

2016-2017 Influenza Season Week 47 ending November 26, 2016

All data are preliminary and may change as more reports are received.

Synopsis:

During week 47 (November 20-26, 2016), influenza activity increased slightly, but remained low in the United States.

- Viral Surveillance:** The most frequently identified influenza virus subtype reported by public health laboratories during week 47 was influenza A (H3). The percentage of respiratory specimens testing positive for influenza in clinical laboratories increased slightly, but remained low.
- Pneumonia and Influenza Mortality:** The proportion of deaths attributed to pneumonia and influenza (P&I) was below the system-specific epidemic threshold in the National Center for Health Statistics (NCHS) Mortality Surveillance System.
- Influenza-associated Pediatric Deaths:** No influenza-associated pediatric deaths were reported.
- Outpatient Illness Surveillance:** The proportion of outpatient visits for influenza-like illness (ILI) was 1.8%, which is below the national baseline of 2.2%. Three regions reported ILI at or above their region-specific baseline levels. Puerto Rico experienced high ILI activity, one state experienced moderate ILI activity, New York City and five states experienced low ILI activity, 44 states experienced minimal ILI activity, and the District of Columbia had insufficient data.
- Geographic Spread of Influenza:** The geographic spread of influenza in Guam, Puerto Rico, the U.S. Virgin Islands, and one state was reported as regional; 12 states reported local activity; the District of Columbia and 36 states reported sporadic activity; and one state reported no activity.

National and Regional Summary of Select Surveillance Components

HHS Surveillance Regions*	Out-patient ILI [†]	Data for current week		Data cumulative since October 2, 2016 (week 40)						
		Number of jurisdictions reporting regional or widespread activity [§]	% respiratory specimens positive for flu in clinical laboratories [‡]	A(H1N1)pdm09	A (H3)	A (Subtyping not Performed)	B Victoria lineage	B Yamagata lineage	B lineage not performed	Pediatric Deaths
Nation	Normal	4 of 54	3.6%	65	731	53	34	21	40	0
Region 1	Normal	0 of 6	1.1%	0	34	0	0	0	0	0
Region 2	Elevated	2 of 4	1.3%	0	67	0	14	4	3	0
Region 3	Normal	0 of 6	0.7%	6	42	1	1	1	4	0
Region 4	Elevated	1 of 8	5.8%	4	58	4	3	2	25	0
Region 5	Normal	0 of 6	1.1%	2	60	29	6	3	0	0
Region 6	Normal	0 of 5	2.1%	8	16	0	5	5	0	0
Region 7	Normal	0 of 4	0.9%	0	12	5	2	0	0	0
Region 8	Normal	0 of 6	2.2%	28	80	2	0	0	0	0
Region 9	Normal	1 of 5	2.1%	16	188	11	1	6	4	0
Region 10	Elevated	0 of 4	8.3%	1	174	1	2	0	4	0

*HHS regions (Region 1 CT, ME, MA, NH, RI, VT; Region 2: NJ, NY, Puerto Rico, US Virgin Islands; Region 3: DE, DC, MD, PA, VA, WV; Region 4: AL, FL, GA, KY, MS, NC, SC, TN; Region 5: IL, IN, MI, MN, OH, WI; Region 6: AR, LA, NM, OK, TX; Region 7: IA, KS, MO, NE; Region 8: CO, MT, ND, SD, UT, WY; Region 9: AZ, CA, Guam, HI, NV; and Region 10: AK, ID, OR, WA).

† Elevated means the % of visits for ILI is at or above the national or region-specific baseline

Â§ Includes all 50 states, the District of Columbia, Guam, Puerto Rico, and U.S. Virgin Islands

‡ National data are for current week; regional data are for the most recent three weeks

U.S. Virologic Surveillance:

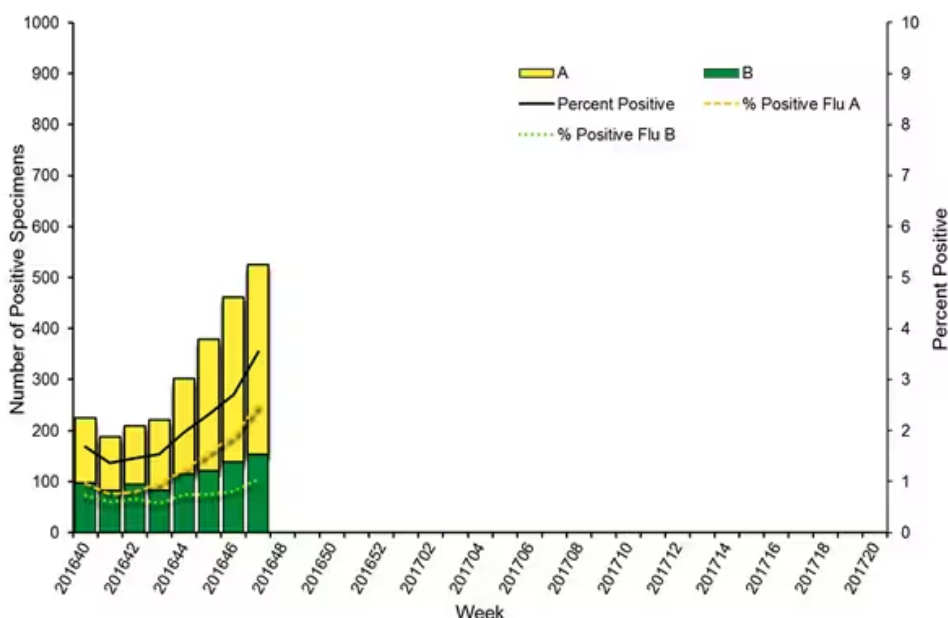
WHO and NREVSS collaborating laboratories, which include both public health and clinical laboratories located in all 50 states, Puerto Rico, and the District of Columbia, report to CDC the total number of respiratory specimens tested for influenza and the number positive for influenza by virus type. In addition, public health laboratories also report the influenza A subtype (H1 or H3) and influenza B lineage information for the viruses they test and the age or age group of the persons from whom the specimens were collected.

Additional data are available at <http://gis.cdc.gov/grasp/fluview/fluportaldashboard.html> and http://gis.cdc.gov/grasp/fluview/flu_by_age_virus.html.

The results of tests performed by clinical laboratories during the current week are summarized below.

	Week 47	Data Cumulative since October 2, 2016 (Week 40)
No. of specimens tested	14,787	119,242
No. of positive specimens (%)	525 (3.6%)	2,510 (2.1%)
Positive specimens by type		
Influenza A	372 (70.9%)	1,626 (64.8%)
Influenza B	153 (29.1%)	884 (35.2%)

**Influenza Positive Tests Reported to CDC by U.S. Clinical Laboratories,
National Summary, 2016-2017 Season**



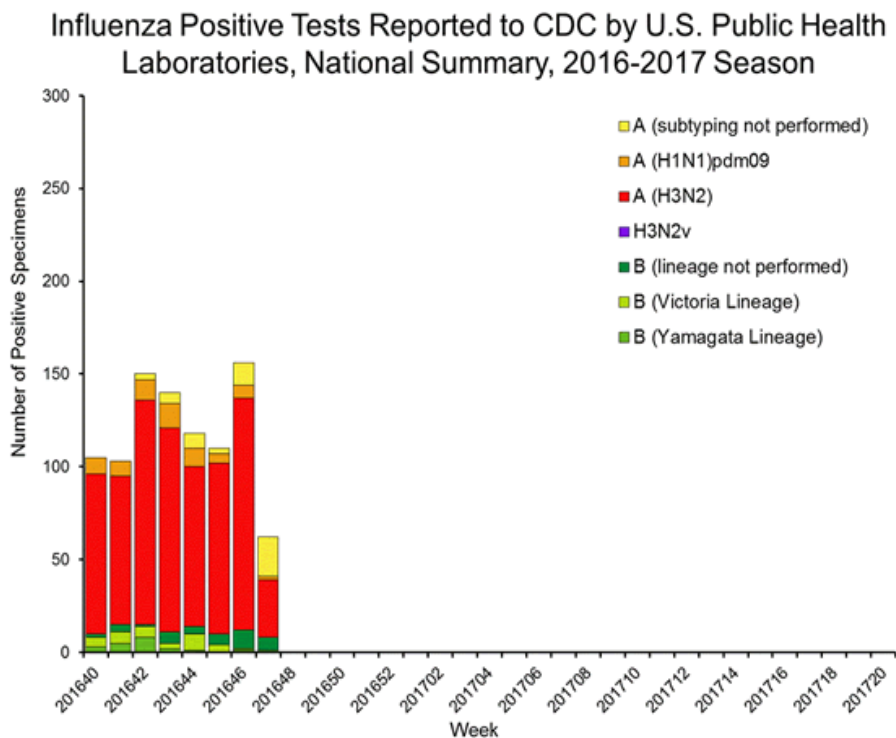
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The results of tests performed by public health laboratories, as well as the age group distribution of influenza positive tests, during the current week are summarized below.

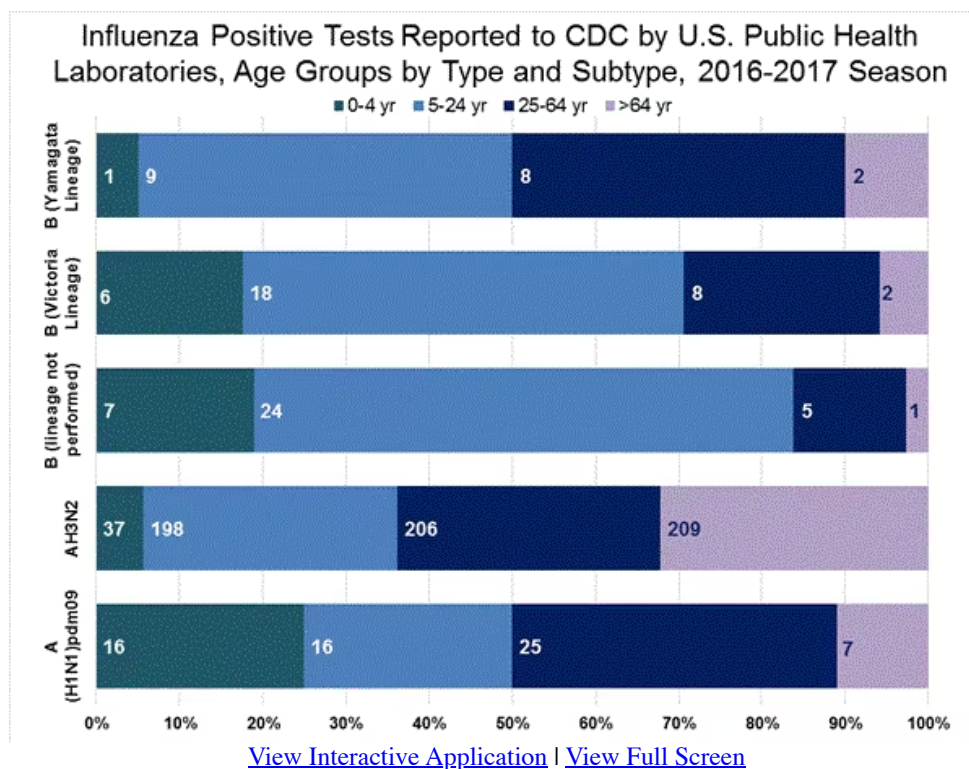
	Week 47	Data Cumulative since October 2, 2016 (Week 40)
No. of specimens tested	541	7,728
No. of positive specimens*	62	944
Positive specimens by type/subtype		
Influenza A	54 (87.1%)	849 (89.9%)
A(H1N1)pmd09	2 (3.7%)	65 (7.7%)
H3	31 (57.4%)	731 (86.1%)
Subtyping not performed	21 (38.9%)	53 (6.2%)
Influenza B	8 (12.9%)	95 (10.1%)
Yamagata lineage	1 (12.5%)	21 (22.1%)

	Week 47	Data Cumulative since October 2, 2016 (Week 40)
Victoria lineage	0 (0%)	34 (35.8%)
Lineage not performed	7 (87.5%)	40 (42.1%)

*The percent of specimens testing positive for influenza is not reported because public health laboratories often receive samples that have already tested positive for influenza at a clinical laboratory and therefore percent positive would not be a valid indicator of influenza activity. Additional information is available at <http://www.cdc.gov/flu/weekly/overview.htm>.



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Influenza Virus Characterization:

CDC characterizes influenza viruses through one or more tests including [genomic sequencing](#), [hemagglutination inhibition \(HI\)](#) and/or neutralization assays. These data are used to compare how similar currently circulating influenza viruses are to the reference viruses used for developing influenza vaccines, and to monitor for changes in circulating influenza viruses. Historically, HI data have been used most commonly to assess the similarity between reference viruses and circulating viruses to suggest how well the vaccine may work until such a time as [vaccine effectiveness estimates](#) are available.

For nearly all virus positive surveillance samples received at CDC, next-generation sequencing is performed to ascertain genomic data of circulating influenza viruses. Viruses can be classified into genetic groups/clades based on analysis of their HA gene segments using phylogenetics and key amino acid changes ([Klimov Vaccine 2012](#)).

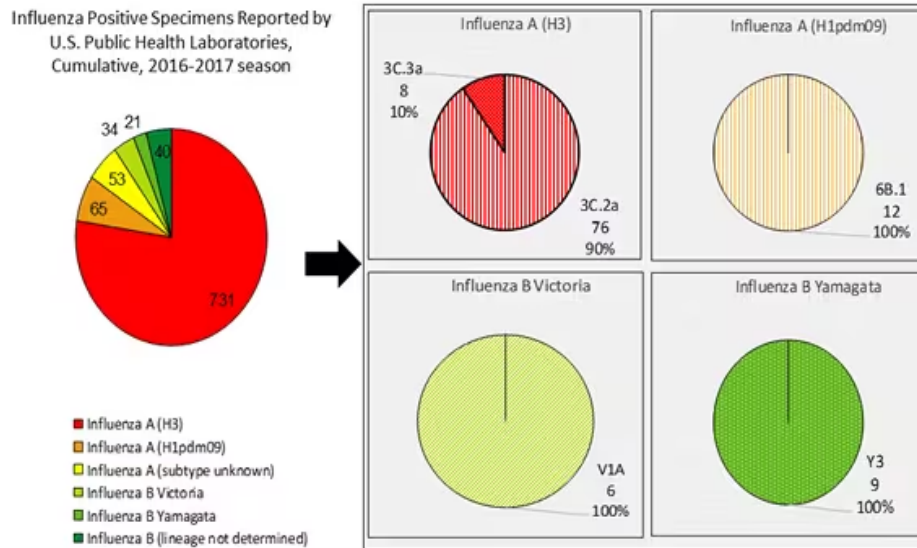
A proportion of influenza A (H3N2) viruses don't yield sufficient hemagglutination titers for antigenic characterization using the hemagglutination inhibition test. Therefore, CDC selects a subset of influenza A (H3N2) viruses to test using a focus reduction assay for supplementary antigenic characterization.

Genetic Characterization

During the 2016-2017 season, 944 influenza positive specimens have been collected and reported by public health laboratories in the United States (figure, left). CDC genetically characterized 111 influenza viruses [12 influenza A (H1N1)pdm09, 84 influenza A (H3N2), and 15 influenza B viruses] collected by U.S. laboratories. The HA gene segment of all influenza A (H1N1)pdm09 viruses analyzed belonged to genetic group 6B.1. Influenza A (H3N2) virus HA gene segments analyzed belonged to genetic groups 3C.2a or 3C.3a. Genetic group 3C.2a includes a newly emerging subgroup known as 3C.2a1. The HA of influenza B/Victoria-lineage viruses all belonged to genetic group V1A. The HA of influenza B/Yamagata-lineage viruses analyzed all belonged to genetic group Y3.

The majority of U.S. viruses submitted for characterization come from state and local public health laboratories. Due to [Right Size Roadmap](#) considerations, specimen submission guidance issued to the laboratories request that, if available, 2 influenza A (H1N1), 2 A influenza (H3N2), and 2 influenza B viruses be submitted every other week. Because of this, the number of each virus type/subtype characterized should be approximately equal. In the figure below, the results of tests performed by public health labs are presented on the left and sequence results by genetic group of specimens submitted to CDC are presented on the right.

Sequence Results, by Genetic Group, of Specimens Submitted to CDC
by U.S. Public Health Laboratories, Cumulative, 2016-2017 season



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Antigenic Characterization

CDC has antigenically characterized 34 influenza viruses [7 influenza A (H1N1)pdm09, 15 influenza A (H3N2), and 12 influenza B viruses] collected by U.S. laboratories since October 1, 2016.

Influenza A Virus [22]

- **A (H1N1)pdm09 [7]:** All 7 (100%) influenza A (H1N1)pdm09 viruses were antigenically characterized using ferret post-infection antisera as A/California/7/2009-like, the influenza A (H1N1) component of the 2016-2017 Northern Hemisphere vaccine.
- **A (H3N2) [15]:** All 15 (100%) influenza A (H3N2) viruses were antigenically characterized as A/Hong Kong/4801/2014-like, a virus that belongs in genetic group 3C.2a and is the influenza A (H3N2) component of the 2016-2017 Northern Hemisphere vaccine, by HI testing or neutralization testing.

Influenza B Virus [12]

- **Victoria Lineage [5]:** All 5 (100%) B/Victoria-lineage viruses were antigenically characterized using ferret post-infection antisera as B/Brisbane/60/2008-like, which is included as an influenza B component of the 2016-2017 Northern Hemisphere trivalent and quadrivalent influenza vaccines.
- **Yamagata Lineage [7]:** All 7 (100%) B/Yamagata-lineage viruses were antigenically characterized using ferret post-infection antisera as B/Phuket/3073/2013-like, which is included as an influenza B component of the 2016-2017 Northern Hemisphere quadrivalent influenza vaccines.

Antiviral Resistance:

Testing of influenza A (H1N1)pdm09, influenza A (H3N2), and influenza B virus isolates for resistance to neuraminidase inhibitors (oseltamivir, zanamivir, and peramivir) is performed at CDC using a functional assay. Additional influenza A (H1N1)pdm09 and influenza A (H3N2) clinical samples are tested for mutations of the virus known to confer oseltamivir resistance. The data summarized below combine the results of both testing methods. These samples are routinely obtained for surveillance purposes rather than for diagnostic testing of patients suspected to be infected with antiviral-resistant virus.

High levels of resistance to the adamantanes (amantadine and rimantadine) persist among influenza A (H1N1)pdm09 and influenza A (H3N2) viruses (the adamantanes are not effective against influenza B viruses). Therefore, data from adamantane resistance testing are not presented below.

**Neuraminidase
Inhibitor
Resistance
Testing Results
on Samples
Collected
Since October
1, 2016**

	Oseltamivir		Zanamivir		Peramivir	
	Virus Samples tested (n)	Resistant Viruses, Number (%)	Virus Samples tested (n)	Resistant Viruses, Number (%)	Virus Samples tested (n)	Resistant Viruses, Number (%)
Influenza A (H1N1)pdm09	17	0 (0.0)	17	0 (0.0)	17	0 (0.0)
Influenza A (H3N2)	79	0 (0.0)	79	0 (0.0)	61	0 (0.0)
Influenza B	20	0 (0.0)	20	0 (0.0)	20	0 (0.0)

The majority of recently circulating influenza viruses are susceptible to the neuraminidase inhibitor antiviral medications, oseltamivir, zanamivir, and peramivir; however, rare sporadic instances of oseltamivir-resistant and peramivir-resistant influenza A (H1N1)pdm09 viruses and oseltamivir-resistant influenza A (H3N2) viruses have been detected worldwide. Antiviral treatment as early as possible is recommended for patients with confirmed or suspected influenza who have severe, complicated, or progressive illness; who require hospitalization; or who are at [high risk](#) for serious influenza-related complications. Additional information on recommendations for treatment and chemoprophylaxis of influenza virus infection with antiviral agents is available at <http://www.cdc.gov/flu/antivirals/index.htm>.

Pneumonia and Influenza (P&I) Mortality Surveillance:

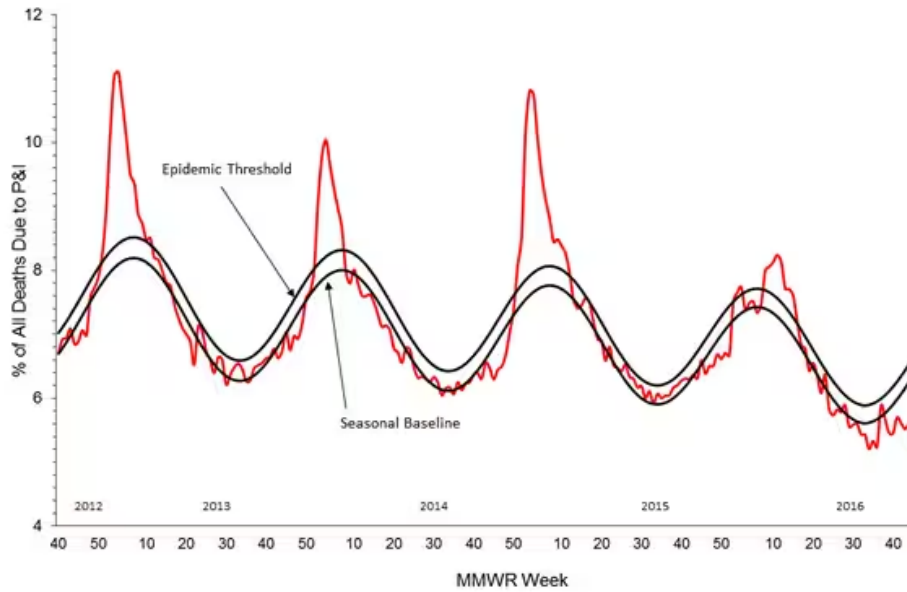
Based on National Center for Health Statistics (NCHS) mortality surveillance data available on November 30, 2016, 5.2% of the deaths occurring during the week ending November 12, 2016 (week 45) were due to P&I. This percentage is below the epidemic threshold of 6.9% for week 45.

Weekly mortality surveillance data includes a combination of machine coded and manually coded causes of death collected from death certificates. A backlog of data requiring manual coding continues to exist within NCHS mortality surveillance data. The percentages of deaths due to P&I are higher among manually coded records than more rapidly available machine coded records and may result in initially reported P&I percentages that are lower than percentages calculated from final data. Efforts continue to reduce and monitor the number of records awaiting manual coding. During week 47, it was determined that data from the summer months were sufficient to allow re-calculation of seasonal baseline and epidemic threshold values. Those modified values are used in the current report and will be used going forward.

Beginning in the week ending October 8, 2016 (week 40), CDC retired the 122 Cities Mortality Reporting System and uses only the NCHS Mortality Surveillance System.

Region and state-specific data are available at <http://gis.cdc.gov/grasp/fluview/mortality.html>.

**Pneumonia and Influenza Mortality from
the National Center for Health Statistics Mortality Surveillance System**
Data through the week ending November 12, 2016, as of November 30, 2016



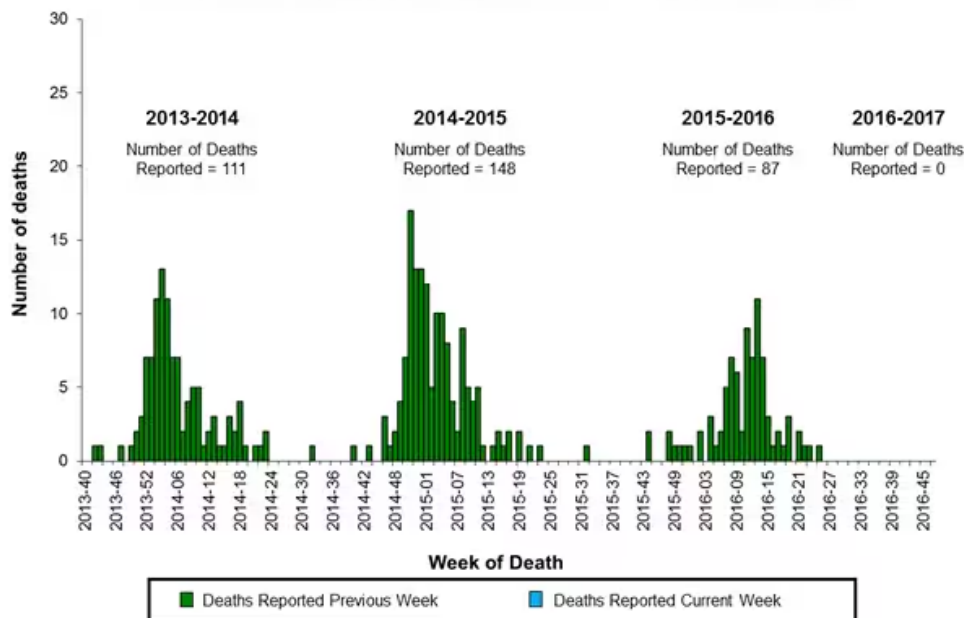
[View Regional and State Level Data](#) | [View Chart Data](#) | [View Full Screen](#) | [View PowerPoint Presentation](#)

Influenza-Associated Pediatric Mortality:

No influenza-associated pediatric deaths were reported to CDC during week 47.

Additional data can be found at: <http://gis.cdc.gov/GRASP/Fluview/PedFluDeath.html>.

Number of Influenza-Associated Pediatric Deaths by Week of Death: 2013-2014 season to present



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Influenza-Associated Hospitalizations:

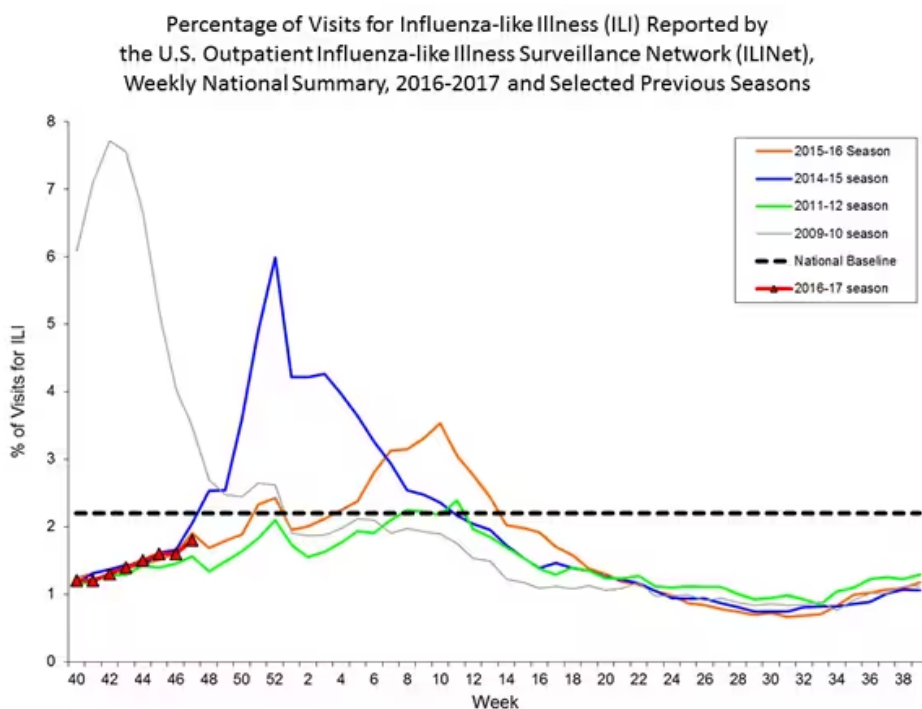
The Influenza Hospitalization Surveillance Network (FluSurv-NET) conducts population-based surveillance for laboratory-confirmed influenza-related hospitalizations in select counties in the Emerging Infections Program (EIP) states and Influenza Hospitalization Surveillance Project (IHSP) states. FluSurv-NET estimated hospitalization rates will be updated weekly starting later this season. Additional FluSurv-NET data can be found at: <http://gis.cdc.gov/GRASP/Fluview/FluHospRates.html> and <http://gis.cdc.gov/grasp/fluview/FluHospChars.html>.

Outpatient Illness Surveillance:

Nationwide during week 47, 1.8% of patient visits reported through the U.S. Outpatient Influenza-like Illness Surveillance Network (ILINet) were due to influenza-like illness (ILI). This percentage is below the national baseline of 2.2%.

(ILI is defined as fever (temperature of 100°F [37.8°C] or greater) and cough and/or sore throat.)

Additional data are available at <http://gis.cdc.gov/grasp/fluview/fluportaldashboard.html>.



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On a regional level, the percentage of outpatient visits for ILI ranged from 0.8% to 3.5% during week 47. Three regions (regions 2, 4, and 10) reported a proportion of outpatient visits for ILI at or above their region-specific baseline levels.

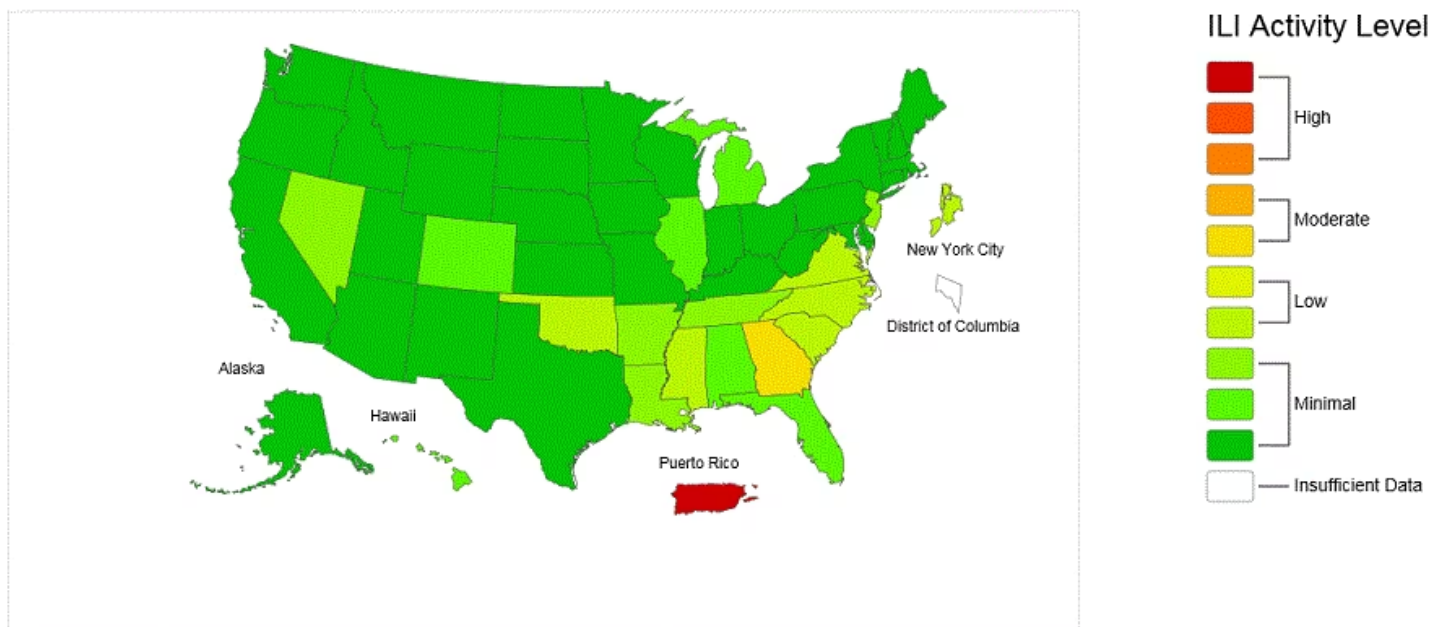
ILINet State Activity Indicator Map:

Data collected in ILINet are used to produce a measure of ILI activity* by state. Activity levels are based on the percent of outpatient visits in a state due to ILI and are compared to the average percent of ILI visits that occur during weeks with little or no influenza virus circulation. Activity levels range from minimal, which would correspond to ILI activity from outpatient clinics being below, or only slightly above, the average, to high, which would correspond to ILI activity from outpatient clinics being much higher than average.

During week 47, the following ILI activity levels were experienced:

- Puerto Rico experienced high ILI activity.
- One state (Georgia) experienced moderate ILI activity.
- New York City and five states (Mississippi, North Carolina, Oklahoma, South Carolina, and Virginia) experienced low ILI activity.
- 44 states (Alabama, Alaska, Arizona, Arkansas, California, Colorado, Connecticut, Delaware, Florida, Hawaii, Idaho, Illinois, Indiana, Iowa, Kansas, Kentucky, Louisiana, Maine, Maryland, Massachusetts, Michigan, Minnesota, Missouri, Montana, Nebraska, Nevada, New Hampshire, New Jersey, New Mexico, New York, North Dakota, Ohio, Oregon, Pennsylvania, Rhode Island, South Dakota, Tennessee, Texas, Utah, Vermont, Washington, West Virginia, Wisconsin, and Wyoming) experienced minimal ILI activity.
- Data were insufficient to calculate an ILI activity level from the District of Columbia.

Influenza-Like Illness (ILI) Activity Level Indicator Determined by Data Reported to ILINet 2016-17 Influenza Season Week 47 ending Nov 26, 2016



[Click on map to launch interactive tool](#)

*This map uses the proportion of outpatient visits to health care providers for ILI to measure the ILI activity level within a state. It does not, however, measure the extent of geographic spread of flu within a state. Therefore, outbreaks occurring in a single city could cause the state to display high activity levels.

Data collected in ILINet may disproportionally represent certain populations within a state, and therefore, may not accurately depict the full picture of influenza activity for the whole state.

Data displayed in this map are based on data collected in ILINet, whereas the State and Territorial flu activity map is based on reports from state and territorial epidemiologists. The data presented in this map is preliminary and may change as more data are received.

Differences in the data presented here by CDC and independently by some state health departments likely represent differing levels of data completeness with data presented by the state likely being the more complete.

[Geographic Spread of Influenza as Assessed by State and Territorial Epidemiologists](#)

The influenza activity reported by state and territorial epidemiologists indicates geographic spread of influenza viruses, but does not measure the severity of influenza activity.

During week 47, the following influenza activity was reported:

- Regional influenza activity was reported by Guam, Puerto Rico, the U.S. Virgin Islands, and one state (North Carolina).
- Local influenza activity was reported by 12 states (Alabama, Connecticut, Georgia, Indiana, Louisiana, Maine, Massachusetts, Nevada, New Hampshire, Oregon, Texas, and Washington).

- Sporadic influenza activity was reported by the District of Columbia and 36 states (Alaska, Arizona, Arkansas, California, Colorado, Delaware, Florida, Hawaii, Idaho, Illinois, Iowa, Kansas, Kentucky, Maryland, Michigan, Minnesota, Mississippi, Missouri, Montana, Nebraska, New Jersey, New Mexico, New York, North Dakota, Ohio, Oklahoma, Pennsylvania, South Carolina, South Dakota, Tennessee, Utah, Vermont, Virginia, West Virginia, Wisconsin, and Wyoming).
- No activity was reported by one state (Rhode Island).



[Flu Activity data in XML Format](#) | [View Full Screen](#)

Additional National and International Influenza Surveillance Information

FluView Interactive: FluView includes enhanced web-based interactive applications that can provide dynamic visuals of the influenza data collected and analyzed by CDC. These FluView Interactive applications allow people to create customized, visual interpretations of influenza data, as well as make comparisons across flu seasons, regions, age groups and a variety of other demographics. To access these tools, visit <http://www.cdc.gov/flu/weekly/fluviewinteractive.htm>.

U.S. State and local influenza surveillance: Click on a jurisdiction below to access the latest local influenza information.

Alabama	Alaska	Arizona	Arkansas	California
Colorado	Connecticut	Delaware	District of Columbia	Florida
Georgia	Hawaii	Idaho	Illinois	Indiana
Iowa	Kansas	Kentucky	Louisiana	Maine
Maryland	Massachusetts	Michigan	Minnesota	Mississippi
Missouri	Montana	Nebraska	Nevada	New Hampshire
New Jersey	New Mexico	New York	North Carolina	North Dakota
Ohio	Oklahoma	Oregon	Pennsylvania	Rhode Island
South Carolina	South Dakota	Tennessee	Texas	Utah
Vermont	Virginia	Washington	West Virginia	Wisconsin
Wyoming	New York City	Puerto Rico	Virgin Islands	

World Health Organization: Additional influenza surveillance information from participating WHO member nations is available through [FluNet](#) and the [Global Epidemiology Reports](#).

WHO Collaborating Centers for Influenza located in [Australia](#), [China](#), [Japan](#), the [United Kingdom](#), and the [United States](#) (CDC in Atlanta, Georgia).

Europe: For the most recent influenza surveillance information from Europe, please see WHO/Europe and the European Centre for Disease Prevention and Control at <http://www.flunewseurope.org/>.

Public Health Agency of Canada: The most up-to-date influenza information from Canada is available at <http://www.phac-aspc.gc.ca/fluwatch/>

Public Health England: The most up-to-date influenza information from the United Kingdom is available at <https://www.gov.uk/government/statistics/weekly-national-flu-reports>

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An overview of the CDC influenza surveillance system, including methodology and detailed descriptions of each data component, is available at: <http://www.cdc.gov/flu/weekly/overview.htm>.
