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Risk factors and micro-geographical heterogeneity of *Schistosoma haematobium* in Ndumo area, uMkhanyakude district, KwaZulu-Natal, South Africa

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ABSTRACT

Schistosomiasis is a snail-transmitted parasitic disease endemic in most rural areas of sub-Saharan Africa. However, the currently used prediction models fail to capture the focal nature of its transmission due to the macro-geographical levels considered and paucity of data at local levels. This study determined the spatial distribution of *Schistosoma haematobium* and related risk factors in Ndumo area, uMkhanyakude District, KwaZulu-Natal province in South Africa. A sample of 435 schoolchildren between 10 to 15 years old from 10 primary schools was screened for *S. haematobium* using the filtration method. Getis-Ord Gi* and Bernoulli model were used to determine the hotspots of *S. haematobium* infection intensity based on their spatial distribution. Semiparametric-Geographically Weighted Regression (s-GWR) model was used to predict and analyse the spatial distribution of *S. haematobium* in relation to environmental and socio-economic factors. We confirmed that schistosomiasis transmission is focal in nature as indicated by significant *S. haematobium* cases and infection intensity clusters ($p < 0.05$) in the study area. The s-GWR model performance was low ($R^2 = 0.45$) and its residuals did not show autocorrelation (Moran's $I = -0.001$; z-score = 0.003 and p-value = 0.997) indicating that the model was correctly spelled. The s-GWR model also indicated that the coefficients for some of the socio-economic variables such as distances of households from operational piped water collection points, distance from open water sources, religion, toilet use, household head and places of bath and laundry significantly (t-values +/−1.96) varied across the landscape thereby determining the variation of *S. haematobium* infection intensity. This evidence may be used for control and management of the disease at micro scale. However, there is need for further research into more factors that may improve the performance of the s-GWR models in determining the local variation of *S. haematobium* infection intensity.

1. Background

Schistosomiasis is a snail-borne parasitic disease caused by *Schistosoma haematobium* and *Schistosoma mansoni.* The disease is of public health importance in sub-Saharan Africa where approximately 200,000 deaths per year are associated with it (WHO, 2014) despite the control efforts (Fenwick et al., 2009). The estimated global burden of the diseases is 3.3 million disability–adjusted life years (Murray et al., 2013). Distribution of the diseases is dependent on presence of intermediate hosts (*Bulinus* species for *S. haematobium* and *Biomphalaria* species for *S. mansoni*) (Brown, 1994). Approximately 76% of the sub-Saharan population lives close to open water bodies including rivers, ponds and dams which are infested with the intermediate snail hosts that transmit schistosomiasis (Steinmann et al., 2006). In South Africa, schistosomiasis is endemic in KwaZulu-Natal province, north east of the country where *S. haematobium* is the predominant species (Schutte et al., 1995).

Schistosomiasis transmission is very focal and heterogeneous in nature, thus necessitating local-scale studies in endemic areas (Rudge et al., 2008). The focality and heterogeneity in schistosomiasis transmission reflect the local complex interaction of human and snail host as well as environmental and socio-economic fac-

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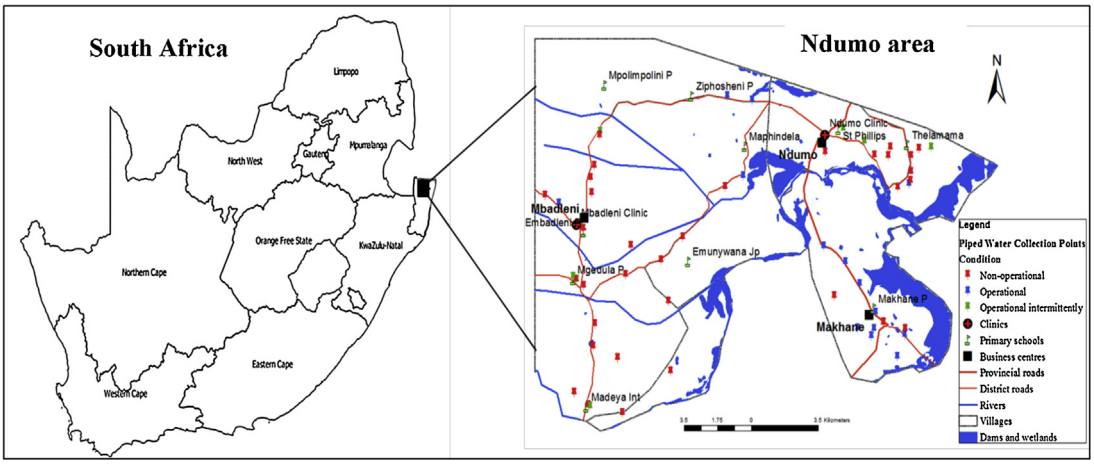

Fig. 1. Study area—Ndumo, uMkhanyakude District, KwaZulu-Natal, South Africa.

tors (Fenwick et al., 2006; Woodhall et al., 2013). For transmission to occur people must be in contact with water contaminated by schistosome cercariae from infected snails (Woodhall et al., 2013). Distance to water contact sites, land-use and the distribution of infected intermediate host snails and socio-economic factors such as sex, sources of drinking water, latrine availability at home and inadequate sanitation have been reported to contribute to the heterogeneity at local level (Chandiwana et al., 1988; Gryseels and Nkulikyinka, 1988, 1990; Chimbari et al., 2003; Raso et al., 2005, 2007; Gazzinelli et al., 2006; Kapito-Tembo et al., 2009; Odiere et al., 2011; Grimes et al., 2014). Thus, intensity of infection is influenced considerably by the frequency and duration of human contact with contaminated water (Kloos et al., 1998). This is complementary to the continental and national scales where climatic factors (temperature and rainfall) and physical factors (vegetation, altitude, large water bodies) have been identified as major determinants of the heterogeneous geographical distribution of schistosome infections (Tsang et al., 1997; Handzel et al., 2003; Simoonga et al., 2008; Brooker and Clements, 2009; Clements et al., 2009). The small scale heterogeneity of schistosomiasis is mainly due to locally determined factors, and characterisation of these factors has long been considered to have important implications for control programmes (Woolhouse et al., 1997). The knowledge on spatial heterogeneity of schistsosmiasis at local levels helps to understand the local transmission dynamics and identification and location of communities at high risk and transmission sites. Such knowledge will provide insights into the drivers of transmission and help in designing schistosomiasis control and elimination efforts that are multifaceted, but selectively focused in space and time (Ekpo et al., 2008; Peng et al., 2010).

The geographical distribution of schistosome infections has been modelled using different methods including Bayesian geostatistical modelling (Clements et al., 2006; Brooker et al., 2009). Predictive maps have been generated to guide schistosomiasis control programmes but these maps have a limitation in clearly predicting the distribution of the diseases due to the focal nature of transmission mainly determined by distribution of intermediate hosts (Clements et al., 2006; Brooker et al., 2009). Thus, there is a paucity of data on the micro-geographical and micro-epidemiological information of schistosomiasis in endemic areas (Mccreesh and Booth, 2013). The quantification of heterogeneities in the distribution of schistosomiasis and its use in targeting control interventions at micro-geographic level is scarce and can only be ascertained by micro-geographical studies within endemic communities to determine the extent and causes of small-scale heterogeneity (Rudge et al., 2008).While accurate data are needed, an attempt to reduce transmission and efforts to eliminate schistosomiasis are getting on the international public health agenda (Knopp et al., 2013) there is need to develop or use innovative mapping methodologies that consider focality of schistosomiasis (Ruberanziza et al., 2015). There are several disaggregate spatial statistical techniques available for empirical analysis (Nkeki and Osirike, 2013) including the geographically weighted regression (Fotheringham et al., 2002), local indicator of spatial association (Anselin, 1995); local Gi* Statistics (Ord and Getis, 1995); local Moran's *I* (Anselin, 1995) and the Bernoulli and Poisson regression models in Kulldorff's scan (Kulldorff, 1997b). The use of these local spatial statistics has become widespread and prominent especially among spatial analysts, geographers, medical practitioners, physical and social scientists mainly because it is fast becoming an established fact that global statistics can no longer satisfy contemporary policy needs (Nkeki and Osirike, 2013). However, these techniques are yet to be fully tested or used especially at small scale schistosomiasis modelling.

The aim of this study was to determine the spatial distribution of *S. haematobium* and related risk factors in Ndumo area, uMkhanyakude District, KwaZulu-Natal province in South Africa based on the null hypothesis of uniform distribution of *S. haematobium* at micro-scale. The Bernoulli model and the Getis-Ord models were used to determine the spatial distribution or pattern of *S. haematobium* infections. A semi-parametric Geographically Weighted Regression (s-GWR) model was used to explore the relationship between *S. haematobium* and environmental and socio-economic factors.

2. Methods

2.1. Study area

This study was conducted in Ndumo area of uMkhanyakude Health District in KwaZulu-Natal (KZN) province, South Africa (Fig. 1). The area is approximately 60 km by 30 km. There are seasonal streams/rivers flowing towards the Pongola flood plain and two main dams (Nsunduza and Namaneni) in the area. Almost 20% of the population in Ndumo are unemployed and over 70% are not economically active, resulting in high levels of poverty (Lankford et al., 2011). UMkhanyakude district experiences hot and wet summer and a cold and dry winter. More than half of the households in this area lack clean water and sanitary facilities (Pschorn-Strauss, 2005) hence they are more vulnerable to vector-borne diseases (VBDs) like schistosomiasis. Fig. 1 also shows the distribution of piped water collection points in Ndumo area during the study

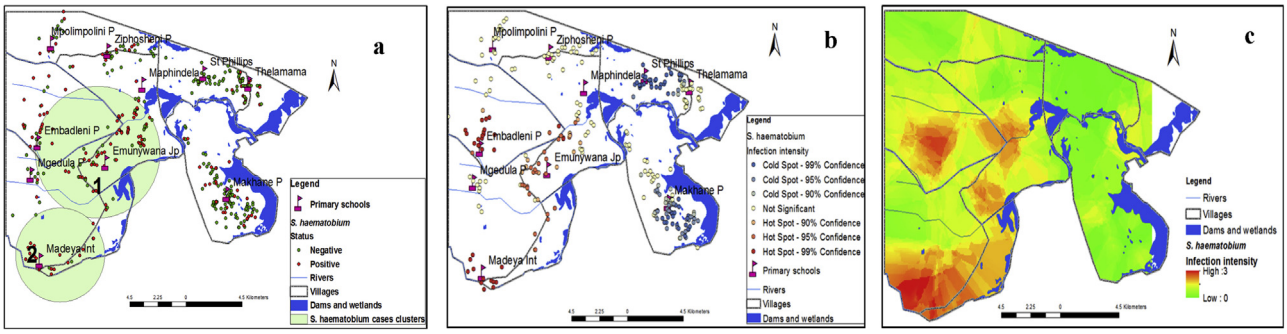

Fig. 2. (a) *Schistosoma haematobium* clusters by cases (Bernoulli model in SatScan) in Ndumo area of uMkhanyakude district (b) *Schistosoma haematobium* spatial clusters by intensity (Getis-Ord Gi*) in Ndumo area of uMkhanyakude district (c) Spatial distribution of the 3 classes of *S. haematobium* infection intensity: 0-no case, 2-light infection (1–49 eggs per 10 ml of urine) and 3 – heavy infection (greater than 50 eggs per 10 ml of urine) from Empirical Bayesian Model (EBK) in ArcGIS 10.2.

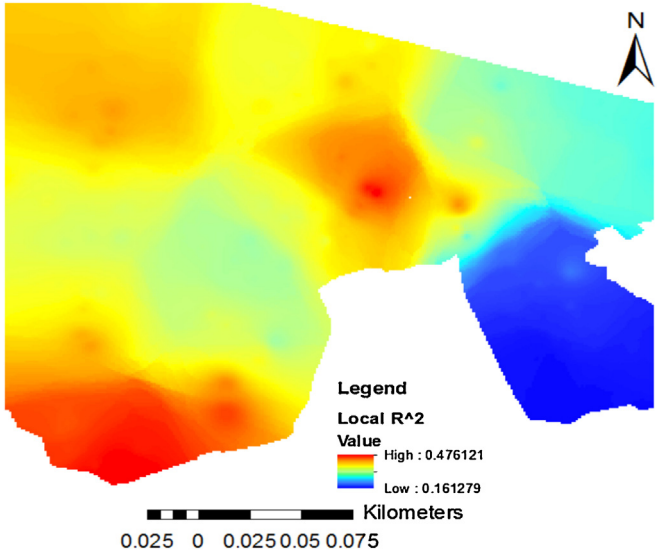

Fig. 3. Local R^2 variation of the semiparametric-Geographically weighted Regression (s-GWR) model of the *Schistosoma haematobium* in Ndumo area, uMkhanyakude district, South Africa.

period. The larger part of the south western part of Ndumo area covering Madeya, Mgedula and Mbadhleni primary school had no operational piped water collection points (Fig. 1). Schistosomiasis intermediate host snails (*Bulinus globosus* and *Biomphalaria pfeiffferi)* are also present in the study area.

2.2. Parasitological survey

A sample of 435 schoolchildren between the ages of 10–15 years from 10 primary schools (Fig. 1) was screened for *S. haematobium* using the filtration method in September 2014. Equal selection of participants from both sexes was guaranteed and systematic sampling was used to avoid biased selection of participants. Urine specimens were collected between 10 am and 2 pm when egg excretion is usually maximal (Despommier et al., 2012) and processed using the filtration method for detection of *S. haematobium* eggs (Mott, 1983; Chimbari et al., 1993). *S. haematobium* eggs were microscopically identified and quantified as number of eggs per 10 ml of urine (Despommier et al., 2012).

2.3. Questionnaire survey

A questionnaire was administered to 320 schoolchildren who participated in the parasitology survey described above. However, only 314 questionnaires were analysed as the other 6 were not well georeferenced. The questionnaire solicited for data on socio-economic factors related to *S. haematobium* infections. The factors included age, gender, religion, household head, toilet at home, toilet use, place of bath and laundry and household livelihoods.

2.4. Mapping

The primary schools and homesteads with school going children aged 10 to15 years selected for this study were geo-referenced using the hand held Differential Global Position System (DGPS) receivers (Trimble Geoexplorer, Sunnyvale, CA). Water sources such as rivers, dams and operational public piped water were also captured using DGPS. Distance calculator functionality of ArcGIS 10.x was used to calculate the distance between the households and the nearest river or dam as well as the nearest operational public piped water collection points.

2.5. Ethical considerations

The study was part of a larger project on malaria and bilharzia in Southern Africa (MABISA). Ethical approval was obtained from Biomedical Research Ethics Committee (BREC) at University of KwaZulu-Natal for the main MABISA project and this particular study. We also obtain the gate keeper permission from the Ministry of Health and worked hand in hand with the local health centres. Informed consent and assent was sought from the parents or legal guardians of the child and the child respectively since this project involved children less than 18 years of age. Only pupils with signed consent and assent forms were eligible for participation as the participation in the study was absolutely voluntary. We guaranteed confidentiality of participants' information including results. Positive cases of schistosomiasis were treated with praziquantel.

2.6. Spatial statistical analysis

2.6.1. Schistosomiasis cases spatial-clusters detection

The widely used Kulldorff's scan statistic in SaTScan™ (Kulldorff, 1997c, 1997b, 2015; Huang et al., 2007; Warden, 2008) tests whether events such as disease cases are distributed randomly in space and, if not, identifies the approximate location of significant geospatial clusters (Kulldorff, 1997b; Meurs et al., 2013). The Bernoulli method in SaTScan™ uses the "0"and "1" event data to detect prevalence clusters. The same approach was adopted in this study, "1" represented the cases of *S. haematobium* while "0" was none cases of *S. haematobium* (controls). Thus cases and controls were used to determine if there was significant clustering of

the case location distribution as compared to the controls location distribution (Kulldorff and Nagarwalla, 1995; Kulldorff, 1997a; Warden, 2008). SaTScan™ uses a moving, window of varying diameter to detect and evaluate clusters. For each window location and size, the number of observed and expected observations are calculated, percentage cases in area and relative risk inside the window and in turn, calculates the likelihood function for each window, the form of which differs depending on the assumed distribution of events. The advantage of this method is that it is independent of the underlying population distribution (Warden, 2008). The SaTScan Bernoulli model uses a likelihood ratio test of the probability of a group of cases within a potential cluster defined by a circle. The likelihood function for the Bernoulli model was calculated as described by Kulldorff (1997c) Warden (2008) and Kulldorff (2015). Relative risk is the estimated risk within the cluster divided by the estimated risk outside the cluster.

In this study the significant ($p < 0.05$) and non-overlapping clusters are reported. These high-risk clusters were based on maximum radius of 5 km, 50% of the total number of subjects and no adjusting for more likely clusters. The 999 Monte-Carlo replications were conducted to evaluate statistical significance of the clusters (Meurs et al., 2013; Nagi et al., 2014).

2.6.2. *S. haematobium* infection intensity spatial clusters detection

S. haematobium infection intensity ranged from 0 to 2104 eggs per 10 ml of urine which was classified into 3 classes according to WHO guidelines (WHO, 2002). The classes include: 0 eggs/10 ml of urine (no case), 1–49 eggs per 10 ml of urine (light infections) and ≥50 eggs per 10 ml of urine (heavy infections). Spatial autocorrelation analysis methods were used to determine if similar values (number of eggs per 10 ml of urine) in a dataset were closer to each other than expected thus clustered. The spatial statistics used in this study include the Global Moran's *I* (1950), and the local indicators of spatial association (LISA) (Anselin, 1995)—Getis-Ord Gi* (Getis and Ord, 1992; Ord and Getis, 1995) Global Moran's *I* was used to evaluate or quantify the overall spatial autocorrelation or spatial pattern of *S. haematobium* intensity in the whole study area and was tested for significance. Global Moran's *I* was used with a row standardisation to take care of the possible errors in sampling. Moran's *I* values range from −1 to 1. While 1 indicates a perfect positive correlation, 0 implies perfect spatial randomness and −1 suggests a perfect negative spatial autocorrelation (Tu and Xia, 2008). The Getis-Ord Gi* (G/Gi*) measures the degree of spatial autocorrelation at each specific location thus it was used to detect *S. haematobium* hot spots. This method gives the level of confidence or significance of each point that is its probability of being part of cluster or hotspot in relation to the surrounding points. The Empirical Bayesian Kriging (EBK) in ArcGIS 10.2 was used to model the spatial distribution of the 3 classes of *S. haematobium* infection intensity in the study area for visualisation.

2.6.3. Modelling the spatial relationship between S. haematobium and related risk factors

Geographically weighted regression (GWR) approaches were proposed so as to cope with spatially nonstationary processes (Fotheringham et al., 2002). In this study we used semiparametric GWR (s-GWR) model to explore the spatial relationship between classified *S. haematobium* infection intensity and socio-economic and environmental factors. The semi-parametric model proposed by Nakaya et al. (2005) accommodates situations where some covariate effects (parameters) may not vary geographically (Ribeiro et al., 2015). Using s-GWR makes it possible to estimate local rather than global parameters and thus provides a way of accommodating the local geography (Nakaya et al., 2005) of the relationship between *S. haematobium* and socio-economic and environmental factors. The statistical output of s-GWR software includes a baseline global model result (parameter estimates) (Matthews and Yang, 2012).

Semiparametric Gaussian GWR (s-GWR) model is specified by (Nakaya, 2014) as shown in the equation in Eq. (1).

$$y_i = \sum_k \beta_k(u_i, v_i) x_{k,i} + \sum_l \gamma_l z_{l,i} + \varepsilon_i \quad (1)$$

Local terms

Global terms

where y_i, $x_{k,i}$, and ε_i are dependent variable, kth independent variable, and the Gaussian error at the location *i* respectively; (u_i, v_i) is the x-y coordinate of the *i*th location; and coefficients β_k (u_i, v_i) are varying conditional on the location, $z_{l,i}$, is the *l*th independent variable with a fixed coefficient y_l. Thus, the model mixes geographically local and global terms.

We used the adaptive bi-square kernel for geographically weighting since it is suitable for clarifying local extents for model fitting and keeping constant the number of areas to be included in the kernel (Nakaya, 2014). The golden search was also used to automatically and efficiently determine the best or optimal bandwidth size for geographically weighting.

AICc, R^2 and adjusted R^2 were used to select the best model. The model with smaller AICc performs better compared to the one with higher AICc as Ribeiro et al. (2015) noted that if the difference between Aikaike's Information Criteria (AICc) is larger than 2, the model with lower AICc is selected. The Moran's *I* was used to check if there was still autocorrelation in the residuals of the local GWR model which might indicate misspecification of the model or missing of key variables to explain the spatial pattern.

A convenient 5-number summary that defines the extent of the variability in the parameter estimates (minimum, lower quartile, median, upper quartile, and maximum local parameter estimates reported in the GWR model) was presented in a table. The Monte Carlo test result for non-stationarity in each parameter was also presented for visualizing the local parameter estimates and their associated diagnostics as advised by Matthews and Yang, (2012). In addition, GWR models estimate local standard errors, derive local t-statistics, calculate local goodness-of-fit measures including R-squared (R^2), and calculate local leverage measures. We generated maps of the spatial variation of local goodness of fit (R^2), the parameter estimates and local t-statistics from the local GWR as indicated by Matthews and Yang (2012) and Fotheringham et al. (2002). The mapping GWR results facilitates interpretation based on spatial context and known characteristics of the study area (Goodchild and Janelle, 2004). Mapping only the parameter estimate alone is misleading, as the map reader has no way of knowing whether the local parameter estimates are significant anywhere on the map (Matthews and Yang, 2012). Hence, we overlaid the t-values as isolines (or contour lines) on top of the parameter estimate surface to allow the map reader to read both the approximate parameter estimate and the t-value for any location on the map. The t-values indicate the significance of the coefficients (+/−1.96 are significant) across the study area.

Table 1
Properties of the *Schistosoma haematobium* clusters in Ndumo area, uMkhanyakude, South Africa (shown in Fig. 2a).

	Cluster 1 (Centre)	Cluster 2 (South West)
Radius	4.45 km	3.17 km
Population	92	26
Number of cases	66	22
Expected cases	36.8	10.4
Observed/expected	1.79	2.12
Relative risk	2.3	2.28
Percentage cases in area	71.7	84.6
Log likelihood ratio	24.48	11.75
P-value	<0.001	0.0028

3. Results

3.1. S. haematobium *spatial distribution in Ndumo area*

Two spatial clusters (1 and 2 in Fig. 2a and Table 1) of high relative risk of *S. haematobium* were identified through the Bernoulli model (SatScan Statistic). The two Clusters had similar relative risk and were significant ($p < 0.05$) based on the log likelihood ratio. This indicates and strengthens the observation that positive cases were grouped in these areas. *S. haematobium* positive cases were found close together in the identified clusters compared to other parts of Ndumo area indicating that distribution of prevalence or cases of *S. haematobium* are not uniform in this area. There were higher chances of 10–15 years school children in these clusters to be infected compared to other parts of Ndumo area.

3.2. S. haematobium *intensity spatial distribution in Ndumo area*

The Global Moran's Index for the classified *S. haematobium* infection intensity was 0.15 with a corresponding *z-value* of 10.24 and a $p < 0.05$. This indicates that similar values cluster spatially—meaning high intensity values are found closer together, and low intensity values are found closer together, than would be expected from an underlying random spatial process as there is less than 1% likelihood that this clustered pattern could be the result of random choice. The Getis-Ord Gi* method detected two significant clusters of high *S. haematobium* intensity and two significant cold spots for *S. haematobium* indicating the non-uniform distribution of *S. haematobium* intensity (Fig. 2b). These high intensity clusters were located in the same areas as high risk clusters in Fig. 2a. There were higher chances of 10–15 years school going children in these areas to be heavily infected compared to their counterparts in the other parts of Ndumo area. The spatial distribution of these infections can be visualised in Fig. 2c where 0 means no cases and 3 indicate heavy *S. haematobium* infections (number of eggs greater than or equal to 50 per 10 ml of urine). It is prominent in Fig. 2 that heavy infections were found in the middle of Ndumo area to the South East and the most likely factors contributing to this pattern are investigated in the next section.

3.3. S. haematobium *and related risk factors*

The convenient parameter 5-number summary of parameter estimates is shown in Table 2. Most of the variables showed significant variation in relation to spatial distribution of *S. haematobium* infection intensity except age, gender and household livelihoods.

The fitness parameters of the models are shown in Table 3. The Geographically weighted regression (local) model performed better compared to the global regression. However, the local to Global variable selection (where age, gender and household livelihoods were held constant) improved the model by 18.86.

The Moran's *I* of the residuals of the final local GWR model was −0.001 (z-score = 0.003 and p-value = 0.997). This indicates that there was no spatial autocorrelation and that the model was well specified. The local R-squared of the final model is shown in Fig. 3. The Model had higher prediction ability in areas which had higher *S. haematobium* infection intensities and cases. The variation of the estimated local coefficients and the t-statistic which indicate the significance of the coefficients is as shown in Fig. 4.

The local coefficients determined through the local to global variable criteria showed variation across Ndumo area. Most of the coefficients (Household head, places for bath and laundry, distance from piped water collection points and religion) had higher coefficients in the areas with high *S. haematobium* infection intensity and prevalence which is from the central part of Ndumo area to the South West. The coefficients are the marginal effects and they measure how much *S. haematobium* infection intensity (classes 1 to 3) changes for one unit changes in the exploratory variables. In Fig. 4, it is also evident that the significance (+/−1.96) of the coefficients of the exploratory variables varied across the study area.

4. Discussion

Results from this study indicated that *S. haematobium* prevalence, individual positive cases and level of intensity were spatially clustered indicating small-scale focality of the disease even within Ndumo area. The results are consistent with findings from other studies conducted in different endemic areas (Raso et al., 2005; Brooker et al., 2006; Clements et al., 2006; Simoonga et al., 2008). Such variation in exposure to schistosomiasis even in endemic communities has also been observed at micro-geographical level in Kenya (Fulford et al., 1996; Kloos et al., 1997; Stothard et al., 2002; Booth et al., 2004) and Brazil (Bethony et al., 2004) and Zanzibar (Rudge et al., 2008). The observed clusters were around the surveyed schools as previously observed by Stothard et al. (2002) and Rudge et al. (2008). These clusters were in the same areas (prevalence and intensity) indicating the relationship between the two. Meurs et al. (2013) studied the micro-geographical clustering of *Schistosoma* infection (*S. haematobium* and *S. mansoni*) in relation to schistosome specific morbidity including urinary tract morbidity and hepatic fibrosis in a co-endemic area, and found a weak correlation. Therefore this study could pave the way for further specific studies on morbidity and immunology in these clusters as well as outside the clusters.

The local GWR model used in this study showed how the coefficients of socio-economic and environmental factors related to *S. haematobium* intensity may vary across the landscape thereby determining the variation of the disease. As also observed by Feuillet et al. (2015), the non-stationarity of spatial datasets observed in this study has been demonstrated in other studies on health-related outcomes based on different variables and magnitudes. Hence, this study has shown that GWR-based analyses may provide insights into the contribution of different socio-economic variables on the distribution of schistosomiasis and could be used as a tool for place-specific targeting the control and management of the diseases. The local GWR model showed a higher performance in showing the spatial variation of the local parameters compared to global regression model. The local R^2 showed that the local model had higher performance in hotspots areas compared to the other parts of the study area. Although the local GWR model had a higher performance based on AICc and R^2 compared to global model, Ribeiro et al. (2015) has hinted that delivering the choice of model selection exclusively to AIC measure might hide important details in spatial variations of ecological associations, especially when difference between models AIC is marginal (close to 2). However, in this study the difference was far more than 2 which might

Table 2
Geographically Weighted Regression (GWR) model test for spatial variability of parameters in Ndumo area, uMkhanyakude district, KwaZulu-Natal, South Africa.

Variable	Min	Lower quartile	Median	Upper quartile	Maximum	DIFF of criterion[b]
Intercept						−7.100[a]
Gender						3.220[a]
Age						1.131[a]
Household livelihoods						1.489[a]
Religion	−0.375	−0.110	−0.023	0.034	0.168	−2.651
Household head	−0.220	0.040	0.112	0.152	0.171	−6.380
Availability of a toilet at home	−0.439	−0.201	−0.072	0.011	0.205	−1.656
How often they use toilet	−0.491	−0.178	−0.071	0.019	0.144	−7.344
Where they bath or wash during rainy season	−0.042	0.102	0.149	0.275	0.346	0.855
Distance from piped water collection points	−0.464	−0.254	0.046	0.082	0.230	−3.437
Distance from open water sources	−0.284	−0.212	0.008	0.058	0.199	4.20[c]

[a] The variable were considered to be global after the local to global iteration.
[b] Positive value of Diff-Criterion suggests non spatial variability especially greater than or equal to two, suggests that the local term is better to be assumed as global.
[c] After the local to global iteration the variable was not moved to global variable.

Table 3
Comparison of model performances.

Fitness parameters	Global regression	s-GWR(before local to global)	s-GWR (after local to global)
AICc	635.35	616.82	597.96
R square	0.20	0.33	0.45
Adjusted R square	0.17	0.25	0.36

give confidence on the performance of the local model compared to the global model. The model residuals indicated no autocorrelation which can confirm that the variables considered in this study were able to predict the spatial distribution of *S. haematobium* in this area. However, low performance of the model indicates that we may have missed key determinants of the spatial distribution of the disease.

The variation of the coefficients observed could be justified as school children in some homesteads are more exposed to schistosomiasis compared to others based on their location in relation to sources of water and socio-economic activities. For example in this study there were higher *S. haematobium* cases and infection intensities around Mbadleni and Madeya primary schools as they did not have operational public piped water collection points and had better access to open water sources (rivers and dams) as also observed in other endemic areas (Booth et al., 2004; Kapito-Tembo et al., 2009). This study also showed a variation in distances from households and public piped water collection points and open water sources in relation to *S. haematobium* infection. However, Cluster 2 was far from the operational public water collection points such as tanks and tapes. Although Cluster 1 was close to public water collection tanks and tapes the homesteads were pre-exposed to the open water sources as there is a dense network of rivers and a dam that might have exposed them to habitats of the host snail—*B. globosus*. Therefore the high intensity and high prevalence clusters or hotspots might be due to heavy reliance on open water sources such as rivers and small dams.

Religion and household head also varied across Ndumo area and showed the association with the spatial variation of *S. haematobium* infection intensity. This association has been established in non-spatial studies elsewhere (Huang and Manderson, 1992; Ndassa et al., 2007). Religious beliefs may have implications on water-contact behaviour, for example during baptism and healing process by immersion mainly in Zionist and Apostolic Churches (Peltzer, 1999). Religious and cultural beliefs may also determine the health care seeking behaviour. For example those who have poor health care seeking behaviour may have higher infection intensities. The household head may also determine the health status of the family as well as the household income levels which may determine the livelihood activities which may expose children to *S. haematobium*. However household's livelihoods did not show variation in this study hence was moved to global model in the s-GWR.

The role of improved water supply and sanitation on disease transmission and incidence has long been described as necessary for reducing the incidence and prevalence of schistosomiasis (Esrey et al., 1991; Grimes et al., 2014). In this study, high prevalence and high relative risk was observed around Madeya primary school to the South West which is furthest from the public piped water collection points. Various studies have established a direct association between the intensity of the disease and proximity of infected individuals to natural water sources such as lakes, rivers, and ponds and inadequate sanitation (Chimbari et al., 2003; Clennon et al., 2006; Kapito-Tembo et al., 2009). Similar studies showed the same in small-scale studies in communities endemic for *S. mansoni* (Kloos et al., 1997; Booth et al., 2004) and *S. haematobium* (Clennon et al., 2006; Rudge et al., 2008; Meurs et al., 2013). However those studies were considering proximity to the identified transmission sites while this study considered distance from the nearest open sources which may explain why R^2 was low. Our study showed a variation in association between *S. haematobium* infection and sanitation (latrine at the homestead) and how often people use toilets. In their review, Grimes et al. (2014) also noted that 5 out of 12 datasets they reviewed reported a significantly lower odds of *S. haematobium* infection for those with adequate sanitation (mainly latrine) and the remaining 7 did not show a significant difference between those with and without adequate sanitation. Hence, the complex requirements for disease transmission contribute to the focal nature of schistosomiasis (Woodhall et al., 2013). These factors cannot solely or independently predict the spatial distribution of *S. haematobium* prevalence and intensity at this scale. There is need to identify transmission sites and other household socio-economic factors to explain the spatial transmission dynamics of *S. haematobium* at micro-geographical scale. This may improve the performance of the sGWR model. However, the use of non-classified *S. haematobium* intensity using the semiparametric – Geographically Weighted Poisson Regression (s-GWPR) may improve the prediction. The results of this study may give insights on the spatial distribution of the diseases in the view of WHO guidelines based on 3 classes of infections (no case, light infections and heavy infections) and this could guide the local control programmes.

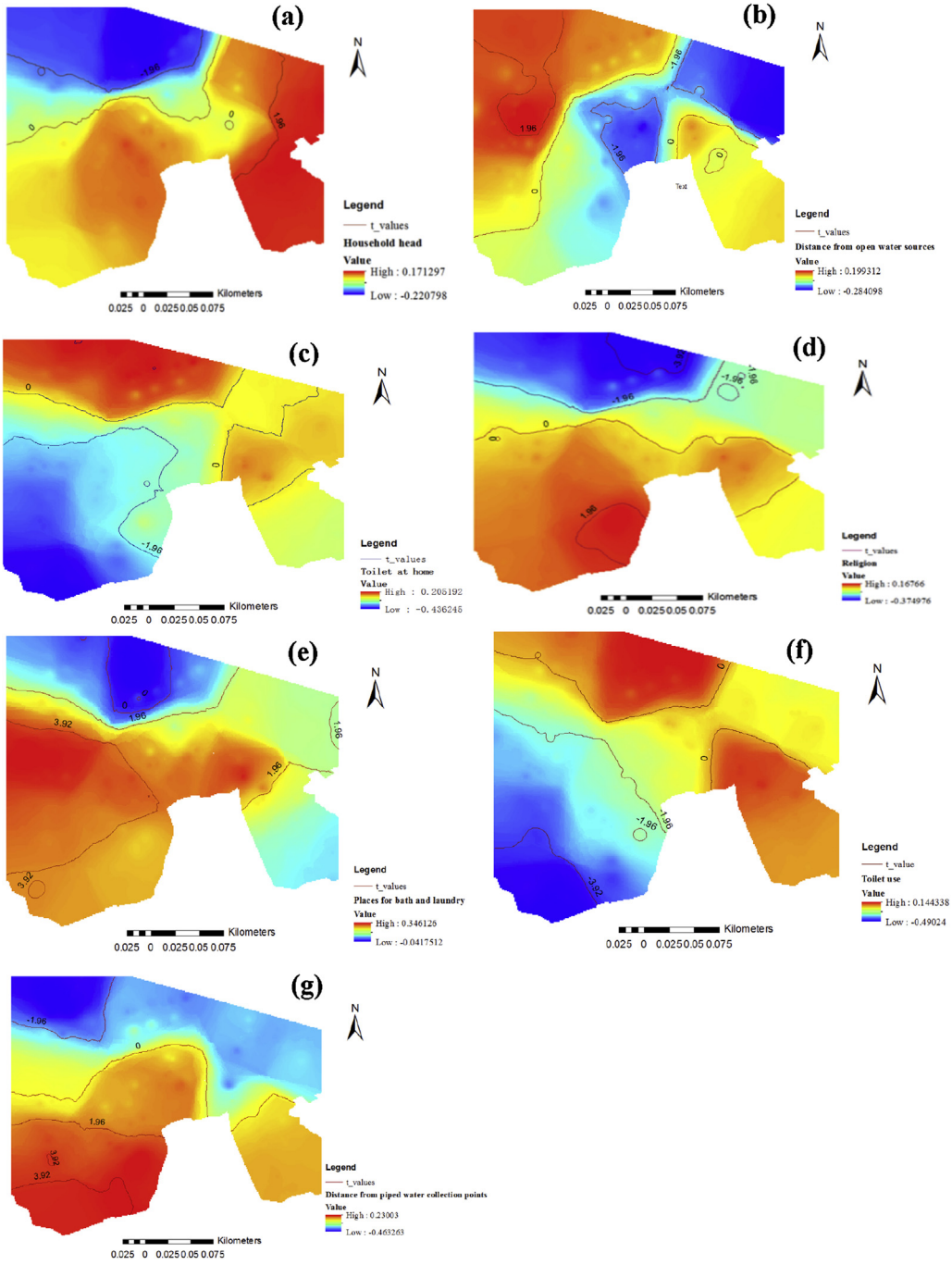

Fig. 4. Local parameters or estimates of semiparametric-Geographically Weighted Regression (s-GWR) model. (a) Household head (b) Distance from open water sources (c) Availability of a toilet at home (d) Religion How often they use toilet (e) Place of bath and laundry Religion (f) Toilet use (g) Distance from piped water collection points.

Identifying transmission epicentres and understanding spatial patterns of human infection, may help to develop more effective, highly focal snail control program in conjunction with targeted chemotherapy (Clennon et al., 2004) and develop less uniform strategies to better tailor control efforts at the local level (Kanwai et al., 2011; Meurs et al., 2013; Rollinson et al., 2013; Campbell et al., 2014; Adenowo et al., 2015). This may also lead to targeting of human water contact behavioural and environmental factors influencing infection exposure (Rudge et al., 2008). The macro-geographical level has been demonstrated in many studies, driven by the fact that decision making for control programmes often takes place at national and district levels (Raso et al. 2005). Hence, micro-geographical studies within endemic communities are required to help in developing and implementation of control programmes (Rudge et al., 2008) at local levels.

5. Conclusion

Our study explored and analysed the spatial distribution of *S. haematobium* and its relationship with the socio-economic factors in Ndumo area, uMkhanyakude district in South Africa. We confirmed that schistosomiasis transmission is focal in nature as indicated by the clusters mostly on the dense river networks and dams where transmission occurs. The local s-GWR model also indicated that some of the socio-economic variables vary across the landscape thereby determining the magnitude or density of *S.*

haematobium infection intensity. This evidence can be used for control and management of the disease at micro scale. However, there is need for further research into more factors that may improve the performance of the s-GWR models in determining the local variation of *S. haematobium* infection intensity.

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