IBM XL Fortran Advanced Edition for Blue Gene, V11.1 on a system where IBM XL C/C++ Advanced Edition for Blue Gene, V9.0 is already installed.

In this case, both compilers will use the IBM MASS library provided with IBM XL Fortran for Blue Gene.

(For information about installing IBM XL C/C++ Advanced Edition for Blue Gene, V9.0 refer to the *IBM XL C/C++ Advanced Edition for Blue Gene, V9.0 Installation Guide* )

- Install an update on a system where IBM XL C/C++ Advanced Edition for Blue Gene, V9.0 has already been installed.

In this case, use the procedure in “Running the `xlf_install` utility to update a basic installation” on page 19.

You should use the `xlf_install` utility to install IBM XL Fortran Advanced Edition for Blue Gene, V11.1 as long as *all* of the following conditions apply:

- You are installing the compiler to the default location, which is  
`/opt/ibmcmp/`
- You agree to remove any previously installed IBM XL Fortran for Blue Gene components.
- The Blue Gene tool chain is installed in the default location:
  - The Blue Gene/L tool chain default path is `/bgl/BlueLight/ppcfloor`.
  - The Blue Gene/P tool chain default path is `/bgsys/drivers/ppcfloor`.

If any of these conditions does not apply, do *not* use the `xlf_install` utility. Instead, see the procedures in Chapter 3, “Advanced installation,” on page 13.

---

### Running the `xlf_install` utility for a new installation

The `xlf_install` utility is located in the root directory of the installation image.

**Note:** Because the `xlf_install` utility is written in Perl, you must ensure that Perl is installed on your system before you run the utility. See “Verifying that the required GNU and Perl packages are installed” on page 8.

When you run the `xlf_install` utility for a new installation, it does the following:

- Checks for all prerequisite software packages
- Checks for the existence of the Blue Gene tool chain in the default location
- Uninstalls any previously installed IBM XL Fortran for Blue Gene components
- Installs all compiler packages into the default location
- Automatically invokes the **new\_install** utility, which installs the license file and generates the default configuration file
- Optionally creates symbolic links in `/usr/bin/` to the compiler invocation commands
- Generates an installation log in the `/tmp/` directory

To run the `xl_f_install` utility to install IBM XL Fortran Advanced Edition for Blue Gene, V11.1:

1. Assuming that the product CD is mounted at the `/cdrom` location in the system, issue the following commands:

```
cd /cdrom
./xl_f_install
```

For additional arguments that you can specify for `xl_f_install`, see “`xl_f_install` options” on page 11.

- If another instance of IBM XL Fortran Advanced Edition for Blue Gene is detected on your system, you are prompted to uninstall it. Confirm that you want to proceed with the uninstallation. If you choose not to uninstall the existing instance of the compiler, the installation process will end.
- If other versions of the IBM SMP and MASS packages are detected on your system either alone or as part of an IBM XL C/C++ Advanced Edition for Blue Gene, V9.0 installation, you are prompted to uninstall them. Confirm that you want to proceed with uninstalling the existing IBM SMP and MASS packages. If you choose not to uninstall the previously installed components, the installation process will terminate.

**Note:** `xl_f_install` will uninstall these packages from their existing location and reinstall them to the default location, `/opt/ibmcmp/`. Therefore, if they were previously installed in a non-default location as part of an IBM XL C/C++ Advanced Edition for Blue Gene installation, you will need to run **vac\_configure** to reconfigure the IBM XL C/C++ compiler to point to the default location for these packages. For procedures, see “Running the **vac\_configure** utility directly” in the *IBM XL C/C++ Advanced Edition for Blue Gene, V9.0 Installation Guide*.

2. You are presented with the licensing agreement and licensing information. Read the licensing agreement and licensing information. If you agree to the licensing terms, accept the license agreement and licensing information to continue installation.

You are prompted to create symbolic links for the compiler invocations in the `/usr/bin/` directory.

3. Optionally, create the symbolic links.

**Note:** An alternative to this step is to add the path that contains the compiler invocations to the `PATH` environment variable. See “Setting the `PATH` environment variable to include the path to the compiler invocations” on page 30.

If you chose to create symbolic links, the following links are created in the `/usr/bin/` subdirectory:

**Blue Gene/L symbolic links**

- blrts\_xlf
- blrts\_xlf90
- blrts\_xlf95
- blrts\_xlf2003
- bgxlf
- bgxlf90
- bgxlf95
- bgxlf2003

#### Blue Gene/P symbolic links

- bgxlf
- bgxlf\_r
- bgxlf90
- bgxlf90\_r
- bgxlf95
- bgxlf95\_r
- bgxlf2003
- bgxlf2003\_r

**Note:** Some command links are not created in `/usr/bin/`, either because they might delete user-defined, IBM XL Fortran for Linux or GCC-related invocations, or because they are not compiler invocation commands. These include:

- f77, f90, f95, fort77, f2003, blrts\_f77, blrts\_fort77, blrts\_f95, blrts\_f2003, bgf77, bgfort77, bgf90, bgf95, bgf2003
- cleanpdf, mergepdf, new\_install, resetpdf, showpdf, xlf\_configure

If all packages are successfully installed:

- A message is displayed confirming the successful installation.
- The configuration file is generated. Its location is `/etc/opt/ibmcmp/xlf/bg/11.1/xlf.cfg`. Any previously generated configuration file is renamed and saved in the same directory.
- The installation log is moved to its permanent location: `/opt/ibmcmp/xlf/bg/11.1/xlf_install.log`.

## xlf\_install options

The `xlf_install` utility provides the following options:

**-h** Displays the installation utility help page.

**-rpmloc** *rpmlocation\_path*

Explicitly specifies the path where all compiler packages are located. The default *rpmlocation\_path* is `./platform/rpms`, which is relative to the path of the installation tool. Therefore, the default *rpmlocation\_path* is:

- `./SLES9-BGL/rpms` (installing Blue Gene/L on SLES9 SP3)
- `./SLES10-BGP/rpms/` (installing Blue Gene/P on SLES10 SP1)

**Note:** Normally, the **-rpmloc** *rpmlocation\_path* option is not required in the installation invocation. If you use the utility directly from the CD, it will automatically determine the source location of the packages.

- U Updates the compiler to the *Version.Release.Modification-Fix* (V.R.M-F) level that the installation utility version supports. For more information, see “Running the xlf\_install utility to update a basic installation” on page 19
- v Displays debugging information generated during the installation of the compiler.
- vv Displays extra debugging information generated during the installation of the compiler.



---

## Chapter 3. Advanced installation

It is highly recommended that you install IBM XL Fortran Advanced Edition for Blue Gene, V11.1 to the default location and use the procedure provided in Chapter 2, “Basic installation,” on page 9. However, you will need to use alternate procedures for customized scenarios, including the following:

- You want to maintain more than one version of IBM XL Fortran Advanced Edition for Blue Gene on the same system. For more information on possible scenarios as well as installation procedures, see “Installing IBM XL Fortran Advanced Edition for Blue Gene, V11.1 to co-reside with earlier versions.”
- You want to upgrade or update an existing version of IBM XL Fortran Advanced Edition for Blue Gene that is installed in a non-default location. For installation procedures, see “Installing IBM XL Fortran Advanced Edition for Blue Gene, V11.1 to co-reside with earlier versions in separate locations on the same system” on page 15.
- You want to try out a new update of the compiler before removing an existing installation from the default location.
- The Blue Gene tool chain is installed in a non-default location:
  - The Blue Gene/L tool chain default path is `/bgl/BlueLight/ppcfloor`.
  - The Blue Gene/P tool chain default path is `/bgsys/drivers/ppcfloor`.

In all of these scenarios, you must use the **rpm** utility to install the compiler; you cannot use the `xlf_install` utility to do so. Once you have successfully installed the compiler to a non-default location, you will need to manually configure the compiler environment using the **new\_install** or **xlf\_configure** utilities; see Chapter 5, “Configuring IBM XL Fortran Advanced Edition for Blue Gene, V11.1 (for advanced users),” on page 23 for procedures.

---

### Installing IBM XL Fortran Advanced Edition for Blue Gene, V11.1 to co-reside with earlier versions

To install IBM XL Fortran Advanced Edition for Blue Gene, V11.1 to co-reside with earlier versions of IBM XL Fortran Advanced Edition for Blue Gene on the same system, you have the following options:

- You can install multiple versions in the same location, while forcing all versions to use the most recent runtime environment. This option is recommended if you want to continue using the different versions of IBM XL Fortran Advanced Edition for Blue Gene over the long term. Multiple versions of IBM XL Fortran Advanced Edition for Blue Gene can co-reside in the same location as long as the later version does not attempt to use runtime packages that pre-date it. If your existing version is installed in the default location, do not try to use `xlf_install` to install the additional version as it will remove the existing version. Instead, use the procedure in “Installing IBM XL Fortran Advanced Edition for Blue Gene, V11.1 to co-reside with earlier versions in the same location” on page 14
- You can allow each version to use the runtime environment that was shipped with it. This option is recommended if you want to phase a migration to the later version. In this case, you will need to install IBM XL Fortran Advanced Edition for Blue Gene, V11.1 in a separate location from all other versions of IBM XL Fortran Advanced Edition for Blue Gene. To do so, follow one of the

procedures in “Installing IBM XL Fortran Advanced Edition for Blue Gene, V11.1 to co-reside with earlier versions in separate locations on the same system” on page 15.

## Installing IBM XL Fortran Advanced Edition for Blue Gene, V11.1 to co-reside with earlier versions in the same location

The following procedure describes how to install IBM XL Fortran Advanced Edition for Blue Gene, V11.1 and update the runtime packages used by an existing version of IBM XL Fortran Advanced Edition for Blue Gene, V10.1 in the same location. This procedure assumes the following:

- You are installing IBM XL Fortran Advanced Edition for Blue Gene, V11.1 to the same location where IBM XL Fortran Advanced Edition for Blue Gene, V10.1 is already installed (by default, /opt/ibmcmp/).
- Your current working directory contains all IBM XL Fortran Advanced Edition for Blue Gene, V11.1 packages, and no other RPM packages.
- The existing runtime component versions listed in Table 10 are installed in the same installation location (by default, /opt/ibmcmp/).

*Table 10. IBM XL Fortran SMP and runtime packages for SLES9 and SLES10 installations*

Existing IBM XL Fortran V10.1 runtime packages	New IBM XL Fortran V11.1 runtime packages
xlsmp.bg.msg.rte-1.6.1-0	xlsmp.bg.msg.rte-1.7.0-0.ppc64.rpm
xlsmp.bg.rte-1.6.1-0	xlsmp.bg.rte-1.7.0-0.ppc64.rpm
xlsmp.bg.lib-1.6.1-0	xlsmp.bg.lib-1.7.0-0.ppc64.rpm
xlfbg.msg.rte-10.1.1-0	xlfbg.msg.rte-11.1.0-0
xlfbg.rte-10.1.1-0	xlfbg.rte-11.1.0-0.ppc64.rpm

To install IBM XL Fortran Advanced Edition for Blue Gene, V11.1, and update the IBM XL Fortran Advanced Edition for Blue Gene, V10.1 XL SMP and runtime packages:

1. To avoid future dependency errors, remove the existing runtime packages by issuing the following commands:

```
rpm -e xlf.bg.msg.rte-10.1.1-0 --nodeps
rpm -e xlf.bg.rte-10.1.1-0 --nodeps
rpm -e xlsmp.bg.lib-1.6.1-0 --nodeps
rpm -e xlsmp.bg.rte-1.6.1-0 --nodeps
rpm -e xlsmp.bg.msg.rte-1.6.1-0 --nodeps
```

**Note:** This example shows package names with no applied updates. The -0 fix level will be different if you have applied any updates.

2. To replace the deleted runtime packages and to install IBM XL Fortran Advanced Edition for Blue Gene, V11.1, issue the following command:

```
rpm -ivh *.rpm
```

3. As a precaution, make a backup copy of any existing configuration file.
4. Modify any existing IBM XL Fortran Advanced Edition for Blue Gene, V10.1 configuration file to use the new configuration path:

```
sed -e "s/xlsmp\1\6/xlsmp\1\7/g"
< /etc/installation_path/xlf/bg/10.1/xlf.cfg >
/etc/installation_path/xlf/bg/10.1/xlf.cfg.new
mv /etc/installation_path/xlf/bg/10.1/xlf.cfg.new
/etc/installation_path/xlf/bg/10.1/xlf.cfg
```

where *installation\_path* is the location in which all IBM XL Fortran packages are installed (by default, /opt/ibmcmp/).

**Note:** The IBM XL Fortran Advanced Edition for Blue Gene, V10.1 path does not change.

5. Generate the default IBM XL Fortran Advanced Edition for Blue Gene, V11.1 configuration file:

```
/installation_path/xlf/bg/11.1/bin/xlf_configure -gcc /usr -gcc64 /usr  
-ibmcmp /installation_path/ /opt/ibmcmp/xlf/bg/11.1/etc/xlf.base.cfg  
-o /etc/installation_path/xlf/bg/11.1/xlf.cfg
```

where *installation\_path* is the location in which all IBM XL Fortran packages are installed (by default, /opt/ibmcmp/).

---

## Installing IBM XL Fortran Advanced Edition for Blue Gene, V11.1 to co-reside with earlier versions in separate locations on the same system

This section provides procedures for two possible installation scenarios:

- You can install all compiler packages to a single non-default location. For example, rather than installing all packages into the default directory /opt/ibmcmp/, you could install them to a directory of your choice, such as /home/mydirectory/. The procedure for doing so is provided in “Installing all packages to a single non-default location.”
- For highly specialized situations only, you can install groups of compiler packages to multiple, different locations. For example, you could install all the compiler library packages to one directory, the runtime environment packages to another directory, and so on. Note, however, that certain packages must be installed together in the same directory; rules for installing packages into multiple non-default directories, as well as procedures for doing so, are provided in “Installing packages to multiple, non-default locations.”

Note that in both of these scenarios, it is highly recommended that you uninstall any previous versions of the compiler from your system before installing any new versions; for uninstallation procedures, see Chapter 7, “Uninstalling IBM XL Fortran Advanced Edition for Blue Gene, V11.1,” on page 33.

### Installing all packages to a single non-default location

To install all compiler packages to a single non-default directory, ensure that your current working directory contains all of the packages for IBM XL Fortran Advanced Edition for Blue Gene, V11.1 and no other RPM packages. From your current working directory, use the following command:

```
rpm -ivh *.rpm --prefix installation_path
```

where *installation\_path* is a directory that is not /opt/ibmcmp/.

### Installing packages to multiple, non-default locations

For highly specialized situations only, you might need to install different packages to different locations.

**Note:** If you want to install packages in different subdirectories, do not install any packages in the /opt/ibmcmp/ directory.

Table 11 provides information about which packages must be installed together in the same directory and which can be installed in any directory.

*Table 11. Rules for installing packages to multiple, non-default locations*

Package Name	Package Description	Rules for installation to a non-default location
xlsmp.bg.msg.rte	IBM SMP messages package	All XL SMP packages must be installed in the same location. For the remainder of this document, the name <i>xlsmpprt_path</i> is used to refer to this location.
xlsmp.bg.rte	IBM SMP runtime package	
xlsmp.bg.lib	IBM SMP static library package	
xlmass.bg.lib	IBM Mathematical Acceleration Subsystem (MASS) package	Any location. For the remainder of this document, the name <i>xlmass_path</i> is used to refer to this location.
xlf.bg.msg.rte	IBM XL Fortran runtime environment messages	Must be installed in the same location as the other runtime packages above.
xlf.bg.rte	IBM XL Fortran runtime package	All IBM XL Fortran runtime packages must be installed in the same location. For the remainder of this document, the name <i>xlrte_path</i> is used to refer to this location.
xlf.bg.rte.lnk	IBM XL Fortran runtime links package	
xlf.bg.lic	IBM XL Fortran license package	Any location. For the remainder of this document, the name <i>lic_path</i> is used to refer to this location.
xlf.bg.lib	IBM XL Fortran compiler libraries package	All IBM XL Fortran compiler and library packages must be installed in the same location. For the remainder of this document, the name <i>xlcmp_path</i> is used to refer to this location.
xlf.bg.cmp	IBM XL Fortran compiler package	
xlf.bg.help.pdf	IBM XL Fortran Help pdf documentation package	Any location (optional). For the remainder of this document, the name <i>doc_path</i> is used to refer to this location.
xlf.bg.man	IBM XL Fortran compiler man pages	
xlf.bg.samples	IBM XL Fortran ANSI class library samples package	Any location (optional). For the remainder of this document, the name <i>smpls_path</i> is used to refer to this location.

To install a relocatable RPM package to any location other than the default location, issue the following command for each group of packages you want to install to a non-default directory:

```
rpm -ivh package --prefix package_installation_path
```

where *package\_installation\_path* is a directory other than /opt/ibmcmp/ and corresponds to one of the appropriate paths listed in Table 11 on page 16.

### **Example : Installing IBM XL Fortran for Blue Gene, V11.1 to multiple non-default directories**

In order to avoid dependency errors during installation of IBM XL Fortran for Blue Gene, V11.1 issue the following commands in the order given:

```
rpm -ivh xlsmp.bg.msg.rte-1.7.0-0.ppc64.rpm --prefix $SMPpath
rpm -ivh xlsmp.bg.rte-1.7.0-0.ppc64.rpm --prefix $SMPpath
rpm -ivh xlsmp.bg.lib-1.7.0-0.ppc64.rpm --prefix $SMPpath
rpm -ivh xlmass.bg.lib-4.4.0-0.ppc64.rpm --prefix $MASS_path

rpm -ivh xlf.bg.msg.rte-11.1.0-0.ppc64.rpm --prefix xlrte_path
rpm -ivh xlf.bg.rte-11.1.0-0.ppc64.rpm --prefix $RTEpath
rpm -ivh xlf.bg.rte.lnk-11.1.0-0.ppc64.rpm --prefix $RTEpath
rpm -ivh xlf.bg.lic-11.1.0-0.ppc64.rpm --prefix $LICpath
rpm -ivh xlf.bg.lib-11.1.0-0.ppc64.rpm --prefix $CMPpath
rpm -ivh xlf.bg.cmp-11.1.0-0.ppc64.rpm --prefix $CMPpath
```

The sample programs and product documentation packages have no dependency on other RPM packages and can be installed in any order using the following commands:

```
rpm -ivh xlf.bg.man-11.1.0-0.ppc64.rpm --prefix $MANPAGpath
rpm -ivh xlf.bg.samples-11.1.0-0.ppc64.rpm --prefix $SAMPpath
rpm -ivh xlf.bg.help.pdf-9.0.0-0.ppc64.rpm
```



---

## Chapter 4. Installing an update

An update of IBM XL Fortran Advanced Edition for Blue Gene, V11.1 provides a fix or multiple fixes to the product. You can download updates from the support web site: <http://www.ibm.com/software/awdtools/fortran/xlfortran/support>

Every PTF update package comes in tar.gz (or compressed) format and includes a version of the xlf\_install utility that is customized to install only the update that accompanies it. If you have any version (including an earlier update) of IBM XL Fortran Advanced Edition for Blue Gene, V11.1 installed on your system, you can apply the latest update. If you are applying the update to an installation in the default location, follow the procedure in “Running the xlf\_install utility to update a basic installation.” If you are applying the update to an installation in a non-default location, you must use one of the procedures in “Installing IBM XL Fortran Advanced Edition for Blue Gene, V11.1 to co-reside with earlier versions in separate locations on the same system” on page 15.

If you want to try out a new update of the compiler before you remove the existing version from the system, you must install the new update to a non-default location. After you have verified that you want to replace the older version with the new update, you can run the xlf\_install utility that comes with the update package, and it will do all of the following:

1. Remove the new update from the non-default location
2. Remove the older version from the default location

**Note:** Do not uninstall the xlf.lic package because this package is required for the next step.

3. Re-install the new update to the default location

For instructions to use the xlf\_install utility to install the new update, see “Running the xlf\_install utility to update a basic installation.”

---

### Running the xlf\_install utility to update a basic installation

You can use the xlf\_install utility to update IBM XL Fortran Advanced Edition for Blue Gene, V11.1 when all the following conditions have been met:

- The base version of IBM XL Fortran Advanced Edition for Blue Gene, V11.1 is already successfully installed in the /opt/ibmcmp/ directory.
- The update package (in tar.gz format) has been uncompressed and unpacked in the /home/root/ directory of the system.

When you run the xlf\_install utility to apply an update, it does the following:

- Checks for all prerequisite software packages
- Uninstalls IBM XL Fortran Advanced Edition for Blue Gene, V11.1 packages
- Installs updated compiler packages into the default location
- Automatically invokes the **new\_install** utility, which installs the license file, renames the old configuration file, and generates a new configuration file
- Optionally creates symbolic links in /usr/bin/ to the compiler invocation commands
- Generates an installation log in the /tmp/ directory

To run the `xlfiinstall` utility to apply an update for IBM XL Fortran Advanced Edition for Blue Gene, V11.1:

1. Change to the directory in which you have unpacked the update package:  

```
cd /home/root/update/xlf/mmmYYYY
```

where *mmmYYYY* is the month and year of the update shipment date. (For example, `aug2007` indicates a shipment date in August of 2007.)

2. Issue the following command:  

```
./xlf_install -U
```

For additional arguments that you can specify for `xlf_install`, see “`xlf_install` options” on page 11.

You are prompted to uninstall any previously installed IBM XL Fortran Advanced Edition for Blue Gene, V11.1 packages.

3. Confirm that you want to proceed with uninstalling the outdated packages.  
You are prompted to uninstall any IBM SMP and MASS packages that were previously installed with IBM XL Fortran Advanced Edition for Blue Gene.
4. Confirm that you want to proceed with uninstalling the existing IBM SMP and MASS packages.

**Note:** `xlf_install` will uninstall these packages from their existing location and reinstall them to the default location, `/opt/ibmcmp/`. Therefore, if they were previously installed in a non-default location as part of an IBM XL C/C++ Advanced Edition for Blue Gene installation, you will need to run `vac_configure` to reconfigure the IBM XL C/C++ compiler to point to the default location for these packages. For procedures, see “Running the `vac_configure` utility directly” in the *IBM XL C/C++ Advanced Edition for Blue Gene, V9.0 Installation Guide*.

You are presented with the licensing agreement and licensing information.

5. Accept the licensing agreement and licensing information.  
You are prompted to create symbolic links for the compiler invocations in the `/usr/bin/` directory.
6. Optionally, create the symbolic links.

**Note:** An alternative to this step is to add the path that contains the compiler invocations to the `PATH` environment variable. See “Setting the `PATH` environment variable to include the path to the compiler invocations” on page 30.

If you choose to create symbolic links, the following links are created in the `/usr/bin/` subdirectory:

#### **Blue Gene/L symbolic links**

- `blrts_xlf`
- `blrts_xlf90`
- `blrts_xlf95`
- `blrts_xlf2003`
- `bgxlf`
- `bgxlf90`
- `bgxlf95`
- `bgxlf2003`

#### **Blue Gene/P symbolic links**



- bgxlf
- bgxlf\_r
- bgxlf90
- bgxlf90\_r
- bgxlf95
- bgxlf95\_r
- bgxlf2003
- bgxlf2003\_r

**Note:** Some command links are not created in `/usr/bin/`, either because they might delete user-defined, IBM XL Fortran for Blue Gene or GCC-related invocations, or because they are not compiler invocation commands. These include:

- `f77`, `f90`, `f95`, `fort77`, `f2003`, `blrts_f77`, `blrts_fort77`, `blrts_f95`, `blrts_f2003`, `bgf77`, `bgfort77`, `bgf90`, `bgf95`, `bgf2003`
  - `cleanpdf`, `mergepdf`, `new_install`, `resetpdf`, `showpdf`, `xlf_configure`
7. If you customized the previously generated configuration file, manually edit `/etc/opt/ibmcmp/xlf/bg/11.1/xlf.cfg` to replicate those changes in the newly generated configuration file.



---

## Chapter 5. Configuring IBM XL Fortran Advanced Edition for Blue Gene, V11.1 (for advanced users)

Before you can run IBM XL Fortran Advanced Edition for Blue Gene, V11.1 you must configure (or re-configure) the compiler if any of the following conditions apply:

- You did not use `xlf_install` to install the compiler.
- The compiler is installed in a non-default location, or compiler components were relocated after installation.

Two configuration tools are provided with the compiler: **`new_install`** and **`xlf_configure`**, both located in the `installation_path/xlf/bg/11.1/bin/` directory after installation.

It is recommended that you use the **`new_install`** utility to configure the compiler, provided that *all* of the following conditions are met:

- Only one version of IBM XL Fortran Advanced Edition for Blue Gene is installed on your system.
- Only one version of GCC is installed in your system and it can be found in the `PATH` environment variable.
- You have root or administrator privileges.
- You want to generate the configuration file in the default directory  
`/etc/opt/ibmcmp/`
- The Blue Gene tool chain is installed in the default location:
  - The Blue Gene/L tool chain default path is `/bgl/BlueLight/ppcfloor`.
  - The Blue Gene/P tool chain default path is `/bgsys/drivers/ppcfloor`.

For instructions, see “Running the `new_install` utility” on page 24.

You should invoke the **`xlf_configure`** utility directly *only* when any of the following is true:

- You have multiple versions of IBM XL Fortran Advanced Edition for Blue Gene installed on your system.
- You receive an error from the **`new_install`** command.
- You want the generated configuration file to be placed in a non-default location.
- You have multiple versions of GCC installed on your system and you need to specify which GCC version you would like to reference in the configuration file.
- The Blue Gene tool chain is installed in a non-default location.

**Note:** If you configure the compiler using **`xlf_configure`**, your output configuration file, `xlf.cfg`, can be written to any location where you have write permission. You would not need root or administrative privileges.

For instructions, see “Running the **`xlf_configure`** utility directly” on page 24.

---

## Running the new\_install utility

The **new\_install** utility does the following:

- Backs up any existing configuration file.
- Queries the RPM database for the paths to the compiler packages and the path to the 32-bit GCC (*gcc32path*) and the 64-bit GCC (*gcc64path*) in the PATH environment variable, and then uses the obtained values to execute the **xlf\_configure** utility.
- Searches for the Blue Gene tool chain in the default location:
  - **Blue Gene/L:** /bgl/BlueLight/ppcfloor/
  - **Blue Gene/P:** /bgsys/drivers/ppcfloor/
- Installs the license file.
- Generates the configuration file in the default location /etc/opt/ibmcmp/xlf/bg/11.1/xlf.cfg.

To run the **new\_install** utility:

1. Change to the directory that contains the compiler executables:

```
cd installation_path/xlf/bg/11.1/bin/
```

where *installation\_path* is the installation location of the compiler packages. If the compiler is installed in the default location, *installation\_path* is /opt/ibmcmp/.

2. Run the following command:

```
./new_install
```

3. Read the license agreement and licensing information. If you agree to the licensing terms, accept the license agreement and licensing information.

---

## Running the xlf\_configure utility directly

You can use the **xlf\_configure** utility to generate the configuration file as long as the compiler has been successfully installed.

To run the **xlf\_configure** utility:

1. Change to the directory that contains the compiler executables:

```
cd installation_path/xlf/bg/11.1/bin/
```

where *installation\_path* is the installation location of the compiler packages. If the compiler is installed in the default location, *installation\_path* is /opt/ibmcmp/.

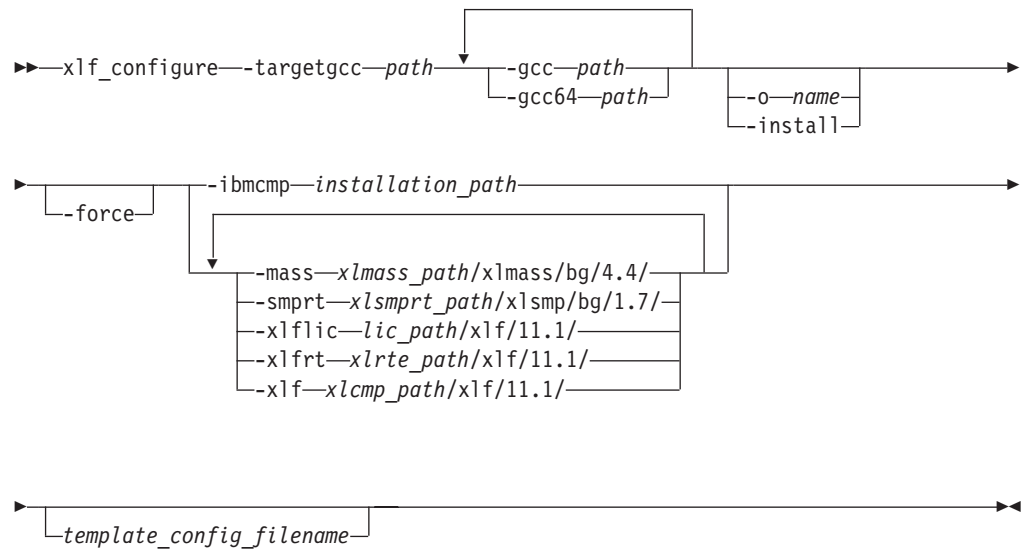
2. Run the following command:

```
./xlf_configure options
```

See the following section for required arguments to the **xlf\_configure** command.

### xlf\_configure options

The **xlf\_configure** command has the following syntax:



where:

**-h** Displays the **xlf\_configure** options help page.

**-targetgcc path**

Specifies the path where the Blue Gene tool chain is installed. For example, if the Blue Gene tool chain is installed in the default directory, you would specify:

**Blue Gene/L**

`-targetgcc /bgl/BlueLight/ppcfloor/blrts-gnu/powerpc-bgl-blrts-gnu`

**Blue Gene/P**

`-targetgcc /bgsys/drivers/ppcfloor/blrts-gnu/powerpc-bgl-blrts-gnu`

**-gcc path**

Specifies the path where the native GCC bin/ directory is installed. For example, if the GCC command is `/usr/bin/gcc`, you would specify:

`-gcc /usr`

**-gcc64 path**

Specifies the path where the native 64-bit GCC bin/ directory is installed. For example, if the 64-bit GCC command is `/usr/bin/gcc -m64`, you would specify:

`-gcc64 /usr`

**-clm path**

Specifies the path where the Common License Manager's license.dat file is located. By default, this is `/opt/clm_ibm`

**-o file\_name**

Specifies the name and path of the configuration file to generate. By default, output is written to the display only.

**-install**

Generates the configuration file as `/etc/opt/ibmcmp/xlf/bg/11.1/xlf.cfg`. By default, output is written to the display only.

- force** Forces the **xlf\_configure** utility to overwrite any existing output file with the same name and path as that specified by the **-o** or **-install** options. By default, if you do not use **-force**, **xlf\_configure** issues an error message and stops if the specified file already exists.
- ibmcmp** *installation\_path*  
Specifies the path where all of the IBM XL Fortran Advanced Edition for Blue Gene packages are installed (if all packages are installed in the same path). By default, the path is `/opt/ibmcmp/`.
- mass** *xlmass\_path/xlmass/bg/4.4/*  
Specifies the path where the `xlmass.bg.lib` package is installed. By default, the full path is `/opt/ibmcmp/xlmass/bg/4.4/`.
- smprt** *xlsmprt\_path/xlsmp/bg/1.7/*  
Specifies the path where the `xlsmp.bg.msg.rte`, `xlsmp.bg.rte`, and `xlsmp.bg.lib` packages are installed. By default, the full path is `/opt/ibmcmp/xlsmp/bg/1.7/`.
- xlflic** *lic\_path/xlf/bg/11.1/*  
Specifies the path where the `xlf.bg.lic` package is installed. By default, the full path is `/opt/ibmcmp/xlf/bg/11.1/`.
- xlfrt** *xlrte\_path/xlf/bg/11.1/*  
Specifies the path where the `xlf.bg.rte` and `xlf.bg.rte.lnk` packages are installed. By default, the full path is `/opt/ibmcmp/xlf/bg/11.1/`.
- xlf** *xlcmp\_path/xlf/bg/11.1/*  
Specifies the path where the `xlf.bg.cmp` and `xlf.bg.lib` packages are installed. By default, the full path is `/opt/ibmcmp/xlf/bg/11.1/`.
- template\_config\_file\_name*  
The input file that is used to construct the configuration file. By default, this is `/opt/ibmcmp/xlf/bg/11.1/etc/xlf.base.cfg`. If you relocated the `xlf.bg.cmp` package to *xlcmp\_path* but want to use the default template, specify:  
`xlcmp_path/xlf/bg/11.1/etc/xlf.base.cfg`.

---

## Chapter 6. After installing IBM XL Fortran Advanced Edition for Blue Gene, V11.1

After installing the compiler, there are verification and setup procedures that you will need, or might need, to follow. These are documented in the following sections:

- “Querying for installed packages”: This section applies to all users.
- “Testing the installation”: This section applies to all users.
- “Enabling the man pages” on page 28: This section applies to all users.
- “Enabling the IBM XL Fortran Advanced Edition for Blue Gene error messages” on page 29: This section applies only to users whose system uses a locale or language encoding other than en\_US.
- “Setting up the environment for the invocation commands” on page 30: This section applies only to users who did not use xlf\_install to install or update the product, or who did not create symbolic links during the installation process with xlf\_install.

---

### Querying for installed packages

To query for an individual package, issue a command such as the following:

```
rpm -q xlf.bg.cmp
```

The result should be:

```
xlf.bg.cmp-V.R.M-F
```

where *V.R.M-F* is the Version.Release.Modification-Fix level of the compiler installed on the system.

If the installation was not successful, you will get a message indicating that the package has not been installed.

To confirm installation of all compiler packages, issue the following command:

```
rpm -qa | grep -e xlf.bg -e xlsmp.bg -e xlmass.bg
```

The result should be a list that contains all of the packages listed in Table 3 on page 2. If none of the packages listed in the table was properly installed, there will be no output from the command.

---

### Testing the installation

To test the product installation and the critical search paths, build and run a sample application.

#### Basic example: Creating and running “Hello World”

1. Create the following Fortran program and name the source file `hello.f`:

```
PRINT *, "Hello World!"  
END
```

**Note:** Each line must have six blank spaces before the first text character.

2. Compile the program:

- If **Blue Gene/L** short invocation commands have been set up, enter the following command:

```
blrts_xlf hello.f -o hello
```

If short invocation commands have not been set up, enter the following command:

```
/opt/ibmcmp/xlf/bg/11.1/bin/blrts_xlf hello.f -o hello
```

- If **Blue Gene/P** short invocation commands have been set up, enter the following command:

```
bgxlf hello.f -o hello
```

If short invocation commands have not been set up, enter the following command:

```
/opt/ibmcmp/xlf/bg/11.1/bin/bgxlf hello.f -o hello
```

3. Run the program by entering the following command:

```
./hello
```

The result should be "Hello World!".

4. Check the exit code of the program by entering the following command:

```
echo $?
```

The result should be 0.

5. Compile the program:

- If **Blue Gene/L** short invocation commands have been set up, enter the following command:

```
blrts_xlf hello.f -o hello
```

If short invocation commands have not been set up, enter the following command:

```
/opt/ibmcmp/xlf/bg/11.1/bin/blrts_xlf hello.f -o hello
```

- If **Blue Gene/P** short invocation commands have been set up, enter the following command:

```
bgxlf hello.f -o hello
```

If short invocation commands have not been set up, enter the following command:

```
/opt/ibmcmp/xlf/bg/11.1/bin/bgxlf hello.f -o hello
```

---

## Enabling the man pages

Man pages are provided for the compiler invocation commands and other utilities that are supplied with the compiler.

IBM XL Fortran Advanced Edition for Blue Gene, V11.1 man pages support the following locales:

- en\_US
- en\_US.utf8

However, before you can read the compiler-supplied man pages, you must add the full directory path to the MANPATH environment variable. The command depends on the Linux shell you are using.



To set the MANPATH environment variable using the Bourne, Korn, or BASH shell, use the following command:

```
export MANPATH=installation_path/xlf/bg/11.1/man/LANG:$MANPATH
```

where LANG is either of the language locales listed above.

---

## Enabling the IBM XL Fortran Advanced Edition for Blue Gene error messages

### Accessing the compiler message catalogs from an I/O node

Before an I/O node can access the compiler message catalogs, it needs to know their location on the Front-end node. This section describes how to set up the I/O node so it can access these messages in a default or non-default location on a Front-end node.

#### Default message location

The default location for the compiler message catalogs is `/opt/ibmcmp/`. To indicate this location to an I/O node, export `/opt/ibmcmp/` from the Front-end node and mount this path to the I/O node.

In the following example, the compiler is installed in the default directory `/opt/ibmcmp/xlf/bg/11.1/` on the Front-end node called `frontend1`. There is one I/O node called `machine1`.

- At `frontend1`, add the following line to the `/etc/exports` file:  
`/opt/ibmcmp/ machine1`
- Run the following command to update the current NFS daemon of `frontend1`:  
`/usr/sbin/exportifs -ra`
- Make sure the empty directory `/opt/ibmcmp/` exists in `machine1`. Then, run the following command:  
`mount frontend1:/opt/ibmcmp/ /opt/ibmcmp/`

#### Non-default message location

If the compiler is installed to a non-default location which is already mounted to the I/O node, the NLSPATH environment variable must be set at the I/O node to point to this location.

For example, if the SMP and runtime message catalogs are installed in the non-default location `/bgl/opt/ibmcmp/` at the Front-end node, run the following command from the I/O node to access them:

```
export NLSPATH=/bgl/opt/ibmcmp/msg/bg/%L/%N:  
/bgl/opt/ibmcmp/msg/bg/%L/%N.cat
```

If your system uses the `en_US` locale and encoding, the compiler message catalogs are automatically configured to display correctly, whether you used the basic or advanced method of installation and configuration. However, if your system uses `en_US.utf8` encoding, you must set the NLSPATH environment variable so that the compiler and runtime functions can find the appropriate message catalogs following installation. If your system uses the `en_US` locale but the runtime packages are installed in a non-default location, you must set the NLSPATH environment variable.

The command to set the NLSPATH environment variable depends on the shell that you are using.

---

## Setting up the environment for the invocation commands

If you used the `xlfc_install` utility to install the compiler and you elected to create the symbolic links at that time, you have already set up the environment for the invocation commands. Do not perform the procedures in this section.

If you did not elect to create the symbolic links when you installed the compiler and want to invoke the compiler without having to specify the full path, you must perform one of the following tasks:

- Set the PATH environment variable, as shown in “Setting the PATH environment variable to include the path to the compiler invocations.”
- Create symbolic links to the compiler invocation commands, as shown in “Creating symbolic links to the compiler invocations.”

### Setting the PATH environment variable to include the path to the compiler invocations

To use IBM XL Fortran Advanced Edition for Blue Gene, V11.1 commands without typing the complete path, you can add the location of the compiler invocations to the PATH environment variable.

If you are using the Bourne, Korn, or BASH shell, use the following command:

```
export PATH=$PATH:installation_path/xlf/bg/11.1/bin/
```

If you are using C shell, use the following command:

```
setenv PATH $PATH:installation_path/xlf/bg/11.1/bin/
```

where *installation\_path* is the location where you have installed the compiler packages (by default, this is `/opt/ibmcmp/`).

**Note:** To set this variable in the Bourne, Korn, or BASH shell so that it applies to all users, add the commands to the file `/etc/profile`. To set it for a specific user only, add the commands to the file `.profile` in the user's home directory. In the C shell, add the commands to the file `/etc/csh.cshrc`. To set it for a specific user only, add the commands to the file `.cshrc` in the user's home directory. The environment variable is set each time the user logs in.

### Creating symbolic links to the compiler invocations

To use the compiler without typing the complete path, you can create symbolic links in the `/usr/bin/` directory for the specific invocations contained in the *installation\_path*/xlf/bg/11.1/bin/ directory.

If you have not already done so when you ran `xlfc_install`, you can create the symbolic links for the following compiler invocations:

#### Blue Gene/L symbolic links

- `blrts_xlf`
- `blrts_xlf90`
- `blrts_xlf95`
- `blrts_xlf2003`

- bgxlf
- bgxlf90
- bgxlf95
- bgxlf2003

#### Blue Gene/P symbolic links

- bgxlf
- bgxlf\_r
- bgxlf90
- bgxlf90\_r
- bgxlf95
- bgxlf95\_r
- bgxlf2003
- bgxlf2003\_r

Links to some invocations are not recommended, either because they delete user-defined, IBM XL Fortran for Blue Gene, or GCC invocations, or because they are not compiler invocation commands. These include the following commands:

- f77, f90, f95, fort77, f2003, blrts\_f77, blrts\_fort77, blrts\_f95, blrts\_f2003, bgf77, bgfort77, bgf90, bgf95, bgf2003
- cleanpdf, mergepdf, new\_install, resetpdf, showpdf, xlf\_configure

Use the following command to create a symbolic link:

```
ln -s installation_path/xlf/bg/11.1/bin/invocation /usr/bin/invocation
```

where:

- *installation\_path* is the location where you have installed the compiler packages (by default, this is /opt/ibmcmp/).
- *invocation* is one of the compiler invocations (such as xlf) in *installation\_path*/xlf/bg/11.1/bin/.

### Basic example: Creating a symbolic link to a compiler invocation

This example assumes that the entire IBM XL Fortran Advanced Edition for LinuxBlue Gene, V11.1 is installed in the default location /opt/ibmcmp/.

#### Blue Gene/L

```
ln -s /opt/ibmcmp/xlf/bg/11.1/bin/blrts_xlf /usr/bin/blrts_xlf
```

#### Blue Gene/P

```
ln -s /opt/ibmcmp/xlf/bg/11.1/bin/bg_xlf /usr/bin/bg_xlf
```

---

## Enabling IBM Tivoli License Compliance Manager

IBM Tivoli® License Compliance Manager (ITLCM) is a Web-based solution that can help you manage software usage metering and license allocation services on supported systems. In general, ITLCM recognizes and monitors the products that are installed and in use on your system.

IBM XL Fortran Advanced Edition for Blue Gene, V11.1 is ITLCM-enabled for inventory support only, which means that ITLCM is able to detect product installation of IBM XL Fortran Advanced Edition for Blue Gene, but not its usage.

**Note:** ITLCM is not part of the IBM XL Fortran Advanced Edition for Blue Gene offering, and must be purchased and installed separately.

Once installed and activated, ITLCM scans your system for product inventory signatures that indicate whether a given product is installed on your system. ITLCM also identifies the version, release, and modification levels of the product. Inventory signature files are not updated after a PTF update package is installed.

If IBM XL Fortran Advanced Edition for Blue Gene is installed in the default location, the signature files are in the `/opt/ibmcmp/xlf/bg/11.1/` directory. For more information about IBM Tivoli License Compliance Manager see: <http://www.ibm.com/software/tivoli/products/license-mgr/>.

---

## Accessing the local documentation

Help using IBM XL Fortran Advanced Edition for Blue Gene, V11.1 is available in PDF format. Manual pages for the compiler invocation commands and other command utilities are also included.

### Viewing the PDF documentation

PDF versions of the IBM XL Fortran Advanced Edition for Blue Gene, V11.1 product manuals are available in the `/doc/en_US/pdf/` directory of the installation media(CD).

After default installation, the PDF documentation can be found in the `/opt/ibmcmp/xlf/11.1/doc/$LANG/pdf/` directory. For non-default installations, the PDF documentation is located in the `$target_dir/xlf/11.1/doc/$LANG/pdf/` directory.

`$LANG` can be `en_US` or `en_US.utf8`

---

## Chapter 7. Uninstalling IBM XL Fortran Advanced Edition for Blue Gene, V11.1

IBM XL Fortran Advanced Edition for Blue Gene, V11.1 does not provide a standalone uninstallation tool. You must use the Linux **rpm** utility to uninstall IBM XL Fortran Advanced Edition for Blue Gene, V11.1.

**Note:**

1. You must have root user access to uninstall the compiler.
2. Whenever you uninstall a package, specify the *V.R.M-F* (Version.Release.Modification-Fix level) of the package.
3. Always uninstall packages in the reverse order of that in which they were installed. In other words, the last package installed is the first package that you remove. *Exception:* The sample programs and product documentation does not have any package dependencies. You can remove them in any order.
4. You cannot uninstall packages that are required by other packages. For example, `xlsmp.bg.rte` is a shared component if IBM XL C/C++ Advanced Edition for Blue Gene, V9.0 is also installed on the same system.
5. The uninstallation commands will not remove any configuration files that were generated by `new_install` or `xlf_configure`.

---

### Example : Uninstalling IBM XL Fortran Advanced Edition for Blue Gene, V11.1

In this example:

- The compiler packages have a *V.R.M-F* of 11.1.0-0
- The IBM MASS library package has a *V.R.M-F* of 4.4.0-0.
- The IBM SMP library packages have a *V.R.M-F* of 1.7.0-0.

To uninstall IBM XL Fortran Advanced Edition for Blue Gene, V11.1 issue the following commands, in the same order:

```
rpm -e xlf.bg.cmp-11.1.0-0
rpm -e xlf.bg.lib-11.1.0-0
rpm -e xlf.bg.lic-11.1.0-0
rpm -e xlf.bg.rte.lnk-11.1.0-0
rpm -e xlf.bg.rte-11.1.0-0
rpm -e xlf.bg.msg.rte-11.1.0-0
rpm -e xlmass.bg.lib-4.4.0-0

rpm -e xlsmp.bg.lib-1.7.0-0
rpm -e xlsmp.bg.rte-1.7.0-0
rpm -e xlsmp.bg.msg.rte-1.7.0-0
```

You can issue the following commands in any order:

```
rpm -e xlf.bg.samples-11.1.0-0
rpm -e xlf.bg.man-11.1.0-0
rpm -e xlf.bg.help.html-11.1.0-0
rpm -e xlf.bg.help.pdf-11.1.0-0
```



---

## Chapter 8. Troubleshooting the installation and configuration

At the beginning of the installation process, the installation utility creates a new log file in /tmp/. The temporary log files are uniquely named.

After the installation is completed successfully, the log file is moved to the default installation location for future reference. If the installation fails, the installation log will stay in the /tmp/ directory. Regardless of whether the installation succeeds or fails, the file name of the corresponding installation log is displayed as part of the standard output.

Use the information in this section to help you respond to any problems you may encounter when you install and configure IBM XL Fortran Advanced Edition for Blue Gene, V11.1.

---

### Error messages and recommended actions

The compiler generates messages to help you recognize and respond to error conditions. This section provides recommended responses.

#### The specified directory *rpmlocation\_path* does not exist.

##### Scenario

You are running the xlf\_install utility to install the compiler to the default location when you get the following error message:

ERROR: The specified directory, "*rpmlocation\_path*", does not exist.

##### Action

Ensure that you have specified the location of the existing compiler packages correctly. You might need to use the **-rpmloc** *rpmlocation\_path* option if you moved the xlf\_install utility to a different location than the one provided in the installation image. For more information, see "xlf\_install options" on page 11.

#### *rpmlocation\_path* does not contain . . .

##### Scenario

You are running the xlf\_install utility to install the compiler to the default location when you get the following error message:

ERROR: *rpmlocation\_path* does not contain all of the RPM packages for the XL compiler.

##### Action

Ensure you have all of the packages listed in Table 3 on page 2 in the path before running the xlf\_install utility again. You might need to use the **-rpmloc** *rpmlocation\_path* option if you have moved the xlf\_install utility to a different location than the one provided in the installation image. For more information, see "xlf\_install options" on page 11.





---

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