An Introduction to SeqHound
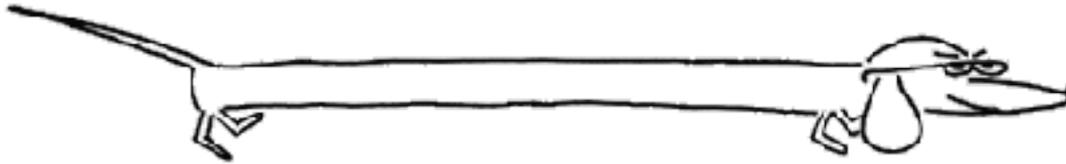
Ian Donaldson
BOSC 2004

What is SeqHound?

Sequences

Sequence annotation

Structure

Literature

Interactions

SeqHound

Access Methods

User

Blueprint

What is SeqHound?

GenBank

Taxonomy, GO, LocusLink, CDD

MMDB

MedLine

BIND

SeqHound

Database Interface

Application Programing Interface (API)

Remote API

Remote Programmer
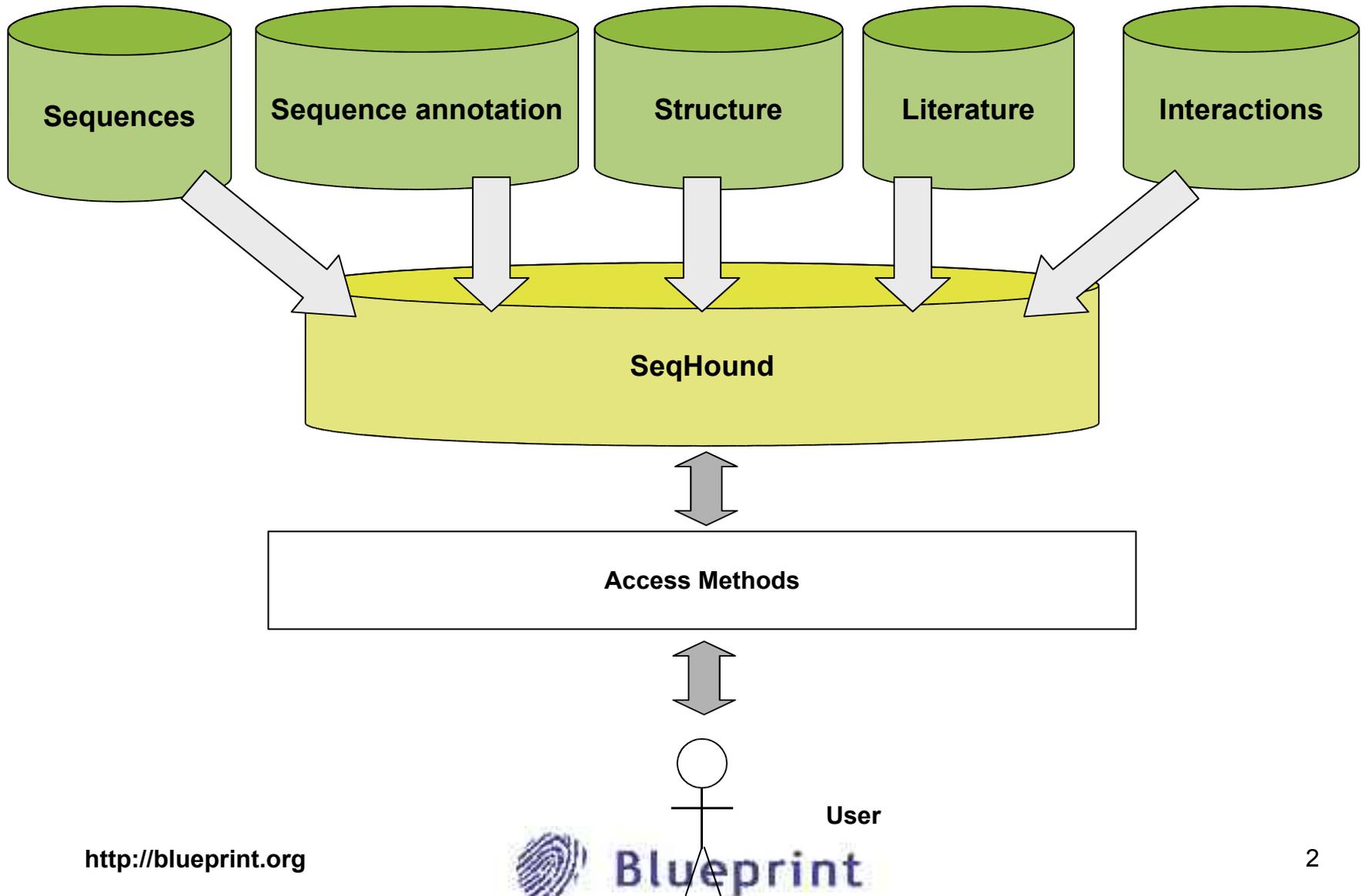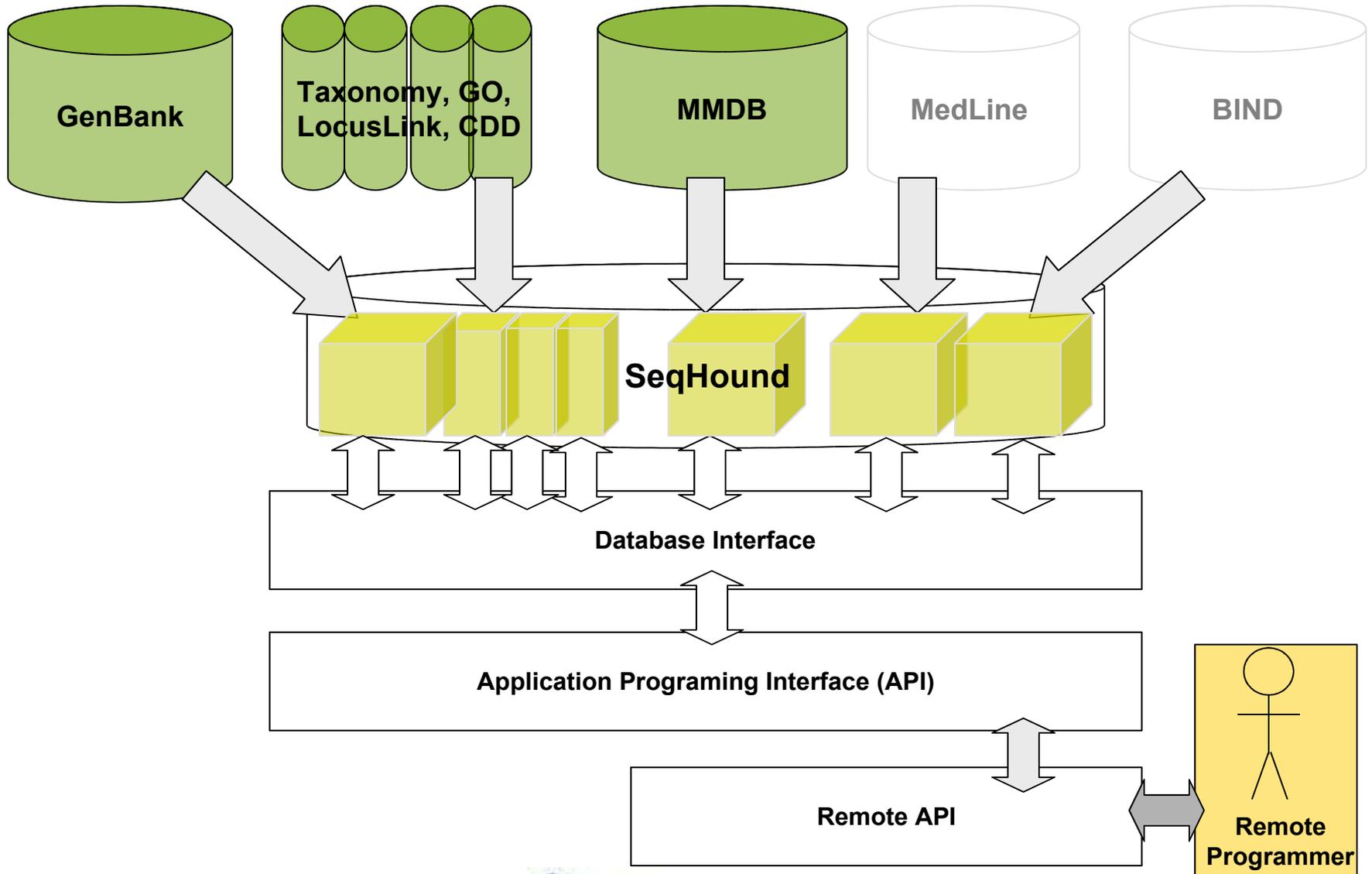
Remote API

Over 140 calls including

SHoundGetFasta

SHoundGetDefLine

Sequence

SHoundGetGenBankff

SHoundGetPDB3D

Structure

SHoundProteinsFromTaxID

Complete Genomes

SHoundRedundantGroup

SHoundNeighboursFromFromGi

Identity/Similarity

SHoundGOIDFromGi

Annotation

SHoundGetDomainsFromGi

Blueprint
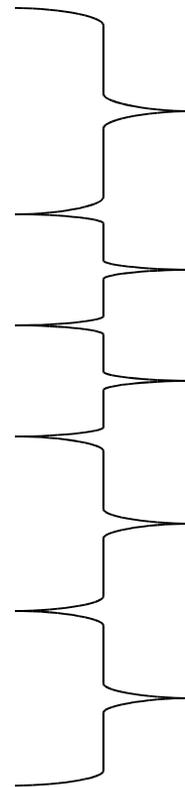
Remote API

Perl

Java

C

C++

Blueprint

Getting started with the remote API

Perl and Java

Follow the links to the sourceforge ftp site.

Instructions included with release package.

C and C++

Follow the links to the sourceforge ftp site.

Instructions included in the SeqHound manual.

Blueprint

Documentation

Yes

Testing

Yes

Blueprint

Updating

Yes

Physical architecture:

Unrestricted 24/7 global access

Supported systems:

BIND Interaction Viewer
BIND Index
BIND BLAST
BIND curation
MMDBIND

In house research

BioMOBY services

Great teaching tool

An open source local installation based on MySQL:

Introduced with Release 3.0

More information:

http://blueprint.org

Blueprint booth (#33)

Software demo (9:30 Sunday morning)

Poster (C-11)

seqhound.usergroup email list

seqhound@blueprint.org