

Profiles Research Networking Software Read Me First

Documentation Version: July 5, 2021

Software Version: ProfilesRNS_3.1.0

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Introduction

Profiles Research Networking Software (RNS) is an open source tool used to speed the process of finding researchers with specific areas of expertise for collaboration and professional networking. Profiles RNS imports and analyzes "white pages" information, publications, and other data sources to create and maintain a complete searchable library of web-based electronic CV's. Built-in network analysis and data visualization tools allow administrators to generate research portfolios of their institution, discover connections between parts of their organization, and understand what factors influence collaboration.

Profiles RNS has had four major releases since 2011, which are summarized below:

Profiles RNS Beta (2011): Automated Disambiguation and Network Visualizations

From the beginning, a key feature of Profiles RNS has been the ability to generate searchable researcher profiles automatically using a "disambiguation engine" that discovers information about people, such as publications they have authored. The software then uses data mining algorithms to identify ways researchers are connected (e.g., prior collaboration, similar interests, same department, etc.) and displays these as interactive network visualizations.

Version 1 (2012-2013): Semantic Web Standards and FAIR Open Data

The focus of our initial production version of Profiles RNS was adopting Semantic Web standards, based on the Resource Description Framework (RDF) data model. In RDF, every entity (e.g., person, publication, concept) is given a unique URI. Entities are linked together (Linked Open Data) using "triples" that contain three URIs--a subject, predicate, and object. For example, the URI of a Person can be connected to the URI of a Concept through a predicate URI of *hasResearchArea*. An instance of Profiles RNS can have millions of URIs and triples. Semantic Web applications use an ontology, which describes the classes and properties used to define entities and link them together. Profiles RNS uses the VIVO Ontology, which was developed as part of an NIH-funded grant to be a standard for academic and research institutions. The combination of Linked Open Data and the VIVO Ontology makes data in Profiles RNS Findable, Accessible, Interoperable, and Reusable (FAIR).

Version 2 (2014-2019): Plugins and Modular Extensions

With this version, numerous new features were added to the software as a result of contributions from both academic and industry members of the Profiles RNS open source community. These include OpenSocial "gadgets" (e.g., videos, presentations, Twitter feeds, links to external websites, etc.); integration with ORCID and research resources (through eagle-i); enhanced publication lists (Altmetric Badges, links to PubMed Central, etc.); grants and funding; education and training; and, "Group Profiles" for research centers, laboratories, and research teams.

Version 3 (2020-): Reports, Data Downloads, and Dashboards

This version of Profiles RNS adds new functionality to users (researchers or administrators) who are logged into the website. Person Lists enable users to select an arbitrary set of profile pages and generate various reports, maps, and network graphs, or export data about those profiles. An upcoming Dashboards feature will display site usage and other statistics.

Where to Go Next

This document provides a brief introduction to Profiles RNS and information on the resources that are available to help you install and use the software. The other documentation files are:

- [ProfilesRNS_InstallGuide.pdf](#) – Follow the instructions in this document to install a new instance of Profiles RNS or upgrade from an older version.
- [ProfilesRNS_APIGuide.pdf](#) – An important feature of Profiles RNS is its ability to share data. The API Guide describes the various types of ways this can be done. It also contains a brief introduction to the ontology used by Profiles RNS. The API_Examples folder contains related files, such as XSDs and example API request messages.
- [ProfilesRNS_ArchitectureGuide.pdf](#) – This document describes how Profiles RNS works and how you can extend the ontology, add custom data feeds, or modify the user interface.
- [ProfilesRNS_ReleaseNotes.pdf](#) – This document lists new features, bug fixes, and known issues with each release of Profiles RNS.

More Information

For more information about Profiles RNS, please visit

<http://profiles.catalyst.harvard.edu>

The Harvard development team can be reached at profiles@hms.harvard.edu. We will try to reply promptly, though we cannot guarantee that we will be able to answer all questions.

Acknowledgements

Profiles Research Networking Software was developed under the supervision of Griffin M Weber, MD, PhD, with support from Grant Number 1 UL1 RR025758-01 to Harvard Catalyst, The Harvard Clinical and Translational Science Center from the National Center for Research Resources and support from Harvard University and its affiliated academic healthcare centers.

Harvard Development Team

The software implementation is led by the Harvard Medical School Information Technology Department. The current and past members of the development team include Nick Benik, Nick Brown, Niraj Desai, Paul Gomez, John Halamka, Ken Huling, Shashank Jain, Melissa Kenny, Kevin Laitinen, Kellie Lucy, Krishna Nellutla, James B. Norman, Rob Piscitello, George Rakauskas, Jeff Rosen, Michele Sinunu, Franco Valentino, Marlon Violette, Griffin Weber, and Steve Wimberg.

UCSF Development Team

The UCSF Profiles team includes Mini Kahlon, Eric Meeks, Kristine Moss, Rachael Sak, and Leslie Yuan. UCSF has developed innovative promotional strategies for research networking, assisted with quality assurance, and are adding OpenSocial support to Profiles RNS. Mini Kahlon was the co-chair with Griffin Weber of the National CTSA Research Networking Group, where they led an effort to create a national pilot that demonstrated interoperability among different research networking platforms.

Recombinant Data Corp.

We thank the team at Recombinant Data Corp for their many years as an Authorized Support Provider for Profiles RNS: Kimber Barton, Nick Brown, Peter Emerson, Dan Housman, Mike Klumpenaar, Dave Legge, Mark Mischke, Matvey Palchuk, Chris Parisi, and Nancy Pickard.

Profiles RNS Users Group

We thank the member institutions of the Profiles RNS Users Group for their willingness to be early adopters of the software and their continued feedback. For a list of member sites, please visit the Community page on <http://profiles.catalyst.harvard.edu>.