



## IHEC on Twitter: First Year

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### Abstract

The IHEC Communications Working Group launched a Twitter account in August 2015. The primary aims of this first IHEC social media venture are to drive traffic to the IHEC Data Portal, annual meeting pages, and main website, and to increase the use of Consortium data and other resources by the wider epigenetics and epigenomics community. The secondary aim is to position IHEC as a valuable member of this community by disseminating useful third-party content (such as methods and review papers, news, events, job openings, and training opportunities) to Consortium members and other followers.

The number of people who follow the IHEC Twitter account has climbed steadily to 370 as of May 2016. Followers include individual scientists, other genomics consortia, academic journals and societies, funding agencies, and science outreach groups. A full breakdown of follower categories will be presented.

The most popular content categories comprise tweets about events and job openings, followed by public outreach articles and videos. The most popular individual tweet to date is a description of and link to the IHEC data portal. Other popular tweets include program and registration links for the 2015 and 2016 IHEC annual meetings, and for events organized by the CEEHRC (Canada) and Roadmap Epigenomics (USA) member projects; links to various videos, articles, and events intended for non-scientists; and a methods paper about Nanopore bisulphite sequencing. Full content metrics (views, engagements, retweets etc.) will be presented.

The Twitter account has directed a modest amount of additional traffic to the IHEC Data Portal, 2015 and 2016 annual meeting websites, and home page. The account has received feedback from followers (e.g. suggestions of epigenetics videos to be added to the IHEC website), and questions about issues such as how to cite IHEC and IHEC data in academic publications. The Communications Working Group will continue to use the IHEC Twitter account to engage with the wider epigenetics and epigenomics community, as part of our overall strategy to increase uptake of the Consortium's valuable data and other resources.