Introduction In 2015, the estimated HIV prevalence in Brazil was 0.4%. This figure has been stable in recent years, but it can mask disparities among regions. In this study we present the spatial distribution of the variation in HIV incidence rates (IR) in Brazilian municipalities from 2009–14 and assess the existence of spatial clustering of increase or decrease in these IR.

Methods We used the AIDS reporting system (Sinan) and programmatic data on Viral Load (VL) exams and ARVs. The diagnosis date used was the earliest among 1st detectable VL, 1st ARV dispensation or diagnosis date in Sinan. Annual IR were generated by municipality. To smooth the IR, we used 3 year averages and applied the local empirical Bayesian method. To assess IR time trends, we calculated the percent IR variations in the period. For spatial statistical analysis, a simple adjacency matrix was generated, and Global and Local Moran’s I autocorrelation tests were applied.

Results The Global Moran’s I for the IR variation was 0.42 (p<0.001) which points to spatial clustering. We generated 2 maps, one for the percent IR variation and another to represent the statistically significant high-high and low-low clusters. In the 1st, we observed that most municipalities in the North (N) and Center-West (CW) present increases in the period; in the Southeast (SE), the state of Sao Paulo (SP) reveals the most relevant decreases in the country; the Northeast (NE), South (S) and some areas of the SE show mixed patterns. The 2nd map makes regional disparities even clearer. There are big clusters of increasing IR in most states of the N, and smaller ones in areas of the CW and NE. Several clusters of declining IR are seen in SP, Minas Gerais (SE), Santa Catarina, Rio Grande do Sul(S), and areas of the NE.

Conclusion Spatial dependency in HIV IR variations in Brazil was evidenced. The methods used in this study have proved useful in monitoring spatiotemporal trends, pointing out important regional differences. Similar analysis can be performed at state and city levels, contributing to improved diagnoses of local epidemics.

P3.150

IMPORTANCE OF REGIONAL OFFICES ON THE IST PROTOCOL OF THE MINISTRY OF HEALTH FOR MULTIPLICATOR FORMATION AND CONTROL OF THESE INFECTIONS IN BRAZIL

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10.1136/sextrans-2017-053264.385

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Introduction According to the World Health Organisation, more than a million STIs are acquired every day. In 2012, an estimated 357 million new cases of curable STIs (gonorrhoea, chlamydia, syphilis and trichomoniasis). The care for clients with STIs is mostly performed in the Primary Care service (AB), in order to stop the signs and symptoms, preventing these infections from becoming complicated, interrupting the transmission chain as effectively and immediately as possible.

After ten years of publication of the Manual on the Control of Sexually Transmitted Diseases, the Department of STIs, HIV/AIDS and Viral Hepatitis (DIAHV) of the Ministry of Health (MS) innovates and launches a Clinical Protocol and Therapeutic Guidelines for Integral Care for Persons with Sexually Transmitted Infections Transmissible - PCDT/IST, considering the need to hold regional workshops for multipliers in the territories. To align and integrate prevention, care, treatment and surveillance actions in the health services, strengthen the work of health professionals in STI/HIV/Aids, according to PCDT/IST; identify the professional’s abilities to perform the appropriate management of care for people with STIs; to discuss the flowcharts and protocols used in the management of STIs.

Methods Using the methodology of the problematization, which proposes the construction of knowledge, based on the reality of the participants and favours the joint reflection and the exchange of experiences. For the realisation of the workshops in the regions, the DIAHV counted on partnership of the states.

Results More than 400 professionals (doctors and nurses) from specialised services and AB were trained in four regions of the country.

Conclusion The realisation of these workshops and the interaction of the DIAHV/MS technicans with care professionals contributed to standardise the management of STIs and to qualify health care for people with STIs. These professionals were certified to multiply the workshop to their peers and send reports of actions to the state.
main age group was 20–24 with speed=106 cases/year, (p=0.043).

Conclusion There was a decreasing trend of AIDS cases and growth in HIV+, with expressive speed among young MSM. This analysis points to the need for discussions of unprotected sexual practices, combined prevention and other actions aimed to controlling the epidemic in greater vulnerability groups.

**P3.152** PREVALENCE OF BACTERIAL VAGINOSIS INFECTION AND ASSOCIATED FACTORS IN WOMEN WHO HAVE SEX WITH WOMEN

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10.1136/sextrans-2017-053264.387

Introduction The present research aims to fill a gap in the national and international literature concerning prevalences and factors related to Bacterial vaginosis (BV) in Women who Have Sex with Women (WSW).

Methods It is a cross sectional, analytical and non-randomized study with 128 WSW from Botucatu - SP and surrounding regions who answered the call from social media, mass communication means, health services and friends or acquaintances from January to November,2015. Data was obtained by the researchers involved in the main study, through interviews ang gynaecological exam. The diagnostic of BV was abted through gram staining. Associations were estimated by multiple regression.

Results The prevalence of BV was 41.1%(%) and factors associated were vaginal douching [OR=3.29 (IC:95%: 1.26–8.59) p=0014] and sex toys use[OR=2.34 (IC:95%: 1.00–5.50), p=0049].

Conclusion Considered as whole, these data lead to conclusion that the individuals of this study presented high vulnerability to STI/AIDS, as shown by the high prevalence of BV. This study clearly shows the need for a specific health assistance to these women, promoting prevention and education in a holistic approach.

**P3.153** SPATIAL AND TEMPORAL ASSOCIATIONS BETWEEN CONGENITAL SYPHILIS CASES AND EPIDEMIOLOGICAL CHARACTERISTICS OF INFECTION SYPHILIS IN ENGLAND


10.1136/sextrans-2017-053264.388

Introduction There has been a rapid rise in infectious syphilis (IS) diagnoses in England since 2011 but congenital syphilis (CS) is rare. In 2016, 3 CS cases were diagnosed in geographically dispersed areas of England. Unusually, their mothers had tested negative at first trimester antenatal screen (screen-negative), indicating syphilis acquisition during pregnancy. Simulation modelling using historical CS cases indicated an event probability of 3%. We investigated the spatial and temporal relationship between screen-negative CS cases and IS epidemiology in the affected areas.

Methods Data from 01/2011-06/2016 were obtained from GUMCADv2, the national electronic surveillance system. England was divided into 3 syphilis epidemiological areas (SEAs): wider incident areas (WIA); the 3 affected and intermediate surrounding counties; endemic areas (with established epidemics in men who have sex with men-MSM) and non-incident non-endemic areas (NINEAs). Time-series analysis (TSA) was used to estimate IS outliers by gender, sexual orientation and SEA. Associations between IS characteristics and SEA (WIA vs. NINEAs) were assessed using Pearson’s chi-square and Kruskal-Wallis tests. Mothers of CS cases were excluded from analyses.

Results In 2011–2016, IS rates/100,000 in WIA; rose in heterosexual women (1.3–3.0) and MSM (8.9–13.9) but fell in heterosexual men (3.7–3.0). In NINEAs rates rose in heterosexual women (1.6–1.9), MSM (5.0–10.8) and heterosexual men (2.7–3.2). On TSA, IS cases significantly exceeded expected bounds in 2016 in heterosexual women in WIA; no exceedance was seen in NINEAs. In 2016, heterosexual women with IS were more likely to be UK-born in WIA than in NINEAs (78% vs. 39%; p<0.001). A greater proportion of MSM were bisexual in WIA than in NINEAs (11% vs. 8%; p<0.001).

Conclusion Increased syphilis transmission in some sexual networks of MSM and a higher proportion of bisexual men in WIA may have created more opportunities for IS acquisition in women. Efforts to raise awareness of the potential risk of acquiring syphilis during pregnancy are needed.

**P3.154** CLONAL SPREAD OF AZITHROMYCIN RESISTANT NEISSERIA GONORRHOEAE IN CANADA (2014–2015)

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10.1136/sextrans-2017-053264.389

Introduction Neisseria gonorrhoeae have acquired resistance to many antimicrobials including third generation cephalosporins and azithromycin, which are the current co-therapy recommended by the Canadian STI guidelines for gonorrhoea treatment. Minimum inhibitory concentrations (MIC) to azithromycin and molecular sequence types were determined for N. gonorrhoeae circulating in Canada.

Methods Between 2014 and 2015, N. gonorrhoeae strains isolated by Canadian provincial public health laboratories were submitted to the National Microbiology Laboratory (NML) (n=4,720) for azithromycin MIC determination (resistance MIC ≥2.0 mg/L) by agar dilution. N. gonorrhoeae multi-antigen sequence typing (NG-MAST) was used for molecular typing.

Results Azithromycin resistance was identified in 3.3% (127/ 3,809) and 4.7% (198/4,190) of N. gonorrhoeae in 2014 and 2015, respectively, a significant increase since 2013 (p<0.001). MICs ranged from 2 to 16 mg/L. The most common sequence types identified in 2014 were ST10451 (n=40), ST10567 (n=38) and ST11765 (n=10). ST11765 is closely related to ST10721 (n=4,720) for azithromycin MIC determination (resistance MIC ≥2.0 mg/L) by agar dilution. N. gonorrhoeae multi-antigen sequence typing (NG-MAST) was used for molecular typing.

Results Azithromycin resistance was identified in 3.3% (127/ 3,809) and 4.7% (198/4,190) of N. gonorrhoeae in 2014 and 2015, respectively, a significant increase since 2013 (p<0.001). MICs ranged from 2 to 16 mg/L. The most common sequence types identified in 2014 were ST10451 (n=40), ST10567 (n=38) and ST11765 (n=10). ST11765 is closely related to ST10451, differing by 1 bp in the por allele. In 2015, the prevalent sequence types were ST12302 (n=110), ST10451 (n=34) and ST9047 (n=23). ST10451, identified in Quebec, Ontario and Alberta, was newly identified in 2014 and also identified in 2015. ST10451 is related to ST1407 (differing by 1 bp in the por allele) which is an internationally-