University of Zurich[UZH]

Determining time of concentration for small lake watersheds in Switzerland for the use in eDNA sampling – a small scale modelling approach

GEO 511 Master's Thesis

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Abstract

Surveying environmental DNA (eDNA) to infer species presence in a landscape is currently at the forefront when it comes to biodiversity monitoring. With a small number of water samples and subsequent laboratory analysis, it is possible to determine the species diversity in areas over large temporal and spatial scales, since all living organisms release DNA into the environment during their interaction with it. Unfortunately, this detectable eDNA does not remain in the environment forever, but has a certain rate of decay. River networks can be seen as conveyor belts of this slowly decaying eDNA, transporting the particles from the outermost point of a catchment area to the next lake. In order to draw conclusions from sampled water over an entire watershed, the eDNA transport distance must exceed its degradation rate. Here, the hydrological concept of time of concentration, which determines how far a single drop of water has from the hydraulically outermost point of a catchment to the point of investigation, is useful.

In this work, three methods, which include different parameters in their calculation, were used to estimate the times of concentration of a total of 217 inflows into eight Swiss lakes. Despite different watershed sizes, different stream gradients or different riverbed characteristics, it was possible to show that time of concentration does not exceed the half-life time of eDNA for the eight areas of interest. At the same time this work can also show how strongly the three modelling methods used differ and which parameters are subject to the greatest uncertainty.

Based solely on the time of concentration calculated for the eight catchments considered in this thesis, I conclude that eDNA is likely transported to lakes from entire lake catchments, even though the results should be taken with caution due to some uncertainties. Further research is needed to ground truth the parameters used in the modelling, but the current understanding suggest that lakes may act as accumulators of eDNA in these eight catchments or similar catchments to these in the world.

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Secondly, I would like to thank Anish Kirtane, who was able to introduce me to the topic of eDNA, which was foreign to me. A special thank for joining a field trip to Lake Pfäffikon at the very beginning of my work and giving me background on eDNA. In addition, his data from his field visits to the study sites helped me validate my own input data and verify its accuracy.

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Basil Frefel, November 2021

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List of Abbreviations

a	Cross-sectional flow area
Agri	Agriculture
C	Celsius
cm	Centimetres
DNA	Deoxyribonucleic acid
eDNA	Environmental DNA
Fo	Forest
ft	Feet
GHV	Grassy and herbaceous vegetation
GIS	Geographical Information Systems
km	Kilometres
km^2	Square Kilometres
L	Channel length
Lt	Runoff travel length
m	Meters
m^2	Square Meters
mi	Mile
mi^2	Square Miles
n	Manning's roughness coefficient
NRCS	Natural Resource Conservation Service
P_w	Wetted Perimeter
Q	Flow rate
R	Hydraulic radius
RuS	Rocks and unconsolidated sediments
s	Second
S	Slope
T_C	Time of concentration
$T_{C\_1m/s}$	Time of concentration 1m/s-method
$T_{C\_Kirpich}$	Time of concentration Kirpich-method
T_{C_NRCS}	Time of concentration NRCS-method
t_t	Travel time
t_O	Overland flow time
UA	Urban area
UV	Ultraviolet
V	Velocity

1. Introduction

1.1 Motivation

Already before my university studies and during my bachelor and finally when visiting master courses, my interest in physical geography has always been very high. I already had the chance to do some internships in this field, for example one in the group of dendrochronology at WSL, the Swiss Federal Institute for Forest, Snow and Landscape. However, my main interest has always been the element water, in all its diversity and as the source of all life. So, in parallel to the courses at the Geographical Institute, I did other internships, including two at EAWAG, the Swiss Federal Institute of Aquatic Science and Technology.

With these premises, it was obvious for me to then write my bachelor thesis in this field. I dealt with global and local water use conflicts and especially included the aspect of citizen science, the extent to which lay people can help solve problems related to water use. During my master's degree, I took additional courses in hydrology and my interest in the subject increased so it was clear that I would write my master's thesis again in this field. When I came across the advertised work with the title "Determining time of concentration for lake watersheds in Switzerland" during the decision phase, it was clear to me that this would definitely be a topic for me. My favourite field of physical geography, hydrology, combined with some GIS modelling as well as a subject field completely foreign to me, eDNA, this combination did it for me right away.

1.2 Human-driven biodiversity changes and why it matters

"Biological diversity means the variability among living organisms from all sources including, inter alia, terrestrial, marine and other aquatic ecosystems and the ecological complexes of which they are part; this includes diversity within species, between species and of ecosystems” (CBD, 1992). The Encyclopaedia Britannica (Primm, 2021) defines the term biodiversity somewhat shorter, but less detailed as the “Quantity of plant and animal species found in a given environment”. Biodiversity, no matter how we define it in the end has always been a major part of man's discussion in his interaction with the environment. Since his existence on earth, humans have always had a great influence on their environment and thus also on the prevailing biodiversity.

While the human-made drivers of biodiversity change several 10'000 years ago were fire, hunting, fishing, logging and then at some point agriculture, in recent years it is invasions of previously untouched islands, pollution of the environment and of course man-made climate change that must be seen as the main driver of anthropogenic biodiversity change (Pereira et al, 2012). Land-use changes in particular have also led to a pace of biodiversity change unprecedented in history (WWF, 2020). Climate change has greatly accelerated habitat destruction and biodiversity loss exceeds global conservation efforts by many times (Zari, 2015). There is a frequent debate about why biodiversity is desirable in the first place and why we as inhabitants of the planet earth should take care. Here are just a few examples:

- Food. While we in developed countries rely and feed mainly on domesticated plants and animals, a large part of the world's population still relies on wild collection (Chigonda, 2017). In addition, wild plant and animal species represent an enormous reservoir of genetic diversity that supports the continuation and security of our agriculture and thus our food supply (Chigonda, 2017). Thousands of species of soil improvers or pollinators, as well as species that are active as natural pest controllers, contribute to our food security (WWF, 2020).
- Plants play a big role in our medicine today. For example, most of the cancer drugs we use today are inspired by nature (Newman & Cragg, 2012). Also, greater biodiversity reduces the risk of spreading infectious diseases (Chigonda, T, 2017).
- Biodiversity also plays an important role for tourism, especially for ecotourism and its related economic considerations. The number of people who are interested in nature-motivated tourism and in ecosystems that are as untouched as possible will tend to increase in the future (Bayliss et al. 2014).

In addition to the points mentioned above, many authors also mention the indirect but nevertheless important ecosystem services, which are also directly linked to biodiversity, such as air filtration and thereby regulation of the gas balance in the atmosphere, nutrient cycling, water resource protection, soil formation and its protection (Chigonda, 2017, Shah, 2014 and many more).

1.3 Biodiversity monitoring and eDNA?

Biodiversity monitoring has a long tradition. Charles Darwin in the 19th century during his circumnavigation of the world is just one example of countless early studies of biodiversity on earth. The Christmas Bird Count, which has taken place annually in the USA since 1900, can also be seen as an early and long-lasting biodiversity monitoring project, even if it only focuses on the species of birds (Silvertown, 2009). While counts used to be made primarily through direct individual observations, new techniques have been developed over the years that have been used to monitor biodiversity. For a long time, live trapping, camera trapping or hair surveys were one of the mostly used techniques for detecting animals, especially terrestrial mammals (Swan et al, 2013). Another traditional and proven method of monitoring is the so-called latrine survey method (Sales et al, 2020).

All the above-mentioned methods work reliably but have a major drawback when the spatial and temporal scale of a biodiversity monitoring project become larger: they are relatively expensive (Sales et al, 2020). This could be remedied by the survey of environmental DNA (eDNA). eDNA has recently become an effective tool for biodiversity monitoring (Thomsen & Willerslev, 2015). The greatest difficulty, however, lies in when and where samples should be taken to obtain reliable results.

Environmental DNA is DNA which can be found in environmental samples, for example in soil samples, in fresh water or in lake sediments (Taberlet et al, 2012). Most of the DNA in environmental samples comes from unicellular microorganisms (viruses, bacteria) which are very abundant overall (Pawlowski et al, 2020). However, genetic material can also be found from multicellular eukaryotes (Rodriguez-Ezpeleta et al, 2021). Discovered DNA in the environment such as from faeces, mucus or skin cells, can be used to detect species in the latter (Deiner et al, 2017 & Iwai et al, 2019). However, the released eDNA undergoes various degradation processes and can be transported by the flow of water bodies (see figure 1).

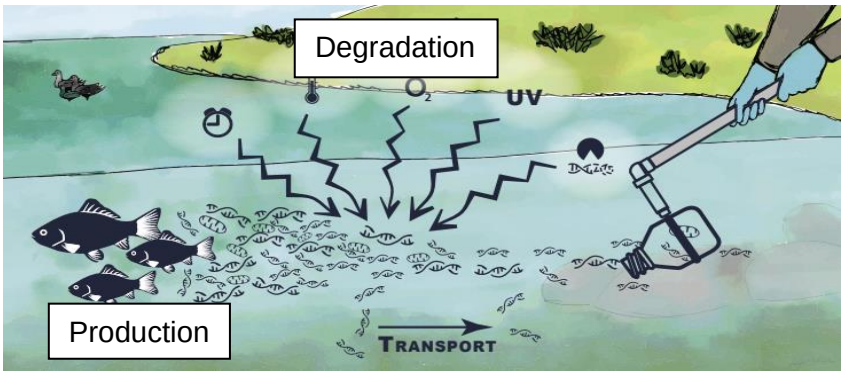

Figure 1: Production and fate of microbial eDNA in aquatic habitats (Pawlowski et al, 2020)

Since the field of eDNA is a relatively young discipline, certain questions are still unanswered. The question of how long DNA traces can be detected in water or how fast they decay, differs greatly from the studies conducted to date (Allan et al, 2020 & Harrison et al, 2019). In this study, only rivers and lakes are considered, but it should be mentioned that there are considerable differences in the half-life of eDNA in water between freshwater and marine systems (Collins et al, 2018). In some literature, eDNA half life spans from 1 hour to 234 hours and is different for different species and depending on water temperature and water chemistry (Allan et al, 2020). Strickler et al. (2015) however identified some of the different factors in the degradation of eDNA in an experimental setup a little more precise: The lowest decay rates were measured in cold water (5°C), low UV irradiance levels, and alkaline water. Here, a different number is given for the retention of eDNA in the water, since traces were still detectable after 58 days (Strickler et al, 2015).

Regarding transport, it has been shown that eDNA can be carried over at least 10 km in smaller streams and up to 100 km in larger rivers (Deiner & Altermatt, 2014 & Pont et al, 2018). Since the direction of flow is clearly given for flowing waters such as rivers or streams, eDNA samples obtained from it allow direct conclusions to be drawn about the upstream catchment area and thus possibly also about its biodiversity (Deiner et al, 2016).

This raises the question of how long the water collected in the field has already been on its way, what part of the total biodiversity of a catchment area can be determined by means of a water sample at a certain point. Assuming that the 1.4 million lakes worldwide (Messager et al, 2016) act as collectors for this eDNA, the biodiversity of entire lake catchment areas could be determined by just sampling water in lakes. For this to be possible at all, the decay rate of eDNA would have to exceed that of transport of particles into a lake – a matter of time of concentration.

1.4 The concept of time of concentration

Although not all factors responsible for the degradation of eDNA are known yet, it can be said that transport and especially transport time play an important role in whether eDNA can be detected in a sample or not. Modelling the transport of substances and thus also of eDNA in streams and rivers is a challenge (Shogren et al, 2017). For modelling eDNA transport in rivers and streams, it is of immense importance to know the physical and biological variables that influence this process (Jerde & Mahon, 2015). In this study, the focus lies on transport times defined by water flow velocities.

Rainwater or melting snow masses in a catchment area follow one of four possible paths: surface runoff or surface flow, surface runoff with transmission losses (infiltration) into the ground, quick return flow where water infiltrates into the ground but rapidly returns to the surface and lastly, the so-called baseflow, whereby the water infiltrates directly into the ground and reaches the groundwater level (USDA, 2010, figure 2a). Within the scope of various applications, the surface runoff is of great interest for both hydrologists and engineers. Provisioning services such as guaranteed access to freshwater, agricultural production and hydroelectricity production or regulatory services such as disaster prevention and risk management are just a few examples where surface runoff has a major influence and is therefore of great importance (Dobriyal et al, 2017).

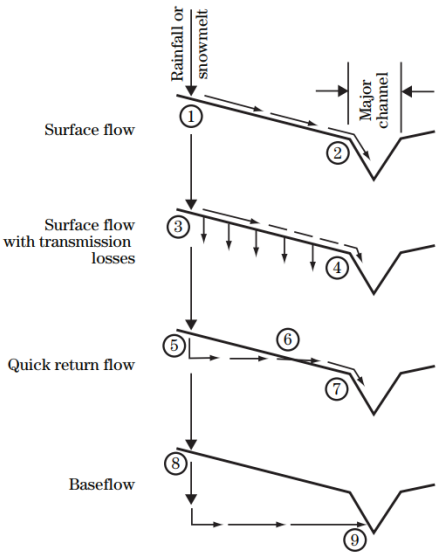

Figure 2a: Types of flow (USDA, 2020)

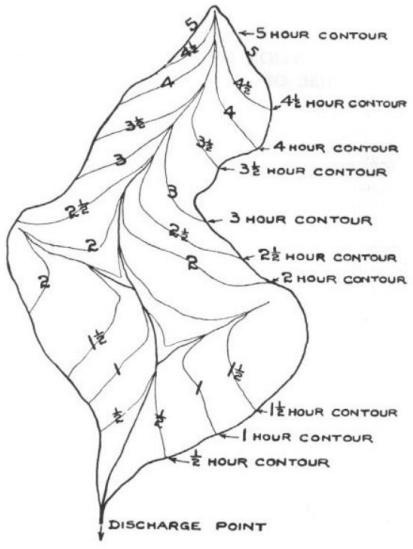

Figure 2b: Schematic isochrones of travel time (Beven, 2020)

The time of concentration (T_c) describes how long a water particle has from the outermost part of a catchment area to its outlet and is strongly connected to water flow velocity (Beven, 2020, figure 2b). This hydraulically most distant point is the point with the longest travel time to the watershed outlet and not necessarily the point with the longest flow distance to the outlet (USDA, 2010). The time of concentration will vary depending on the slope and character of the catchment area and the flow path (USDA 2010). We can therefore say that the travel time and the time of concentration are functions of the length and the flow velocity of a given watercourse (Thomason, 2019). For different catchment area sizes and for different characteristics of the watershed area, countless formulas have been developed to determine the time of concentration as accurately as possible. Table 1 gives an overview of the different methods that can be used for calculating the time of concentration. Table 1 is strongly based on the summary that can be found in Salimi et al (2016).

Model	***Formula***	***Remark***	***Reference***
Kirpich	$T_c = KL^{0.77}*S^{-0.385}$ K = A unit conversion coefficient L = Length of channel from headwater to outlet S = Average slope, ft/ft or m/m	Developed for small basins in Tennessee and Pennsylvania, with basin areas from 0.4 – 45.3 ha.	Kirpich (1940) Li & Chibber (2008)
Williams	$T_c = 60LA^{0.4}*D^{-1}*S^{-0.2}$ L = Basin length, mi A = Basin area, mi^2 D = Diameter (mi) of a circular basin of area S = slope, %	The basin area should be smaller than 129.5km^2	Williams (1922) Li & Chibber (2008)
Johnstone-Cross	$T_c = 300L^{0.5}* S^{-0.5}$ L = Basin length, mi S = Slope, ft/mi	Developed for basins with areas between 64.7 and 4206.1km^2	Johnstone & Cross (1949) Li & Chibber (2008)
NRCS	$T_c = 0.0526[(1000/CN)-9] *L^{0.8}*S^{-0.5}$ CN = Curve number L = Flow length, ft S = Average watershed slope, %	For small rural watersheds	NRCS (1997) Li and Chibber (2008)
Carter	$T_c = 100L^{0.6}*S^{-0.3}$ L = Length of flow, mi S = Surface slope, ft/mi	For natural channels	Carter (1961) Nicklow et al. (2006)
Bransby-Williams	$T_c = 58.5LA^{-0.1}*S^{-0.2}$ L = Mainstream length, km A = Catchment area, km^2 S = Equal area slope, m/km	For big watersheds	Abustan et al. (2008) Department of Transport and Main Roads (2010)

Table 1: A summary of time of concentration methods (Salimi et al, 2016). Abbreviations in this table differ from abbreviations in my work.

As mentioned earlier, the time of concentration indicates how long it takes for water to flow from the hydrologically outermost point of a catchment to the point of investigation. A long but steep stream with high velocity may therefore have a shorter time of concentration than a flat stream, even if the latter is much shorter (Thomason, 2019). It also means, that the shorter the time of concentration, the larger the peak discharge during rainfall events for catchment areas of the same size (INDOT, 2010). As travel time t_t (channel length divided by the average speed of the water) is part of total time of concentration, it must be calculated in advance (INDOT, 2010).

$$t_t = \frac{Lt}{(V)(60)}$$

Equation 1: Water travel time as a function of flow length and flow velocity

Where: t_t = travel time, min
Lt = length which runoff must travel, m
V = estimated or calculated velocity, m/s

The total time of concentration is then by definition:

$$T_c = t_O + t_t$$

Equation 2: Time of concentration as a function of overland flow time and travel time

Where: T_c = total time of concentration
t_O = overland flow time
t_t = travel time, min

Many formulas, as the one just above, include overland flow and sometimes sheet flow when calculating the time of concentration, how long it takes a drop of water in a precipitation event to move overland and build a channel in the first place (Thomason, 2019). However, since the study of eDNA transport is not limited to precipitation events and associated peak discharge, it is rather the continuously existing waterways from their source or point of origin to a certain point downstream that are studied.

Open channel flow is assumed to have begun where cross-sectional information about a stream is available, it is visible in photographs, or where stream channels are shown as such on official maps (Thomason, 2019 & USDA, 2010). Since only the channelled flow is considered in my study for calculating T_c, overland flow is being neglected and some formulas are slightly adjusted. In the following three subchapters, the formulas used in this work are described in more detail.

1.4.1 1m/s-method

In order to get a general overview and to calculate with easily imaginable values, a first calculation of the time of concentration is made with the simple assumption that the water would flow with a constant speed of 1m/s. This flow velocity was also used by Bernhard Lehner (2018) to model the time of concentration on a global scale and produced and shared by our collaborator (Lehner *per com*.). Although there is no value in the literature that would indicate the average global flow velocity, authors such as Schulze et al. (2005) and Fang et al. (2007) have shown in studies that this number settles somewhere between 0.5m/s and 1.5m/s depending on catchment size, streambed roughness and slope. Hence, with a flow velocity of 1m/s, a first, rough result can be calculated.

$$T_{c\_1m/s} = \frac{L}{(1m/s)*60}$$

Equation 3: T_C calculation method using flow velocity of 1m/s

Where: $T_{c\_1m/s}$ = time of concentration (1m/s-method), min
L = Channel length, m

However, selecting flow length alone as the determining parameter for travel time does not cover the whole picture, as the following example illustrates. If time of concentration is calculated using equation 3 for two rivers with a length of 10 km, they will have the same value, regardless of whether one river only descends 50 meters over this flow distance, while the other falls 1000 meters. This obvious error shows that other parameters, such as the slope, must be included in the calculation of the time of concentration to better reflect the conditions.

1.4.2 Kirpich-method

A frequently used and well applicable method to calculate the time of concentration is the Kerby-Kirpich-method (Thomason, 2019). While Kerby's part of the formula calculates the time of overland flow, the Kirpich-method focuses on the channel-flow, the component of interest for eDNA transport. In contrast to equation 3, the Kirpich formula for calculating the time of concentration includes the slope, so greater attention is paid to the shape of the terrain.

$$T_{c\_Kirpich} = 0.0195 * L^{0.770} * S^{-0.385}$$

Equation 4: $T_{C\_Kirpich}$ calculation method

Where: $T_{c\_Kirpich}$ = time of concentration (Kirpich), min
L = Channel length, m
S = Dimensionless main-channel slope

The factor 0.0195 represents a compensation factor for SI units against imperial units and the exponents represent tested best fitting parameter corrections.

1.4.3 NRCS-method

The third method usable for calculating time of concentration for eDNA transport in water is the Natural Resource Conservation Service (NRCS) method, which was developed especially for small, rural watersheds (see table 1). In the NRCS method, the calculation is divided into the different flow processes sheet flow, shallow concentrated flow and channel flow (Thomason, 2019), whereby for eDNA transport only the latter is important, and I therefore concentrate on this part of the formula. Since the NRCS method uses Manning's equation (equation 5) in contrast to the Kirpich-method, two additional parameters are added. First, this is the hydraulic radius, which is derived from the cross-sectional flow area through the wetted perimeter (Water and Rivers Commission, 2001, figure 3) and Manning's *n*, a value that describes the roughness of the riverbed and thus also has an influence on the flow velocity and the time of concentration. Some of Manning's *n* values are presented in table 2.

$$Q = \frac{1}{n} * R^{2/3} * S^{0.5}$$

Equation 5: Manning's equation

Where: Q = flow rate, m/s
R = hydraulic radius, m
= a / P_w
a = cross-sectional flow area, m^2
P_w = wetted perimeter, m
S = Dimensionless main-channel slope
n = Manning's *n* value for open channel flow

$$T_{c\_NRCS} = L / (60 * \frac{1}{n} * R^{2/3} * S^{0.5})$$

Equation 6: T_{C_NRCS} calculation method

Where:
- T_{c_NRCS} = time of concentration (NRCS), min
- L = Channel length, m
- R = hydraulic radius, m
  - = a / P_w
  - a = cross-sectional flow area, m^2
  - P_w = wetted perimeter, m
- S = Dimensionless main-channel slope
- *n* = Manning's *n* value for open channel flow

Type of channel	***Manning's n***
A: Minor streams (top with at flood stage < 30m)	
a) Clean, straight, full, no rifts or deep pools	***0.025 – 0.033***
b) Same as a, but more stones and weeds	***0.030 – 0.040***
c) Clean, winding, some pools and shoals	***0.033 – 0.045***
d) Very weedy, heavy stand of timber and underbrush	***0.075 – 0.150***
e) Mountain streams with gravel and cobbles, few boulders on bottom	***0.030 – 0.050***
f) Mountain streams with cobbles and large few boulders on bottom	***0.040 – 0.070***
B: Excavated or dredged channels – Earth, winding, sluggish	
a) No vegetation	***0.023 – 0.030***
b) Grass, some weeds	***0.025 – 0.033***
c) Deep weeds or aquatic plants in deep channels	***0.030 – 0.040***
d) Winding, sluggish, stony bottom, weedy banks	***0.025 – 0.040***
e) Dense weeds, as high as flow depth	***0.050 – 0.120***
C: Lined Channels	
a) Asphalt	***0.013 – 0.016***
b) Brick (in cement mortar)	***0.012 – 0.018***

Table 2: Manning's Roughness coefficient for Open Channels (Thomason, 2019)

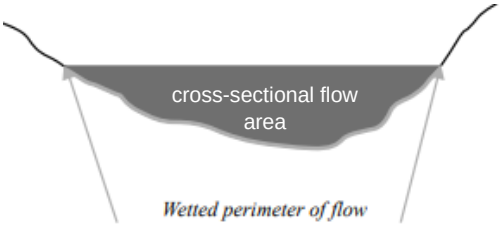

Figure 3: Wetted perimeter and cross-sectional flow area (Water and Rivers Commission, 2001)

1.5 Research questions

The aim of this master's thesis was to test whether the different ways to calculate the time of concentration lead to very different estimates of time of concentration for eight lake catchments in Switzerland. The modelled times of concentration of the watersheds should give information about whether water sampled in lakes could be useful to represent the existing biodiversity by answering the questions:

1. How long does the surface water take to (for the eight given Swiss lake watersheds) travel from the point it enters the stream channel at the outermost part until it reaches the outflow into the lake?
2. How wide is the distribution in the time of concentration for lake watersheds using different approaches?
3. Which data is missing to further improve the models for calculating time of concentration?

The first research question is at the heart of the work, since a suitable formula must be found from among countless existing ones representing the time of concentration for the given catchment areas the best. At the same time, these calculated values form the basis for where eDNA-water samples should be taken to determine the biodiversity present on a landscape scale. The second research question aims to find out whether it matters at all which formula is used to calculate the time of concentration for the catchments in question - in other words, a statistical comparison. Research question 3 is strongly connected with limitations, which arise in the collection and processing of data. This last research question is addressed primarily in the discussion section and the chapter on further research.

2. Study sites

This chapter gives a short overview of the eight lakes I have mainly dealt with in my work, respectively of which I have tried to calculate the time of concentration with my model. These eight lakes were selected for my work because they will also be the primary lakes studied in the overarching study.

2.1 The different lakes and their key numbers

The lakes studied and, of course, the associated hydrological catchments are the following: Lake Greifen, Lake Pfäffikon, Lake Aegeri, Lake Lauerz, Lake Baldegg, Lake Hallwil, Lake Sils and Lake Silvaplana (table 3). All of these lakes are located in Switzerland, more precisely in the “Mittelland” and in the Grisons Alps. They all have a small surface area, ranging from 3.1 km^2 for Lake Lauerz to a maximum of 10.3 km^2 for Lake Hallwil. However, the size of their catchment area differs greatly. Additionally, the surrounding conditions such as surface cover, human influence in the catchment area or the average gradient vary. Lake Sils and Lake Silvaplana are situated at high altitudes and are fed to a certain extent by glaciers. In contrast to the other lakes, this results in a different discharge regime, which makes it exciting for the study. The annual precipitation amounts of the eight catchments range from 1057 mm for Lake Silvaplana to 1762 mm for Lake Lauerz (Hydromaps, 2021). In general, it can be said that in all catchments the most precipitation falls in the summer months of June, July and August, and the least precipitation, with about half of the maximum in each case, in the months of January and February (Hydromaps, 2021).

When looking at table 3, the following must be considered: the catchment area of Lake Greifen includes that of Lake Pfäffikon. This means that the numbers for the size of the catchment area, the mean elevation and the surface cover are related. The same applies to Lake Baldegg and Lake Hallwil as well as Lake Sils and Lake Silvaplana. The catchment areas of Lake Baldegg and Lake Sils are sub-catchment areas of the larger, associated lake watersheds.

	Lake surface area	***Max. Lake depth***	***Surface elevation***	***Catchment area***	***Average catchment elevation***	***Maximum catchment elevation***	***Main portions of surface coverage***	***Additional notes:***
Lake Greifen	8.6 km^2	34m	435m	164 km^2	556m	1105m	Agri: 52% UA: 19% Fo: 18% Water: 7%	Connected to Lake Pfäffikon
Lake Pfäffikon	3.3 km^2	35m	537m	28.9 km^2	665m	1081m	Agri: 43% Fo: 20% UA: 15% Water: 11%	Connected to Lake Greifen
Lake Aegeri	7.2 km^2	82m	724m	48.1 km^2	935m	1556m	Fo: 45% GHV: 35% Water 15% UA: 4%	
Lake Lauerz	3.1 km^2	14m	447m	72.4 km^2	884m	1783m	GHV: 41% Fo: 36% Agri: 13% UA: 4%	
Lake Baldegg	5.3 km^2	66m	463m	73.2 km^2	585m	881m	Agri: 74% Fo: 12% Water: 7% UA: 6%	Connected to Lake Hallwil
Lake Hallwil	10.3 km^2	47m	449m	139.2 km^2	580m	885m	Agri: 64% Fo: 14% Water: 11% UA: 10%	Connected to Lake Baldegg
Lake Sils	4.1 km^2	71m	1797m	45.8 km^2	2328m	3337m	RuS: 42% GHV: 25% Fo: 9% Water: 9% Glaciers: 7%	Connected to Lake Silvaplana Glacier fed
Lake Silvaplana	3.2 km^2	77m	1791m	137.3 km^2	2394m	3408m	RuS: 49% GHV: 23% Fo: 11% Glaciers: 7%	Connected to Lake Sils Glacier fed

Table 3: Overview of the 8 lakes investigated (Swisstopo, 2007) as well as the respective catchment areas (Hydromaps, 2021) including additional information on the land cover of the watersheds where: Agri = Agriculture, Fo = Forest, UA= Urban area, GHV: Grassy and herbaceous vegetation, RuS = Rocks and unconsolidated sediments.

3. Data and Methods

3.1 Data

3.1.1 Datasets from Swisstopo

For the modelling of the times of concentration of the eight lakes, three freely available datasets of the federal office of topography, Swisstopo were used. Namely, these were:

1. A dataset (Swisstopo, 2019) which summarizes all sub catchments in Switzerland. This consists of a mosaic that divides the whole of Switzerland into over 22,000 topographically defined sub-catchments (Swisstopo, 2019). This dataset also contains additional information, for example on surface coverage. However, I did not use this information because it differs from the numbers I used (Hydromaps, 2021, see table 3). This dataset is referred to below as *swiss_subcatchments.*
2. A second dataset containing rivers and lakes, the dataset "Flussordnungszahl nach Strahler" (Swisstopo, 2014). Strahler stream order provides information about the degree of branching of a water network; by definition, springs have a number of 1, and as soon as two rivers of the same order flow together, the number increases by 1. At the same time, this dataset also contains information on the length of individual flow sections as well as the length of all upstream sections. A total of just under 75,000 km of rivers are recorded in Switzerland (Swisstopo, 2014). This data set is referred to below as *FLOZ*.
3. The third dataset contains a digital elevation model of Switzerland. In a grid size of 25 by 25 meters, the height above sea level is recorded for the whole of Switzerland (Swisstopo, 2005). This dataset is referred to below as *chdhm25_ras.*

3.1.2 Ground-truth validation of stream network

To verify the data sets and in particular the FLOZ dataset, individual field inspections took place. These are also of great importance for the data collection within the framework of the overall project, as water sampling to determine the eDNA composition of outflows into the lakes will take place soon and access to the individual sampling locations needed to be found.

Here, such a ground-truth review is shown using the example of Lake Pfäffikon where a visit took place on May 31st, 2021. During a circumnavigation of the lake on the officially marked paths as well as easily accessible areas (nature reserves were not entered), a visual lookout was kept for inflows to the lake. For each inlet, the position was recorded using the smartphone coordinates and a photo was taken (see figures 4-7 and more pictures of inlets in the Appendix C).

Figure 5: Inlet number 9 (own photo)

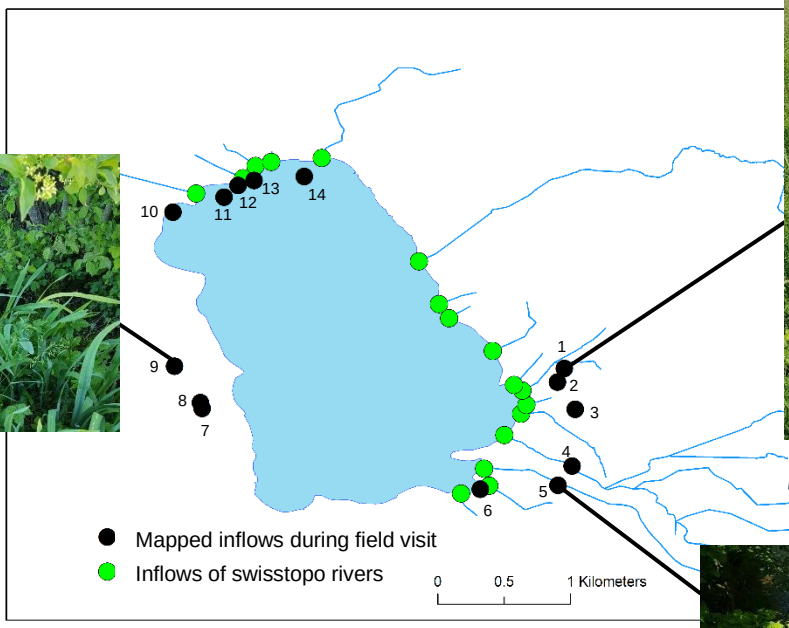

Figure 4: Data-derived and field-visit-mapped inflows into Lake Pfäffikon

Figure 6: Inlet number 1 at north-eastern part of Lake Pfäffikon (own photo)

Figure 7: Main inlet (Chämtnerbach) just before the confluence with the lake (own photo)

3.2 Methods

Since the main part of my work was GIS modelling, most of my workflow took place in ArcGIS (version 10.8.0.12790). The statistical analysis of the calculated times of concentration was then performed in RStudio (version 2021.09.0+351) using the R programming language. The exact workflow in these programs will be explained in the next two chapters.

3.2.1 Work in ArcGis

In this section, the chosen workflow in ArcGIS is presented. As my resulting dataset is a geodatabase and some layers with specific names and data, I refer to them and name them here. For an overview of the metadata, see chapter 3.1.1.

To extract all Swiss lakes, ArcTool: Select (Analysis) was used on the *swiss_subcatchments* dataset with the Expression: "SEE = 'See_stehendesGW'. This results in a new layer called *all_swiss_lakes* containing 203 Objects. Of course, these are effectively not all Swiss lakes but with the data available, this is the shortest and fastest way to get the main Swiss lakes extracted and, important for me, all eight lakes under investigation are included. To further extract the eight lakes, another ArcTool: Select (Analysis) was performed, with corresponding object IDs in the Expression field (see Appendix A). This operation results in a layer called *proposal_lakes* containing the polygons of the eight lakes combined or individually.

To extract the 8 catchments, again ArcTool: Select (Analysis) was used basing the operation on EZGNR in *swiss_subcatchments* (see Appendix A). This results in a layer called for example *Pfäffikersee_catchment* containing all the polygons including Lake Pfäffikon itself forming the complete lake catchment. ArcTool: Merge (Data Management) to produce a merged dataset of the catchment.

The river dataset (*FLOZ*) was first cleaned of lake axes using the ArcTool: Erase (Analysis) resulting in a layer called *FLOZ_without_lakes*. ArcTool: Merge (Feature Vertices to Points) was subsequently used to generate the start and end points for this same dataset (*start_points*, *end_points*).

To assign altitude numbers, *Chdhm25_ras* came into play via ArcTool: Extract Values to Points (Spatial Analyst) resulting in elevation numbers for all Starting- and Endpoints of *FLOZ_without_lakes*-data. Through an ArcTool: Erase (Analysis) operation (*start_points – end_points*) the data set *all_springs* was computed. By ArcTool: Intersect (Analysis) of *end_points* and *all_swiss_lakes* inlets into all Swiss lakes were computed (*inlets_swiss_lakes*). An intersection of *start_points* and *all_swiss_lakes* resulted in *outlets_swiss_lakes*.

ArcTool: Clip (Analysis) of *FLOZ_without_lakes* and for example *Pfäffikersee_catchment* then resulted in *Pfäffikersee_rivers*. The same procedure for clipping the catchment-specific springs and inlets for all 8 lakes was used.

Subsequently, for each lake, respectively the corresponding river dataset, for example *Pfäffikersee_rivers*, a Network dataset was created. A few numbers of manual corrections and removals of individual rivers were necessary to create a functioning and complete network for further calculations. Network Analyst and its function to find the closest facility (facilities: *Pfäffikersee_inlets*, incidents: *Pfäffikersee_springs*) computed the shortest route for every spring to its corresponding lake inlet (including the total length). This layer is called *Pfäffikersee_inflow_possibilties* (and of course analog names for the other lakes) and consists of all relevant information for the calculation of time of concentration.

XY_inflow_possibilties has information on the total length of the river from the spring to the inlet. Elevation above sea level for both the spring and the lake inflow are given, the average slope over the entire course of the river can therefore be calculated. The calculations were performed using ArcTool: Field Calculator (Data Management) into newly created fields (ArcTool: Add Field (Data Management)) in the attribute table.

ToC_1m_s for all *XY_inflow_possibilities* is than calculated by *total_length*/60.

ToC_Kirpich is calculated as follows: $0.0195*([total\_length]^{0.770}) * ([slope]^{-0.385})$ where *slope* = (*elevation_start – elevation_end*) / *total_length*.

For the calculation of time of concentration using NRCS method, additional parameters were added to the dataset *XY_inflow_possibilties*. By consulting aerial photographs, each river was assigned a number for Manning's *n*, the streambed roughness coefficient. Three groups were formed based on table 2:

- Mountain streams with a lot of rocks in the stream bed: $n = 0.05$
- Dug channels / relatively straight, rocky bottom, or algae growth: $n = 0.03$
- Excavated channel, cemented and smooth riverbed: $n = 0.015$

Most rivers were assigned a value of $n = 0.05$, as this category was dominant. Other values were assigned only in the case of clearly visible differences; undefinable river courses were also assigned the number 0.05.

Since the analysis included all river sizes from the smallest mountain stream to the several meters wide inflow into the lakes of the Central Plateau, a compromise had to be found regarding the wetted perimeter and the resulting hydraulic radius. A value of 0.1 was generally assumed for the hydraulic radius. This corresponds for example to a rectangular channel with a water height of 20 cm on a width of 40 cm.

Mannings_velocity was accordingly calculated as follows: (1/[*Mannings_n*]) * $0.1^{2/3}$ * [*slope*]$^{0.5}$.

From this follows **ToC_NRCS** = ([*total_length*]/[*Mannings_velocity*])/60.

At the end of these described calculations, the data set *XY_inflow_possibilties* contains information on all three calculation methods of the time of concentration. However, since this same dataset contains line features and is very difficult to visualize, a further creation of endpoints was performed (ArcTool: Merge (Feature Vertices to Points)).

This resulting dataset, called *XY_inlets_ToC*, contains for each inlet all calculation methods of time of concentration for all upstream branching possibilities. As a final step, only the maximum time of concentration of the flow was selected manually for each inflow (figure 8). Since $T_{C\_Kirpich}$ for branch 1 is higher than the number given by branch 2, this time of concentration is manually added to the final maximum T (figure 8).

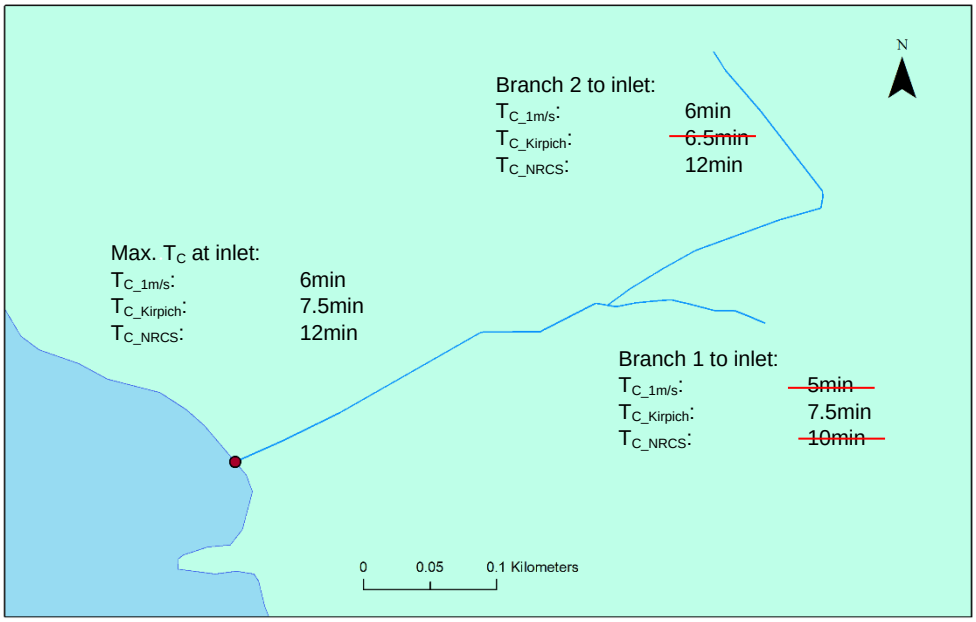

Figure 8: Exemplary procedure for the manual selection of the maximum time of concentration of an inflow

3.2.2 Statistical methods

An analysis of variance was performed to compare the different calculation methods of time of concentration to evaluate the results. In a statistical point of view, each individual outflow is treated as independent (a total of 217 inlets into eight lakes under investigation) and they are measured on the same outcome variable (time of concentration) under three different conditions (different calculation methods). These

conditions normally lead to the application of a within-subjects ANOVA or ANOVA with repeated measures. An ANOVA was thus performed (see Appendix D), but some basic assumptions were not met. On the one hand, my result dataset contains a lot of extreme outliers. On the other hand, the assumption of a normal distribution which must be fulfilled to perform this sort of statistical analysis, is not given. As an alternative to parametric ANOVA, the non-parametric Friedman test was therefore used. This test is used to determine if there are statistically significant differences between the distribution of more than two paired groups (Datanovia, 2021). To run a Friedman test in RStudio, the following packages were used: tidyverse, ggpubr, rstatix. The code of the operation can be found in Appendix D.

4. Results

For all eight lakes and a total of 217 inlets into these lakes, the modelled times of concentration vary from less than one minute for the shortest inflows up to 535 minutes for an inflow into Lake Greifen and resulted from using the NRCS method. For all 217 lake inflows, the average times of concentration were 17.5 minutes for Kirpich-method, 32.3 minutes for 1m/s-method and 29.8 minutes for NRCS-method (table 4, figure 9). The Time of concentration was significantly different for the three different calculation methods (X^2 (2) = 92.53, p = 0.0001).

While the 1m/s calculation method and the NRCS-method provide approximately similar times of concentration on average, the three outliers with high times of concentration in the NRCS-method are particularly noticeable. In general, the Kirpich-method provides the shortest times of concentration and models the time of concentration for outliers to a maximum of just slightly above 200 min. Pairwise Wilcoxon signed rank test between groups revealed significant differences in time of concentration between 1m/s-method and Kirpich-method (p = 4.59*10-21); 1m/s-method and NRCS-method (p = 9.21*10-10); Kirpich-method and NRCS-method (p = 3.48*10-13).

However, the overall picture and individual lakes, their calculated maximum time of concentration has a slightly different picture (table 5). The different methods of calculating the time of concentration also show significant differences over all except for Lake Greifen at lake level, but which measures differ significantly is different for

each lake (table 5 and lake-specific boxplots in Appendix B). To illustrate the calculated values, a four-part overview graphic like that of Lake Aegeri (figure 10) was produced for each lake (Appendix B).

Method	***max. T_C***	***median***	***mean***
1m/s	316 min	16.5 min	32.2 min
Kirpich	200 min	9.11 min	17.5 min
NRCS	535 min	9.89 min	29.8 min

Table 4: Summary of times of concentration for all 217 inflows of the eight lakes studied.

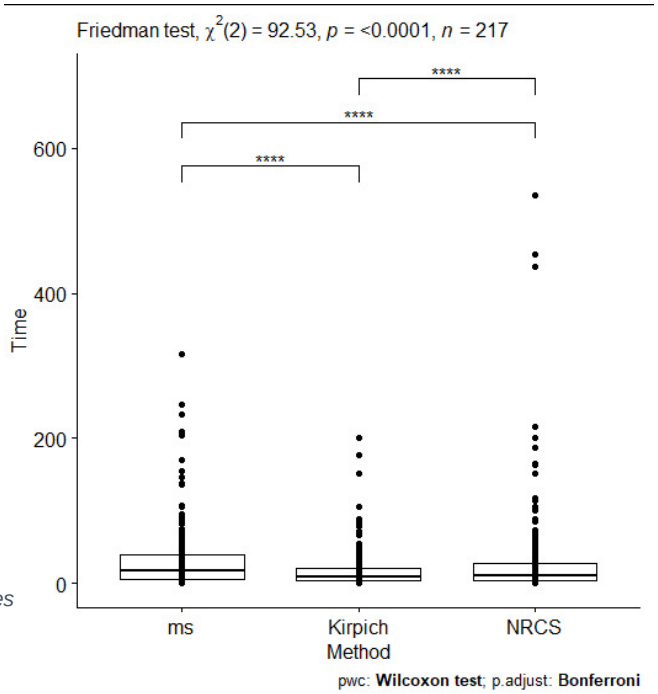

Figure 9: Boxplot summarizing all times of concentration calculations for the eight lakes

	max. $T_{C\_1m/s}$	*max. $T_{C\_Kirpich}$*	*max. T_{C_NRCS}*	*Friedman test*
Lake Greifen	316.4	200.3	535	X^2 (2) = 1.94, p = 0.38
Lake Pfäffikon	169.7	79	187.5	X^2 (2) = 15.18, p = 0.00051
Lake Lauerz	233.3	83	199.9	X^2 (2) = 21.53, p = 0.0001
Lake Ägeri	145.7	55.3	118	X^2 (2) = 47.74, p = 0.0001
Lake Baldegg	245.8	151.6	436.9	X^2 (2) = 29.08, p = 0.0001
Lake Hallwil	138.3	106.3	165.3	X^2 (2) = 25, p = 0.0001
Lake Sils	145.9	49.4	101.9	X^2 (2) = 15.18, p = 0.00051
Lake Silvaplana	209.5	88.2	216.1	X^2 (2) = 29.86, p = 0.0001

Table 5: Summary of all maximum numbers of time of concentration for all three methods used compared for all lakes.

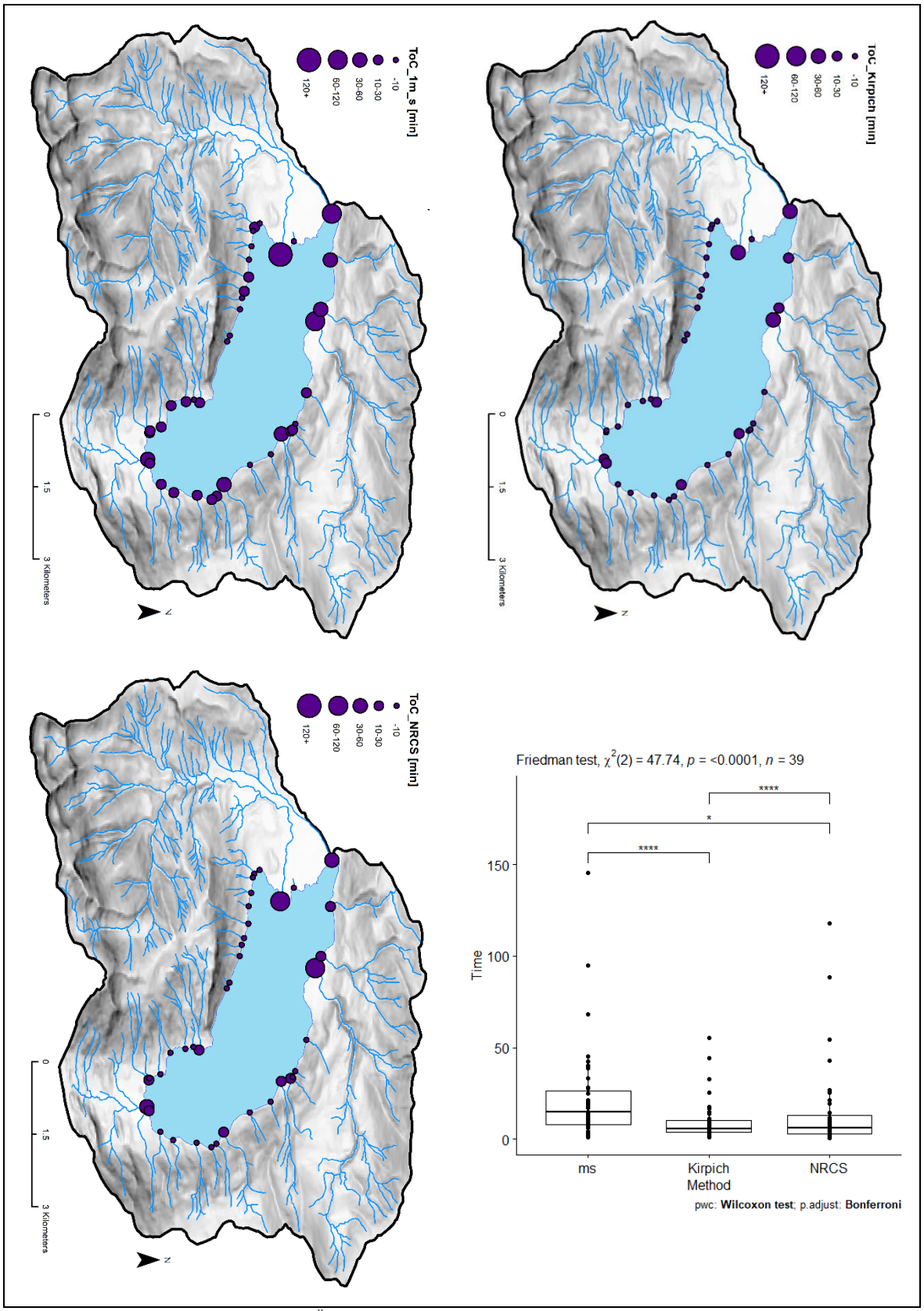

Figure 10: Time of concentration for Lake Ägeri using different calculation methods. Top left: 1m/s. Top right: Kirpich. Bottom left: NRCS. Bottom right: Summary Boxplot. In the background a shaded relief, the darker the steeper the slope.

5. Discussion & Conclusion

5.1 Discussion

For the eight selected Swiss lake catchments, the time of concentration for the inflows ranged from a few minutes to a maximum of just under nine hours. The three models produced significantly different estimates in time of concentration, but their average values differed by a max of 15 minutes. When cross-comparing the individual methods for the eight lakes, it is noticeable that the Kirpich-method, without exception, has the smallest values for the maximum time of concentration. However, the numbers given for Kirpich calculation method must be assumed to be an underestimate due to the assumption of a uniform slope which is not the case (see relief shading in Figure 10). The rivers on the steep southwestern slope of Lake Aegeri have significantly shorter times of concentration (smaller circle diameter) when the slope is included into modelling compared to the 1m/s-method. Although mountain streams and rivers in steep terrain can have rougher streambeds compared to downstream sections, they tend to exceed a flow velocity of 1-m/s for both surface and subsurface flow due to their slope (Lamb et al, 2017). This would mean that the 1-m/s calculation method for steeper areas generally overestimates the values for the time of concentration.

However, even if estimates are underestimated, it is important to put the time of concentration into context for the transport and degradation of eDNA. Empirically it has been shown that eDNA can be detected downstream in flow distances of 10 kilometres for small streams up to 100 kilometres for larger rivers (Deiner & Altermatt, 2014 & Pont et al, 2018). The eight catchments and their rivers modelled here, with a maximum length of 19 kilometres from spring to inlet, are all likely in an order of magnitude to be able to draw conclusions that the eDNA sampled in lakes has been transported from their entire catchment area (Deiner et al, 2016). The times of concentration for all inflows to the lakes studied, regardless of the method used for calculation, are just under nine hours at the maximum and this amount of time does not exceed the experimentally determined decay rates of eDNA for any system studies so far (Allan et al, 2020). Given current knowledge about the decay rate of eDNA in streams, it therefore should be possible for eDNA to reach the lakes for all watersheds analysed. If the flow velocity of the water, which is the basis for all concentration time calculation

methods, is the only component that affects the transport of eDNA in water, it should be possible to consider lakes as accumulators of eDNA.

However, degradation of eDNA is complex and the state in which eDNA resides can determine its properties such as the deposition velocity (Pont et al, 2018). For example, repeated cycles of absorption and deposition to the benthic zone of stream beds could lead to a delay in the transport of eDNA compared to water velocity (Harrison et al, 2019). In addition, during transport downstream, eDNA particles may stick to the streambed or even be adsorbed into the biofilm and thus may never reach the lake (Shogren et al, 2017). In addition, river water characteristics such as temperature, pH or electrical conductivity also play a major role in the degradation process of eDNA during transport (Jia et al, 2021); however, water chemistry and deposition velocity were not considered in more detail in the present study. These would be obvious next parameters to model and include for more realistic estimates of eDNA transport. Based on flow, however, it seems that this is not the limiting factor for the eight catchments modelled here.

5.2 Assumptions and caveats

Despite all the positive results with regard to the transport times of eDNA in water, it should be taken with caution. For the modelling of the concentration times, a lot of assumptions were made, which lead to some notable caveats.

First, caveats concern the data I used, especially Strahler stream order number (Swisstopo, 2014), which did form the basis for my calculations of the time of concentration. As described in section 3.1.2, a field survey was conducted to verify that the field observations of inflows into Lake Pfäffikon matched the dataset. However, as shown in Figure 4, the field observations and the data set used are only moderately consistent. For example, according to Swisstopo (2014), no streams should flow into western Lake Pfäffikon. However, I was able to identify small tributaries there during our visit on site. Another source of error in this field survey presents the inaccuracy of the Google Maps GPS positioning. Figure 4 shows mapped tributaries located in the lake, which is of course hardly possible. Furthermore, this dataset contains many short tributaries (a few meters to a maximum of a few 100 meters), which could be assumed to be drainage channels from marshes near the shore rather than flowing streams. In

addition, obstructions such as falls, small dams, weirs or ponds in the headwaters of the watercourses are not recorded, although they would have a significant influence on the flow velocity (Ohmoto et al, 2016). Due to the absence of such obstacles in the metadata, they could not be included in the modelling and were therefore not considered – rather uniform flow behaviour was assumed over the entire length of a river.

For the calculation of the slope, and thus also the modelling of the concentration times according to the Kirpich-method and the NRCS-method, assumptions were made that likely do not correspond to reality. Since the elevations for each river were extracted only for the springs and the tributaries to the lakes and not for confluences or other intermediate points, the slope results in a constant gradient along the entire length of a river. The fact that different interpretations of the average slope produce different results for the concentration time for this method is hypothetically illustrated with three possible scenarios in figure 11 showing a river that loses a total of 1000 meters of elevation over a flow distance of 10 kilometres.

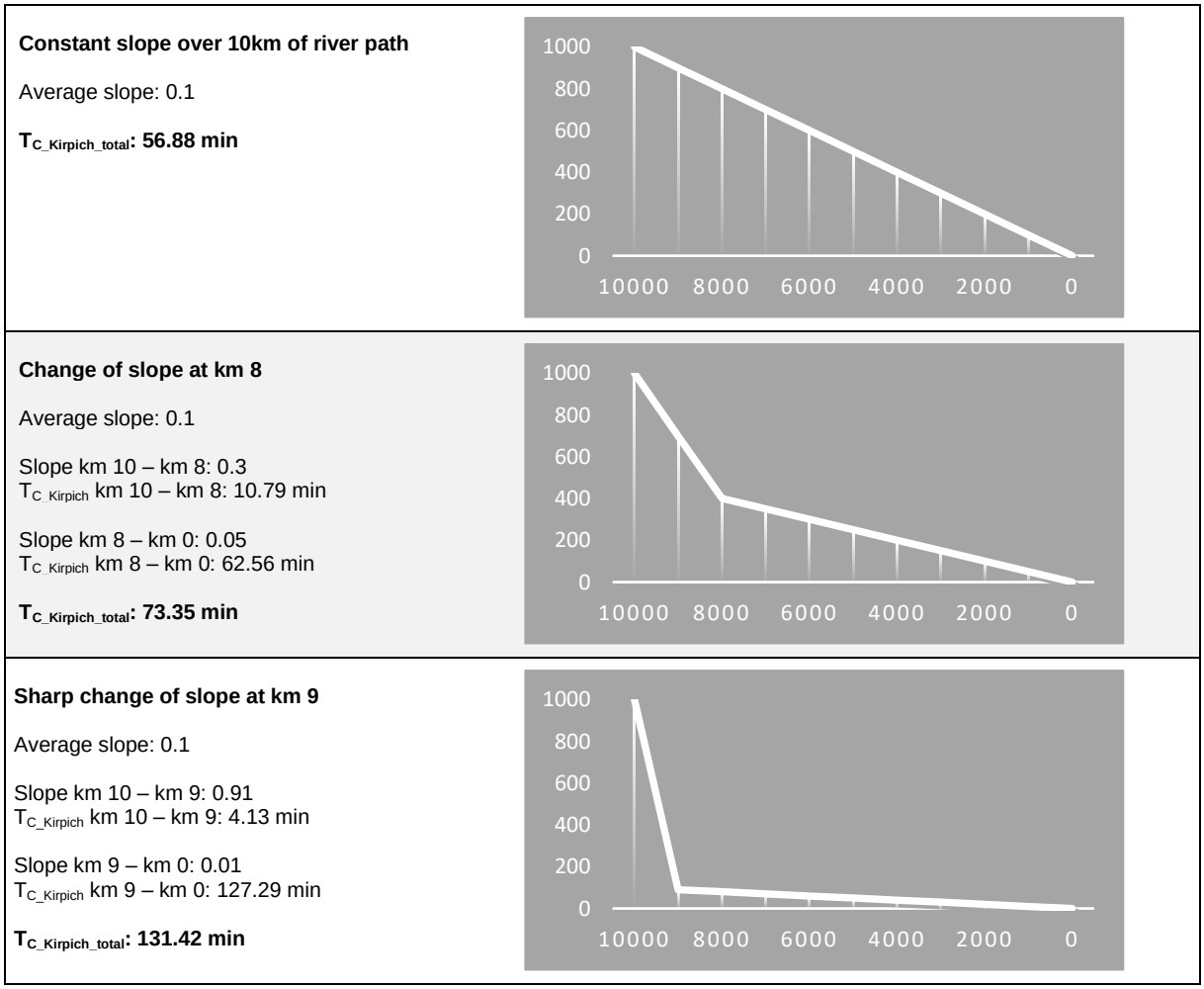

Figure 11: Hypothetical illustration of the importance of slope in calculating time of concentration

The longitudinal profile of most rivers shows relatively large elevation changes over short distances in the headwaters and relatively small elevation changes towards the mouth (Leopold, 1953 & Rhoads, 2020), leading to higher flow speed in the headwaters due to elevation changes compared to river mouth sections. In contrast, the flow velocity also tends to increase downstream due to higher total discharge (Leopold, 1953). The concentration time according to the Kirpich-method calculated in this study is therefore likely to be an underestimation.

In the present study, no attention was paid to the fluctuating discharge values of the rivers in the course of the year or during major events. If bankfull flow conditions are given, the roughness of the body of water, Manning's *n*, tends to decrease and the flow velocity increases at the same time (Yochum et al, 2014). Further, use of Manning's equation, and in particular the hydraulic radius and the roughness value, Manning's *n,* is hard to estimate due to the lack of literature on typical values for mountain streams or rivers in Switzerland. Since the hydraulic radius depends on different flow levels and the form of a streambed (Water and Rivers Commission, 2001), the value of 0.1 was chosen for simplicity, an average stream width of 40 cm and an average stream height of 20 cm was assumed. Using values which exactly double the hydraulic radius to 0.2, the flow velocity of the water in the Manning's formula would be higher and the time of concentration according to the NRCS method would be exactly 37% lower. If the hydraulic radius in the formula is halved to 0.05, the flow velocity is reduced, and the time of concentration would be 57% greater as presented in my results. While this is a large variance that could be assumed for the calculated values, again this amounts to only minutes or hours for the eight catchments under investigation which does not make it more likely that eDNA was degraded before it could be transported to the lake based on flow.

Another estimate that could have led to large variation in times of concentration are that simple aerial photographs were used to select the roughness value of a streambed as part of the NRCS calculation method. This is a very large source of error, since for some rivers, the streambed was not visible at all (dense vegetation cover, turbid water, etc.). Also, the selection of Manning's *n* had to rely on literature descriptions that suggest different values for different channel types. Depending on the interpretation of the observer, this assignment is likely different. Here I chose to follow values presented by Thomason (2019, table 2) and assigned a value of 0.05 to mountain streams, for

example. In other studies, different values are used. Yochum et al. (2014) assign a roughness value of 0.18 to an Italian mountain stream, which could similarly occur in the catchment area of Lake Sils or Lake Silvaplana. If Manning's *n* was doubled, this would also lead to a doubling of the time of concentration according to the NRCS-method. This is again a large variance to consider. For the investigated catchment areas, however, the deviations amounted to a few minutes to a few hours. A decay of eDNA before arrival in the lake is therefore rather unlikely.

6. Outlook, recommendations for further research & improvements

To further advance biodiversity monitoring, much progress is currently being made utilizing the detection of environmental DNA to infer species presence in a landscape. While I could show that water is moving to lakes in a relatively short time, we still need to understand much more about the drivers of eDNA decay. In the field of eDNA research, much is currently done to understand the decay mechanisms and the fate of eDNA in water. However, since most of the studies conducted to date focus on one single species or on a specific environment, a general global overview with reliable parameters for the quantitative decay of eDNA is still lacking. The degradation processes need to be better understood to draw conclusions about how far the transport of eDNA in water is possible and what upstream area can be covered with individual sampling campaigns when biodiversity monitoring is carried out.

Concerning time of concentration, it is unlikely that the accuracy and density of data I was able to access for this study is available on a global level. Therefore, the focus must first be placed on developing a reliable model that provides results for times of concentration based on easily determinable parameters. A first step in this direction has been taken with the present work, although there are still some uncertainties. Since the roughness of the streambed strongly influences the flow velocity of water and thus also the resulting time of concentration, I suggest that a handbook on this subject should be prepared in which images and Manning's *n* values are documented with photographs taken in the field. This would, of course, involve extensive field work, which I consider unavoidable to develop more accurate models that are, above all, also

supported by field testing results. Researchers exploring eDNA transport in river systems should consider collecting such metadata about stream beds such that greater resources exist to incorporate hydrological modelling into predictions. Such continued collaborations will lead to a fruitful interdisciplinary knowledge gain for understanding the potential to use eDNA for biodiversity monitoring on large spatial scale. Given the severity in decline of species and biodiversity, it is paramount we find efficient monitoring tools to aid in decisions to restore and conserve landscapes using the best available science form all disciplines (Lacoursière-Roussel & Deiner, 2021).

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Appendix A: Tables

OBJECTID in swiss_subcatchments		Lake
5992	16371	Silvaplanersee
14929		Silsersee
8416		Greifensee
1559		Pfäffikersee
16871		Ägerisee
11856		Hallwilersee
19913		Lauerzersee
5008		Baldeggersee

Table 6: ObjectID in swiss_subcatchments to extract single lakes

EZGNR in swiss _subcatchments to get Pfäffikersee_catchment		EZGNR in swiss _subcatchments to get Silsersee_catchment		EZGNR in swiss _subcatchments to get Lauerzersee_catchment		EZGNR in swiss _subcatchments to get Aegerisee_catchment	
161826	102758	133831	111701	165037	108424	150519	104534
170562	100163	131999	117939	105128	108766	188351	106077
101443	165966	187174	123387	178225	158888	180066	180323
104191	141078	104386	132553	146203	174992	157572	150531
185726	130678	138602	179638	150318	162285	105379	141627
118576	196672	169677	197625	162371	145144	151597	191080
122785	109175	137840	164024	118189	166587	132186	178753
122785	114514	146731	120961	145898	190553	150519	164331
118515	185449	163772	147583	121023	121073	121644	142999
163562	194981	195492	134491	199906	188701	189923	156398
140410	121163	100945	188227	186322	114725	153956	127675
135397	106401	113810	114915	155225	190803	146046	126657
159685		137515	160259	138083	110953	110002	151964
		142385	139974	199852	101667	158128	157231
		126570	156424	149009	177758	129649	107079
		190092	130726	111122	140180	180076	153232
		101032	156351	169826	102965	179149	150386
		142680	167977	109475	166243	121636	151612
				146325	153098	170553	168598
				139830	182994		176834
				178170	161448		
				129285	159391		
				111290	103053		
				100754	189783		
				158206	131674		
				170550	137420		
				167795	190611		
				187625			

Table 7a: EZGNR in swiss_subcatchments to extract proposal lake catchments

EZGNR in swiss _subcatchments to get Baldeggersee_catchment		EZGNR in swiss _subcatchments to get Hallwilersee_catchment		EZGNR in swiss _subcatchments to get Silvaplanersee_catchment		EZGNR in swiss _subcatchments to get Greifensee_catchment	
117685	105396	192153	138315	104622	193458	175673	194419
129208	104309	158298	175933	154226	159890	187063	145119
155376	172715	129995	185723	158812	138069	175922	188200
113920	159931	154439	146999	142867	162753	139651	161517
100857	183235	147053	152398	190282	199058	106851	185388
181333	106421	128127	140399	102875	131786	128298	143669
181415	101216	130679	153430	189784	196219	126053	112323
110247	130983	148069	128847	108417	138202	151004	169621
131625	177731	121174	178074	151305	141424	166023	160422
162812	136828	150250	168256	106169	168257	103364	182291
140351	144793	160436	151247	181655	142986	172071	116327
188798	139034	150413	183954	119268	124395	190036	199092
173482	116491	153935	183954	188517	128047	132542	132648
181250	128437	147293	114928	105210	178910	166440	153736
194163	142537	116352	127423	119269	149606	164440	168291
189156	111360	190999	175725	163850	143739	187980	182152
107013	110675	176161	177589	105506	141559	121371	168289
110355	139699	148286	107413	190442	126299	124744	165457
165134	157931	124232	144887	172924	156928	100922	133469
102896	114888	178051	178871	137909	163889	151549	176650
163356	126262	127708	152357	100806	156927	199243	179730
171501	129257	105652	127532	174452	152670	132608	198824
172394	162394	147418	133319	105149	124072	198584	126282
164840	125320	195033	105548	191090	191638	165253	117057
184115	196549	128943	100028	108953	149097	166229	183142
188638	187989			170222	150300	133147	152254
158134	172090			198552	159407	183787	135089
110971	166683			127831	174672	159189	107045
118674	154292			192199	179841	133740	185796
138143	123674			141970	151453	164053	161946
125746	141160			112246	114461	180261	142462
182268	103440			161211		170581	134824
180945	151039					137502	177075
121752						150065	151347
						185563	125293
						162949	191666
						120615	137741
						110298	169839
						119874	103197
						175784	188214
						129373	157227
						167429	174170
						144812	161225
						133400	164760
						137710	

Table 7b: EZGNR in swiss_subcatchments to extract proposal lake catchments

Appendix B: Figures

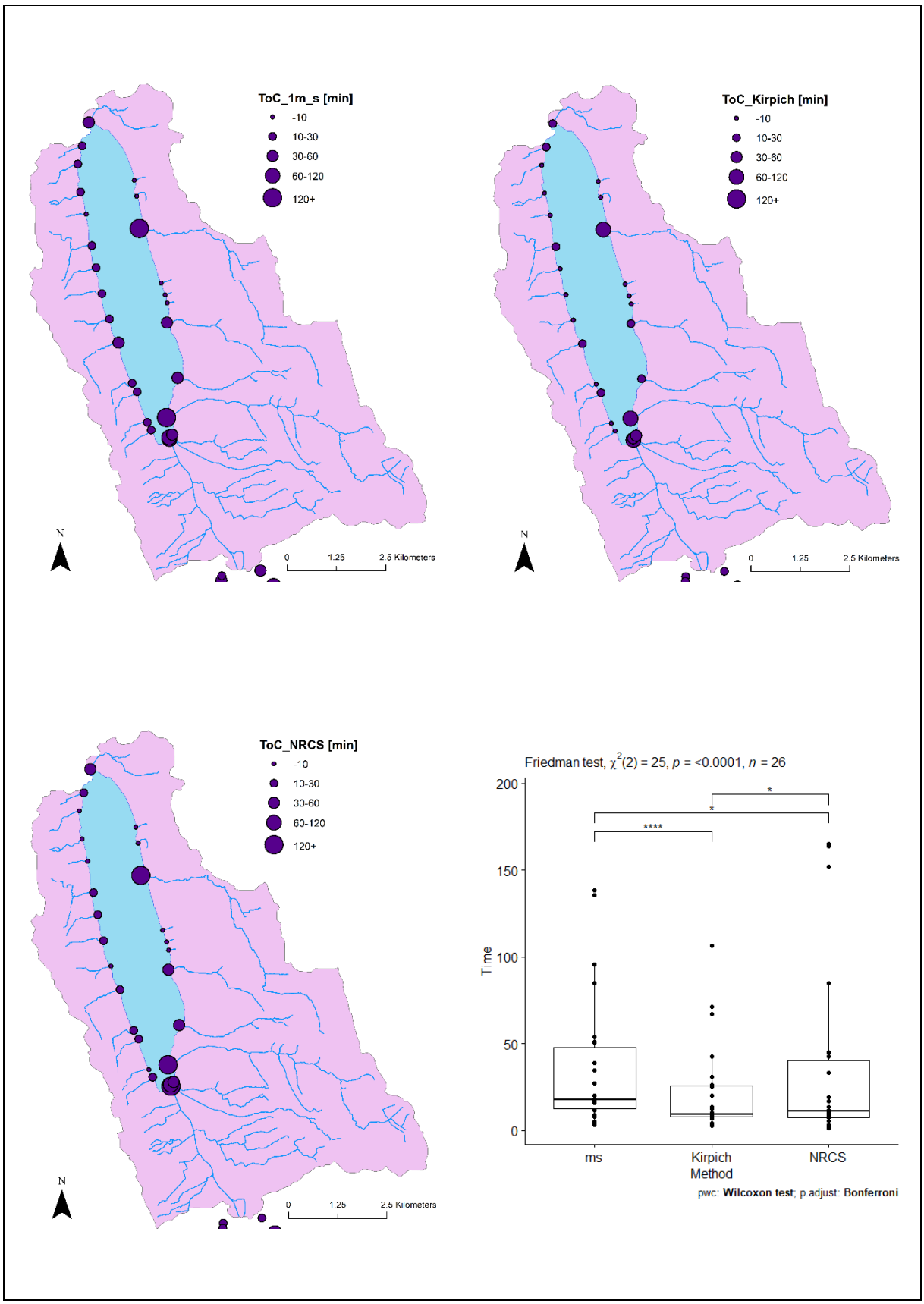


Figure 12: Time of concentration for Lake Hallwil using different calculation methods. Top left: 1m/s. Top right: Kirpich. Bottom left: NRCS. Bottom right: Summary Boxplot.

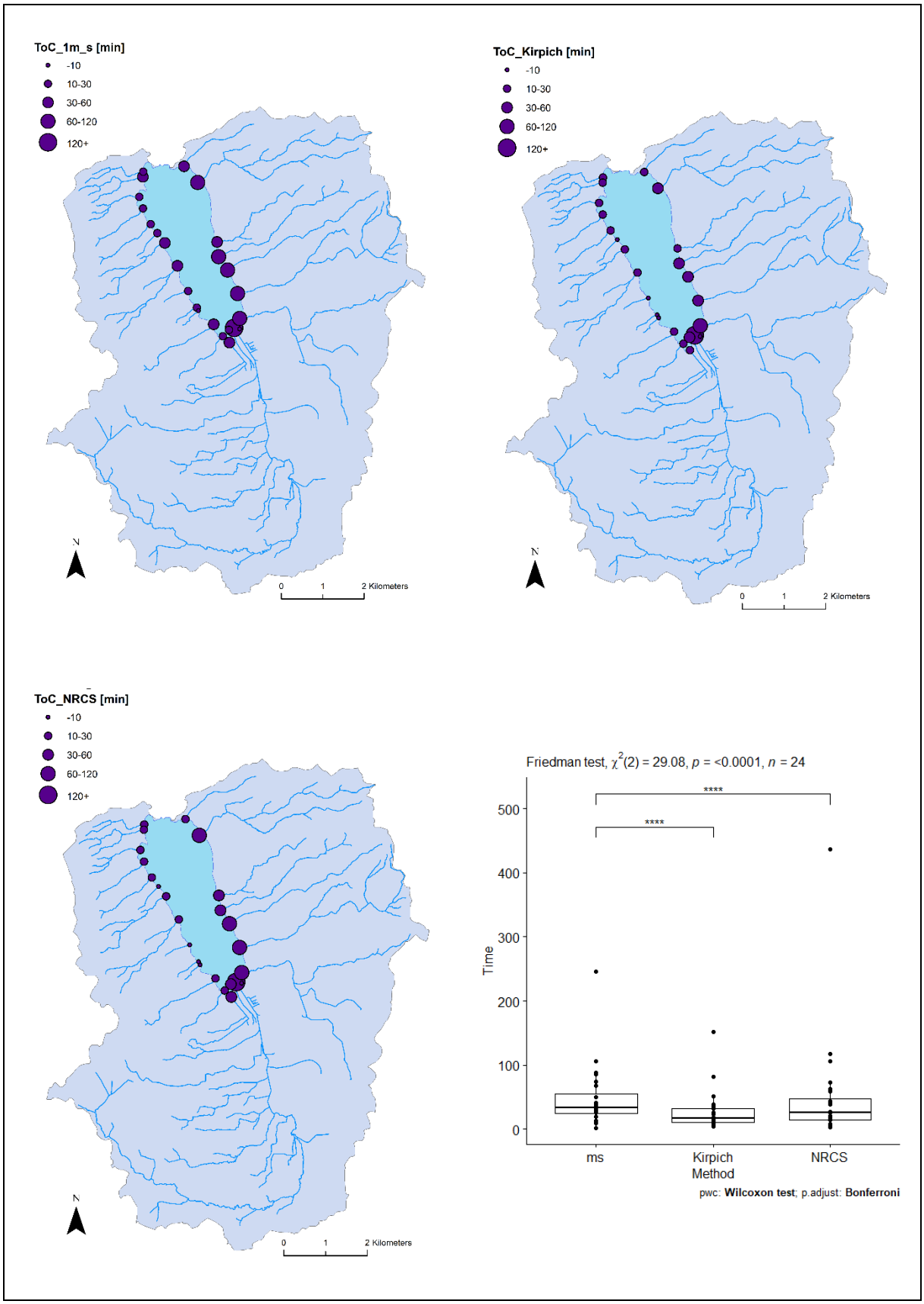


Figure 13: Time of concentration for Lake Baldegg using different calculation methods. Top left: 1m/s. Top right: Kirpich. Bottom left: NRCS. Bottom right: Summary Boxplot.

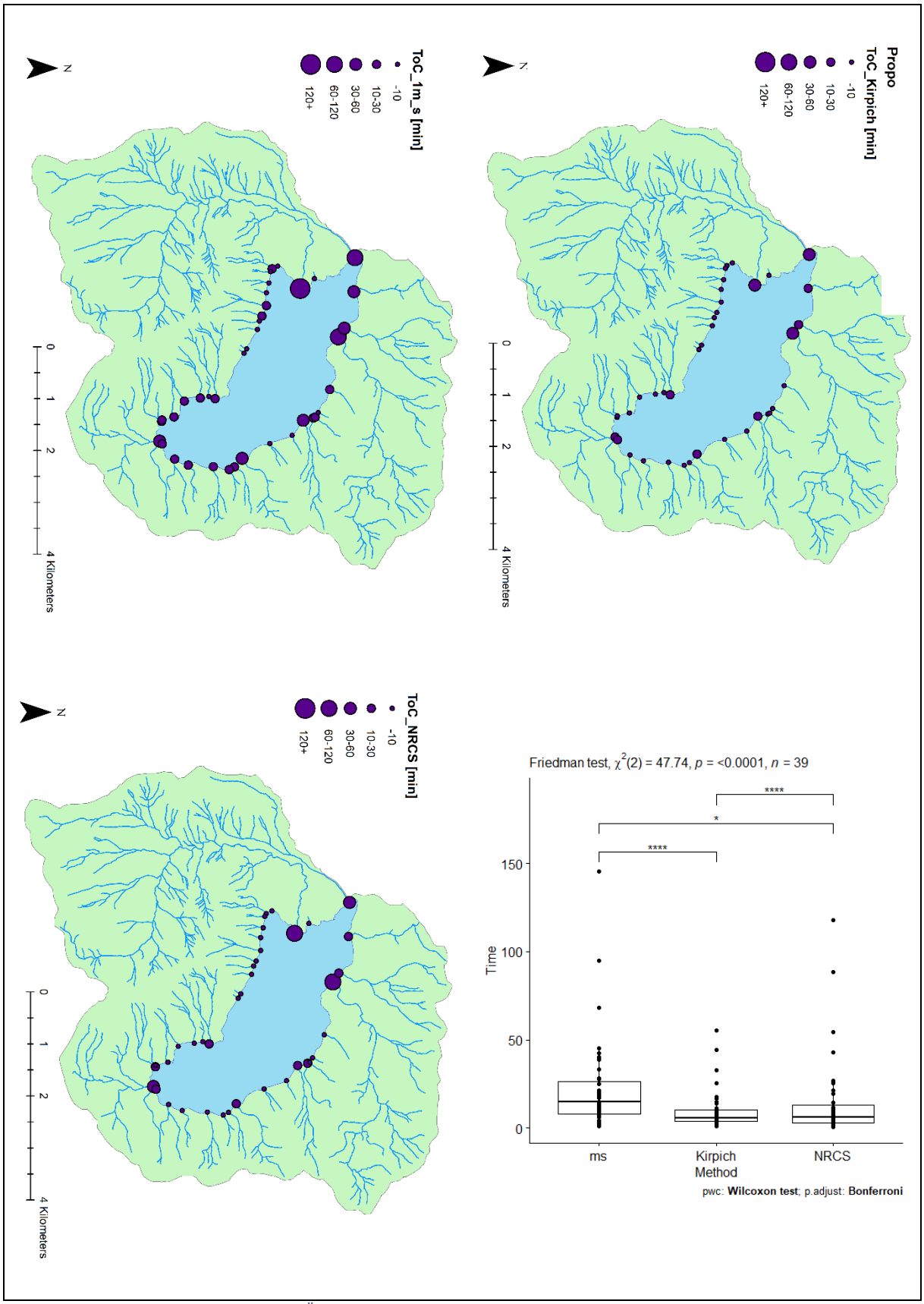


Figure 14: Time of concentration for Lake Ägeri using different calculation methods. Top left: 1m/s. Top right: Kirpich. Bottom left: NRCS. Bottom right: Summary Boxplot.

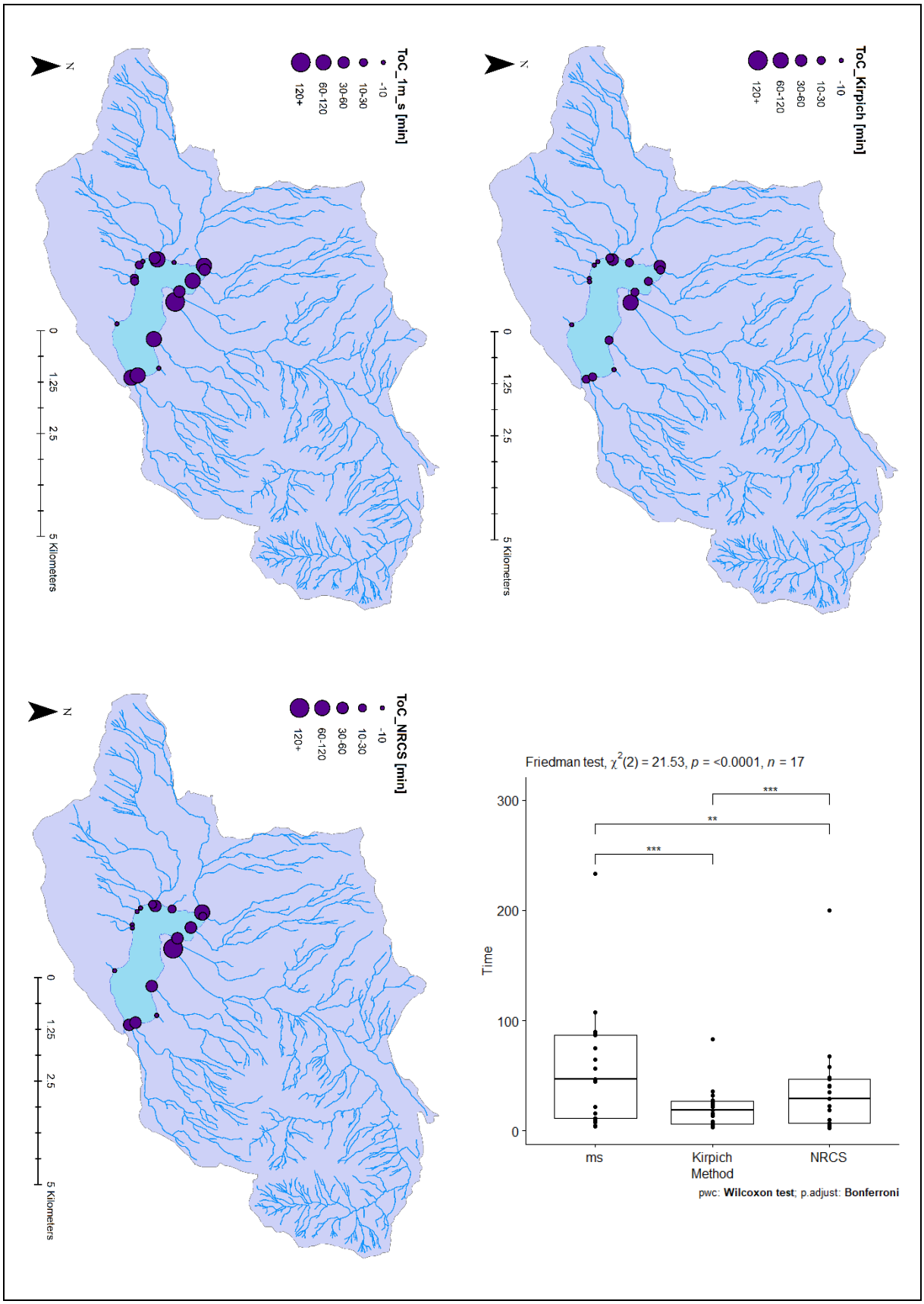


Figure 15: Time of concentration for Lake Lauerz using different calculation methods. Top left: 1m/s. Top right: Kirpich. Bottom left: NRCS. Bottom right: Summary Boxplot.

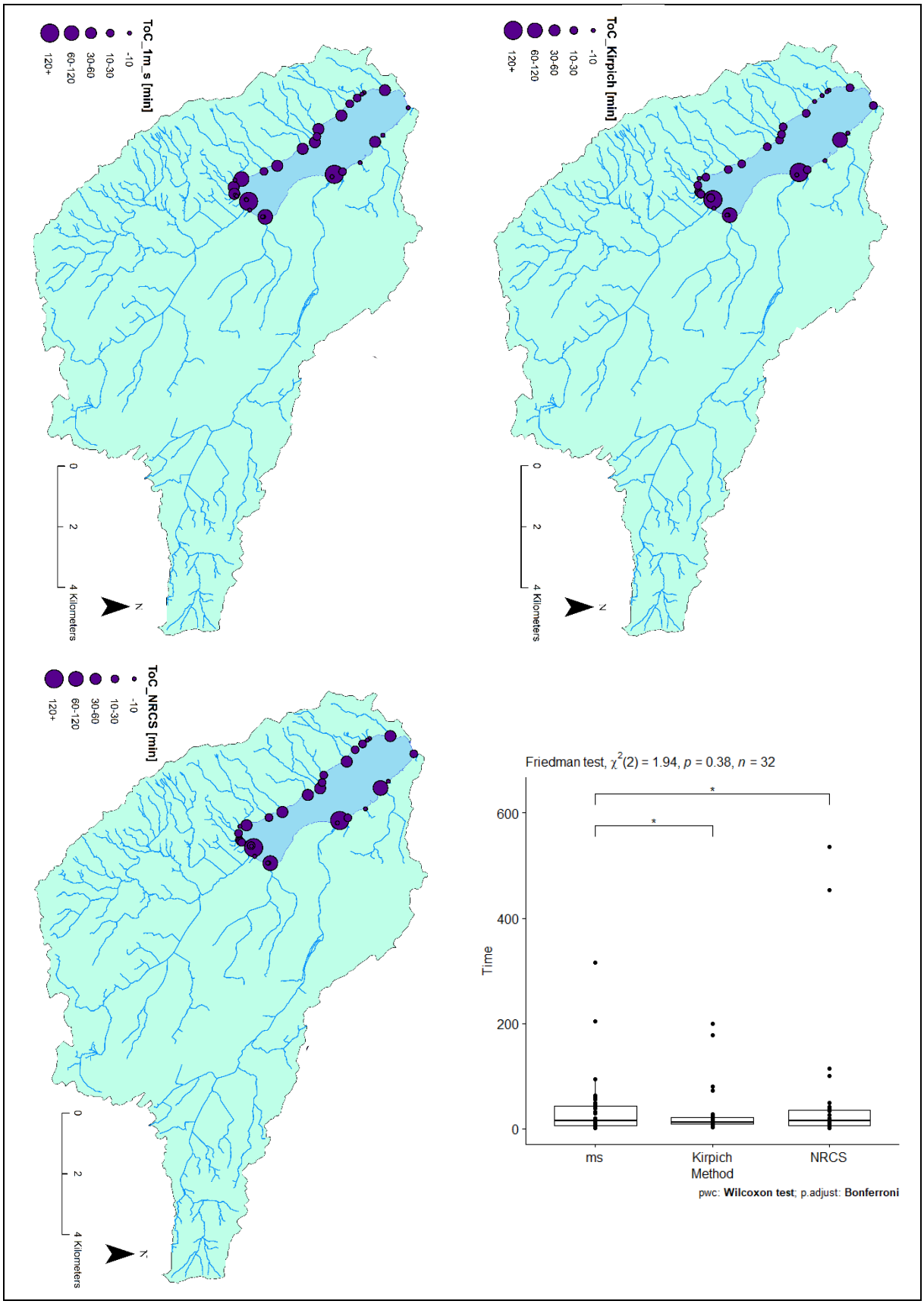


Figure 16: Time of concentration for Lake Greifen using different calculation methods. Top left: 1m/s. Top right: Kirpich. Bottom left: NRCS. Bottom right: Summary Boxplot.

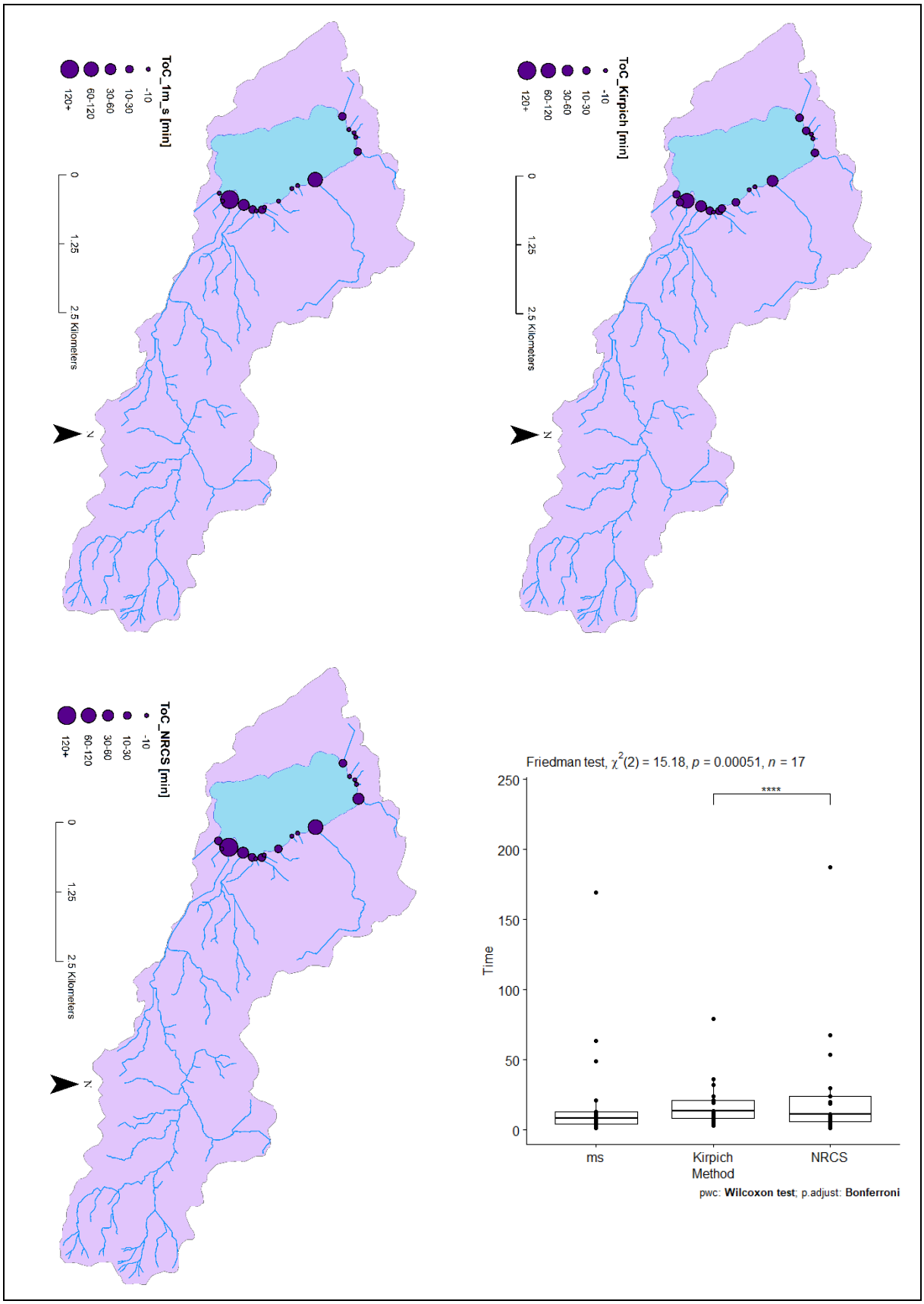


Figure 17: Time of concentration for Lake Pfäffikon using different calculation methods. Top left: 1m/s. Top right: Kirpich. Bottom left: NRCS. Bottom right: Summary Boxplot.

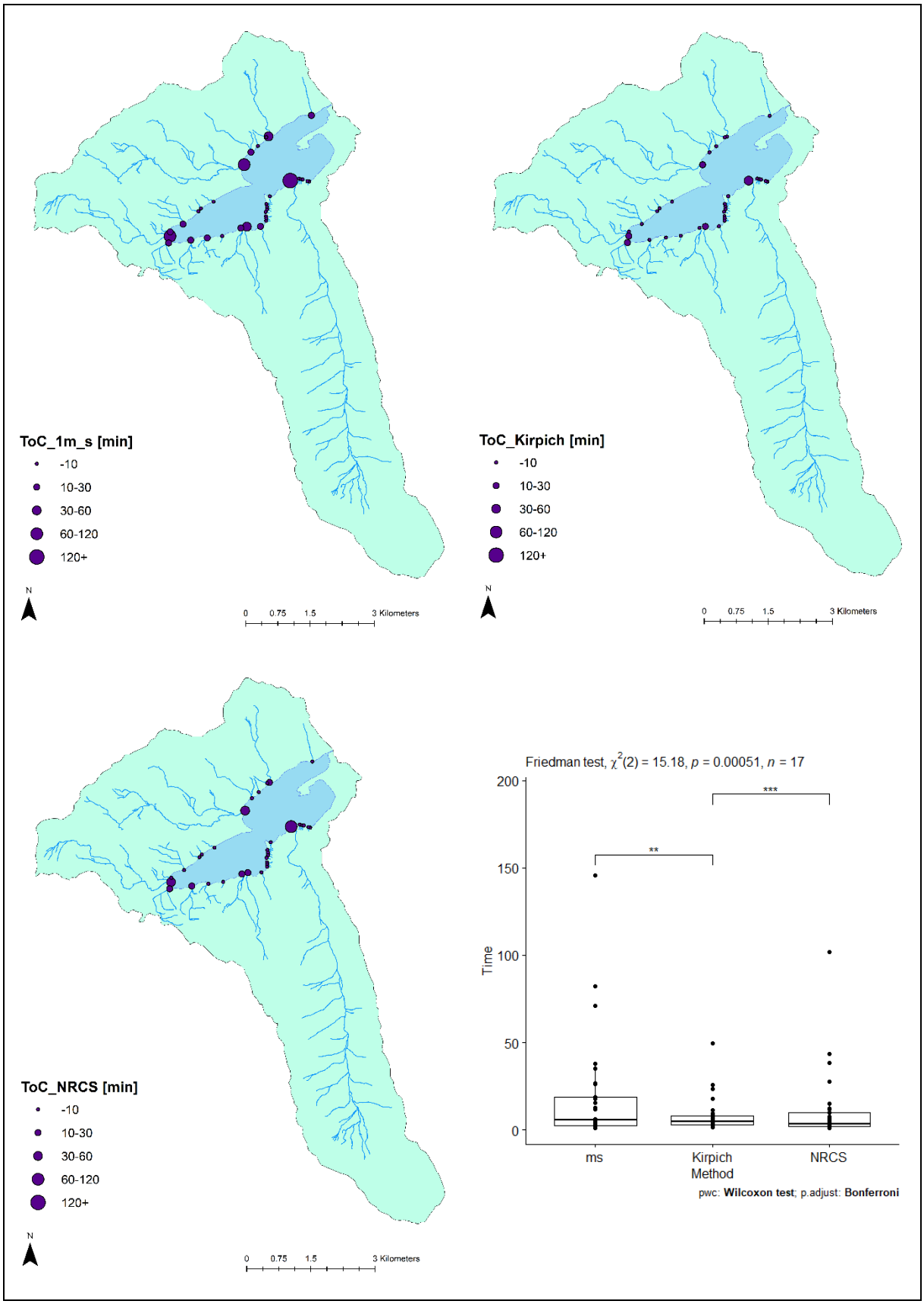


Figure 18: Time of concentration for Lake Sils using different calculation methods. Top left: 1m/s. Top right: Kirpich. Bottom left: NRCS. Bottom right: Summary Boxplot.

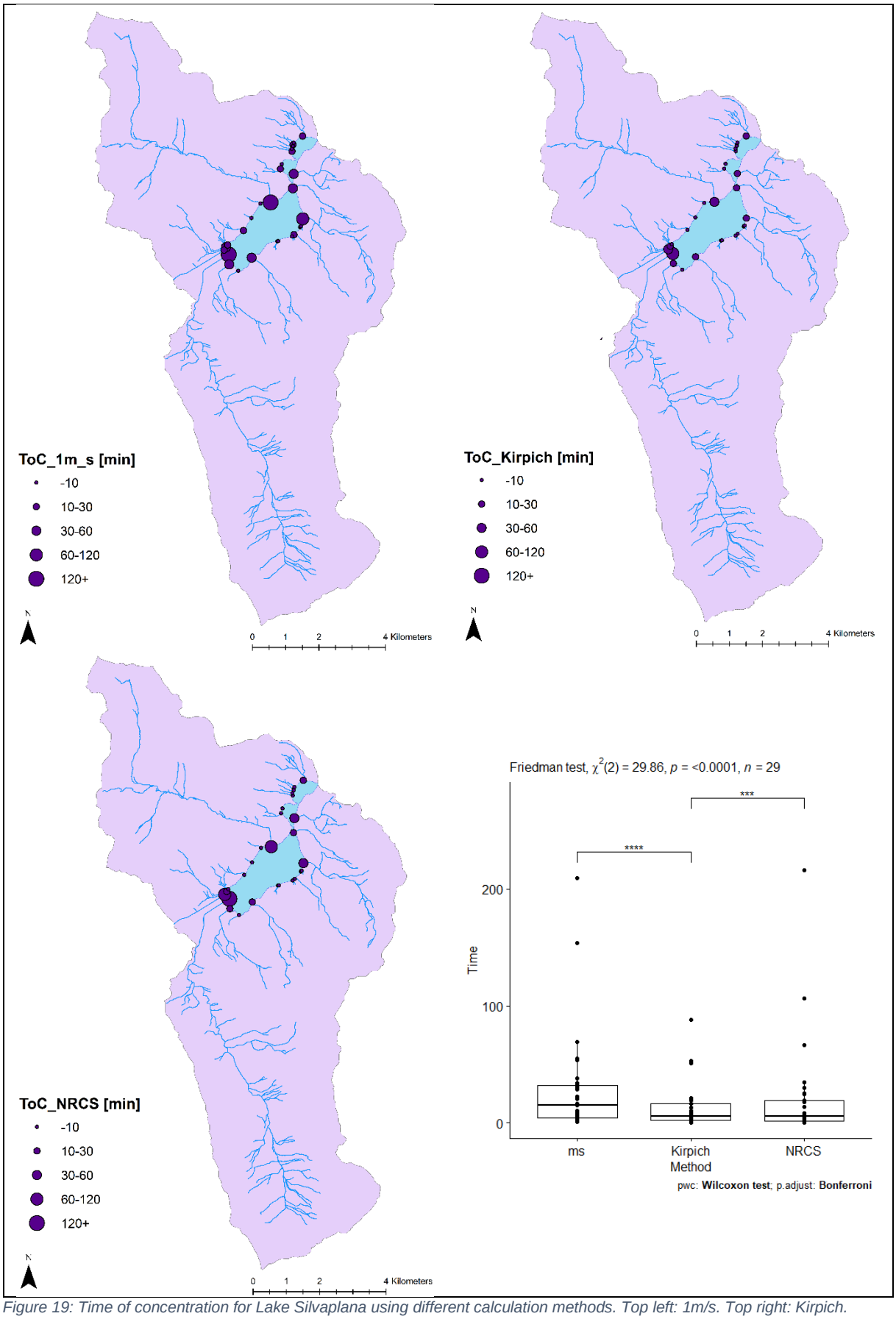


Figure 19: Time of concentration for Lake Silvaplana using different calculation methods. Top left: 1m/s. Top right: Kirpich. Bottom left: NRCS. Bottom right: Summary Boxplot.

Appendix C: Pictures of field visits

Figure 20: Lake Pfäffikon, inlet number 2 (own photo)

Figure 21: Lake Pfäffikon, inlet number 3 (own photo)

Figure 22: Lake Pfäffikon, inlet number 4 (own photo)

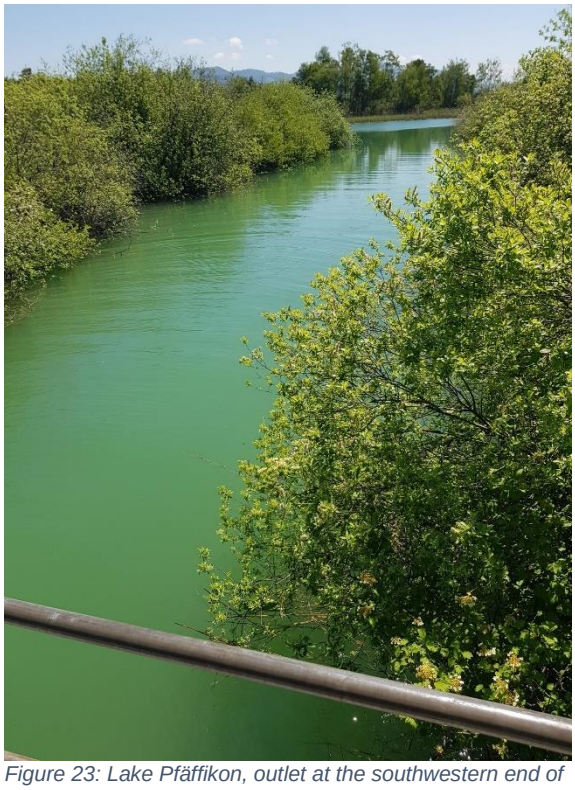


Figure 23: Lake Pfäffikon, outlet at the southwestern end of the lake (own photo)

Figure 24: Lake Pfäffikon, inlet number 8 (own photo)

Figure 25: Lake Pfäffikon, inlet number 10 (own photo)

Figure 26: Lake Pfäffikon, inlet number 13 (own photo)

Figure 27: Lake Pfäffikon, inlet number 14 (own photo)

Figure 28: Lake Sils, main inlet Aua da Fedoz (Kristy Deiner)

Figure 29: Lake Sils, Ova dal Mulin (Kristy Deiner)

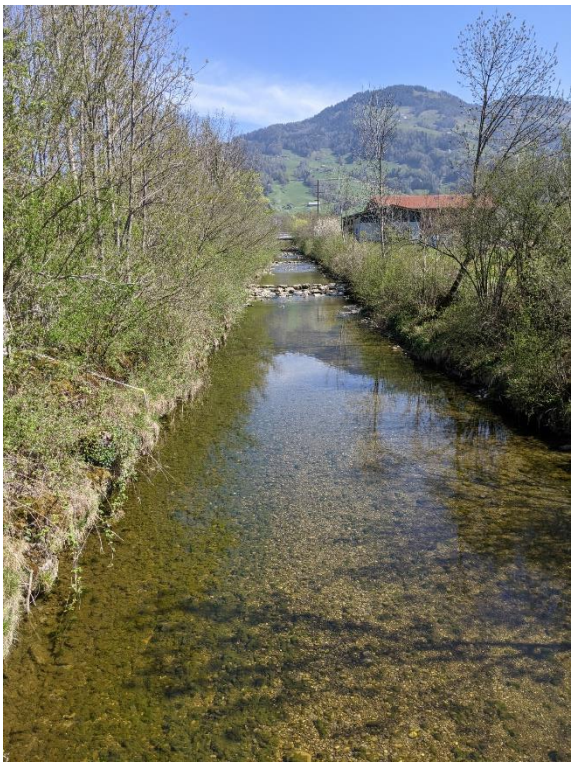


Figure 30: Lake Lauerz main inlet Steiner Aa (Kristy Deiner)

Figure 31: Lake Lauerz, tube inlet (Kristy Deiner)

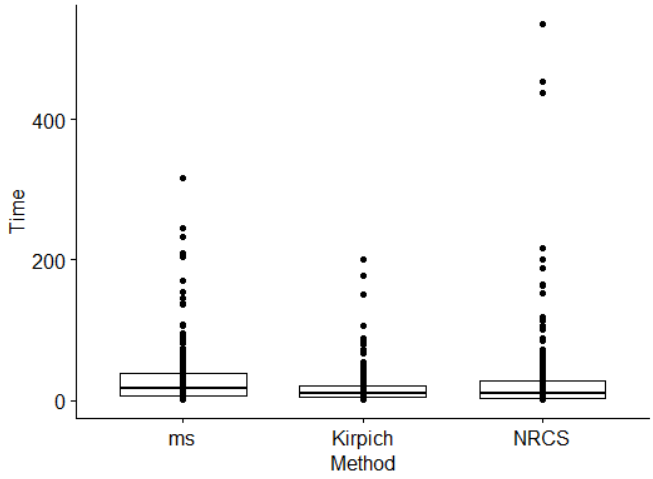
Appendix D: Code in R

R-Code for ANOVA

```
library(tidyverse)
library(ggpubr)
library(rstatix)
proposal_lakes_ToC <-read.csv("C:/Users/bafrefel/Desktop/Times of
concentration of swiss lakes/scratch/xyz.csv", header = T, sep = ";")

#Summary Statistics
proposal_lakes_ToC%>%
  group_by(Method) %>%
  get_summary_stats(Time, type = "mean_sd")
```

Method	variable	n	mean	sd
Kirpich	Time	217	17.5	25.9
ms	Time	217	32.3	45.6
NRCS	Time	217	29.8	64.0

```
# visualization
bxp <- ggboxplot(proposal_lakes_ToC, x = "Method", y = "Time", add =
"point")
bxp
```



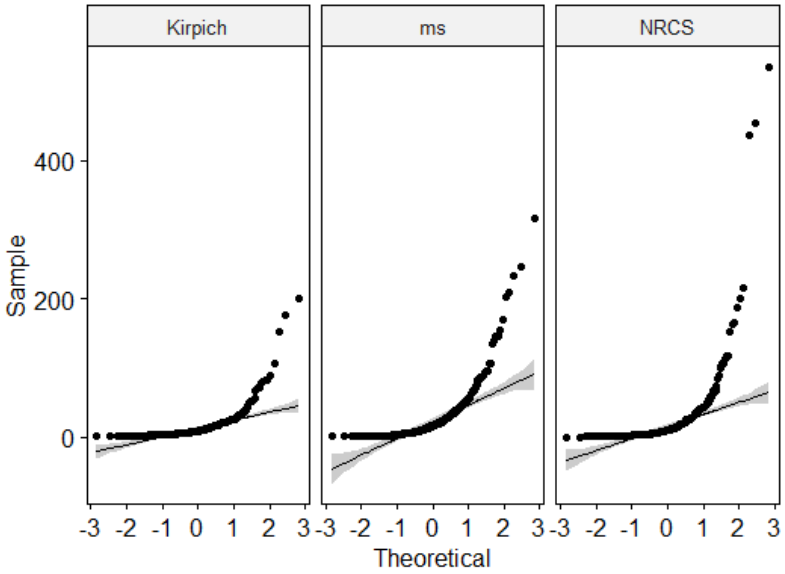

```
#outliers
outliers <- proposal_lakes_ToC %>%
  group_by(Method) %>%
  identify_outliers(Time)
```

→ 58 Outliers, 37 extreme outliers

```
#normality assumption
proposal_lakes_ToC %>%
  group_by(Method) %>%
  shapiro_test(Time)
```

Method	variable	statistic	p
Kirpich	Time	0.562	$4.68*10^{-23}$
ms	Time	0.648	$6.03*10^{-21}$
NRCS	Time	0.430	$9.29*10^{-26}$

```
ggqqplot(proposal_lakes_ToC, ”Time”, facet.by = ”Method”)
```



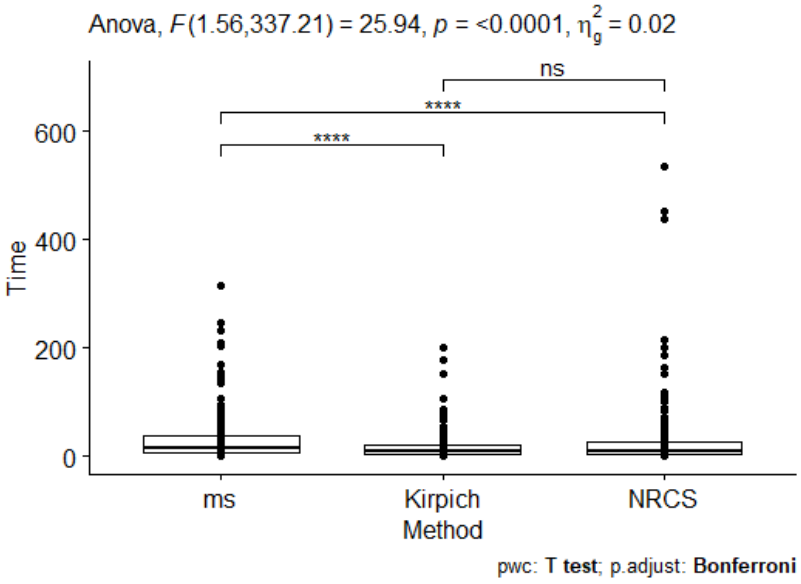

```
#computation of ANOVA
res.aov <- anova_test(data = proposal_lakes_ToC, dv = Time, wid = ï.., 
within = Method)
get_anova_table(res.aov)
```

ANOVA	
Effect	‘Method’
DFn	2
DFd	432
F	25.942
p	$2.29*10^{-11}$
p<.05	*
ges	0.018
Mauchly’s test for sphericity	
Effect	‘Method’
W	0.719
p	$3.9*10^{-16}$
p<.05	*
Sphericity correction	
Effect	Method
GGe	0.781
DF[GG]	1.56, 337.21
p[GG]	$2.19*10^{-9}$
p[GG]<.05	*
HFe	0.785
DF[HF]	1.57, 339.22
p[HF]	$1.99*10^{-9}$
p[HF]<.05	*

```
#pairwise paired t-test
pwc <- proposal_lakes_ToC %>%
  pairwise_t_test(
    Time ~ Method, paired = TRUE,
    p.adjust.method = ”bonferroni”)
pwc
```

Group 1	Group 2	n1	n2	statistic	df	p	p.adj	p.adj.signif
Kirpich	ms	217	217	-8.804631	216	$4.30*10^{-16}$	$1.29*10^{-15}$	****
Kirpich	NRCS	217	217	-4.566128	216	$8.34*10^{-6}$	$2.50*10^{-5}$	****
ms	NRCS	217	217	1.203053	216	$2.30*10^{-1}$	$6.90*10^{-1}$	ns

```
# Visualization: box plots with p-values
pwc <- pwc %>% add_xy_position(x = "Method")
bxp +
  stat_pvalue_manual(pwc) +
  labs(
    subtitle = get_test_label(res.aov, detailed = TRUE),
    caption = get_pwc_label(pwc))
```

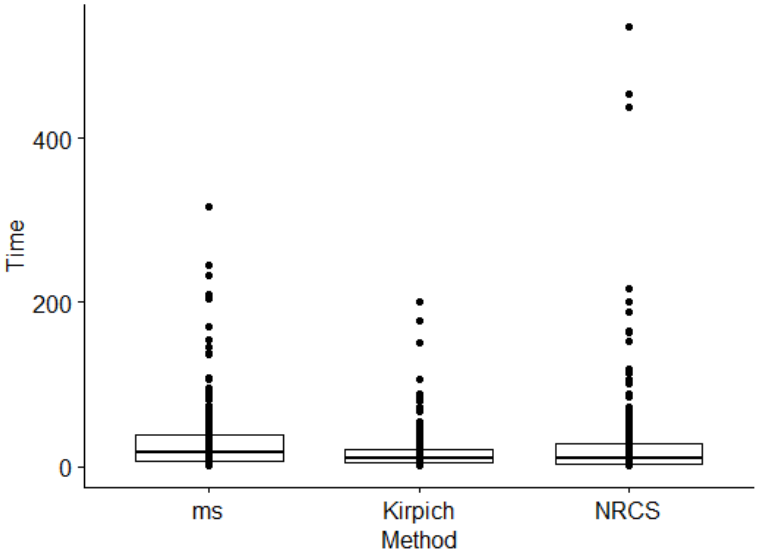


R-Code for Friedman-Test

```
library(tidyverse)
library(ggpubr)
library(rstatix)
proposal_lakes_ToC <-read.csv("C:/Users/bafrefel/Desktop/Times of
concentration of swiss lakes/scratch/xyz.csv", header = T, sep = ";")

#summary statistics
proposal_lakes_ToC%>%
  group_by(Method) %>%
  get_summary_stats(Time, type = "common")
```

Method	Variable	n	min	max	median	iqr	mean	sd	se	ci
Kirpich	Time	217	0.614	200.	9.11	16.0	17.5	25.9	1.76	3.47
ms	Time	217	0.964	316.	16.5	32.6	32.3	45.6	3.09	6.10
NRCS	Time	217	0.341	535	9.89	23.6	29.8	64.0	4.35	8.57

```
# visualization
bxp <- ggboxplot(proposal_lakes_ToC, x = "Method", y = "Time", add =
"point")
bxp
```




```
#computation of Friedman-test
res.fried <- proposal_lakes_ToC %>% friedman_test(Time ~ Method |ï..)
res.fried
```

y	n	statistic	df	p	method
Time	217	92.52535	2	$8.097976*10^{-21}$	Friedman test

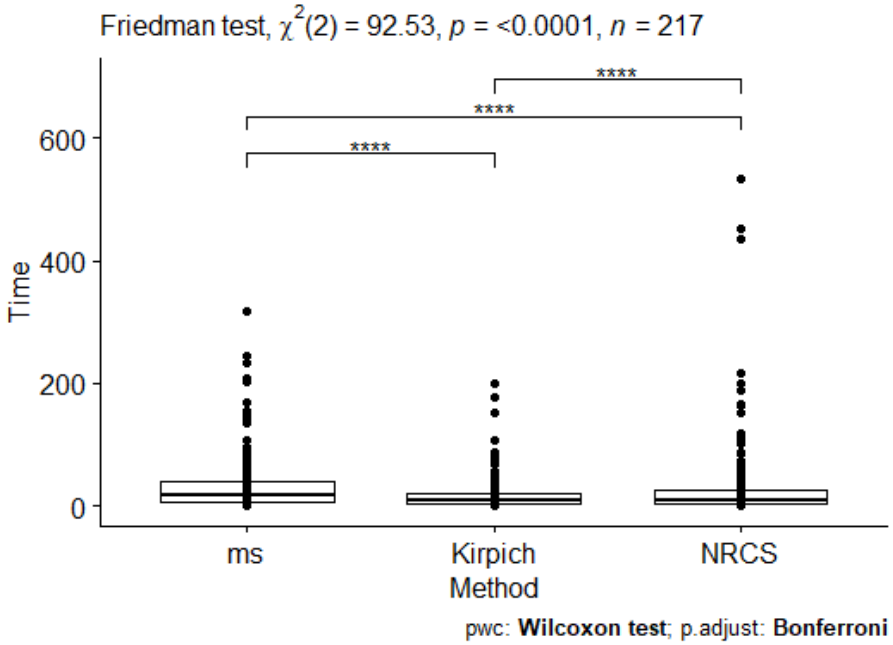
```
#effect size
proposal_lakes_ToC %>% friedman_effsize(Time ~ Method |ï..)

#Multiple pairwise-comparisons
pwc <- proposal_lakes_ToC %>%
  wilcox_test(Time ~ Method, paired = TRUE, p.adjust.method = "bonferroni")
pwc
```

Group 1	Group 2	n1	n2	statistic	p	p.adj	p.adj.signif
Kirpich	ms	217	217	2999	$1.53*10^{-21}$	$4.59*10^{-21}$	****
Kirpich	NRCS	217	217	5997	$3.07*10^{-10}$	$9.21*10^{-10}$	****
ms	NRCS	217	217	18699	$1.16*10^{-13}$	$3.48*10^{-13}$	****

```
pwc2 <- proposal_lakes_ToC %>%
  sign_test(Time ~ Method, p.adjust.method = "bonferroni")
pwc2
```

Group 1	Group 2	n1	n2	statistic	df	p	p.adj	p.adj.signif
Kirpich	ms	217	217	49	217	$1.88*10^{-16}$	$5.64*10^{-16}$	****
Kirpich	NRCS	217	217	90	217	$1.40*10^{-2}$	$4.20*10^{-2}$	*
ms	NRCS	217	217	162	217	$1.98*10^{-13}$	$5.94*10^{-13}$	****

```
# Visualization: box plots with p-values
pwc <- pwc %>% add_xy_position(x = "Method")
ggboxplot(proposal_lakes_ToC, x = "Method", y = "Time", add = "point") +
  stat_pvalue_manual(pwc, hide.ns = TRUE) +
  labs(
    subtitle = get_test_label(res.fried,  detailed = TRUE),
    caption = get_pwc_label(pwc))
```


Friedman test, $\chi^2(2) = 92.53$, $p = <0.0001$, $n = 217$
****
****
****
600
400
200
0
Time
ms
Kirpich
NRCS
Method
pwc: **Wilcoxon test**; p.adjust: **Bonferroni**

Appendix E: Personal Declaration

I hereby declare that the submitted thesis is the result of my own, independent work. All external sources are explicitly acknowledged in the thesis.

Place and Date	**Basil Frefel**
Dübendorf, 30.11.2021